

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 17:31:33 ; Search time 7014.33 Seconds
(without alignments)
10680.938 Million cell updates/sec

Title: US-10-670-454-1
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match of

Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:★

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Query Match 100.0%; Score 1318; DB 6; Length 1318;

ALIGNMENTS

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ACCESSION	BD243009
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REFERENCE	1. (bases 1 to 1318) Thomas,S.G., Hedden,P. and Phillips,A.B. Enzyme
AUTHORS	Patent: JP 2002518005-A 1 25-JUN-2002;
TITLE	THE UNIVERSITY OF BRISTOL
JOURNAL	OS Phaseolus coccineus (scarlet runner bean)
COMMENT	PN JP 2002518005-A/1 PD 25-JUN-2002 PF 11-JUN-1999 JP 2000554938 PR 12-JUN-1998 GB 9812821.8,15-JUL-1998 GB 9815404.0 PT STEPHEN GREGORY THOMAS, PETER HEDDEN, ANDREW LEONARD PHILLIPS PC C12N9/04, A01H5/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/10, PC C12N15/09, PC C12N5/00, C12N5/00, C12N15/00 CC Enzyme FH Key FT source FT bean') FT Location/Qualifiers 1. .1318 /organism="Phaseolus coccineus" /mol_type="genomic DNA" /db_xref="r:ayon:1886"
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VERSION	AX008671.1 GI:9996195		
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AUTHORS	Enzyme								
TITLE	Patent: WO 9966029-A 1 23-DEC-1999;								
JOURNAL	PHILLIPS ANDREW LEONARD (GB); HEDDEN PETER (GB); UNIV BRISTOL (GB);								
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PCO132438
DEFINITION
ACCESSION
VERSION
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SOURCE
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rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.

1
REFERENCE
AUTHORS
TITLE
Thomas, S.G., Phillips, A.L. and Hedden, P.
Molecular cloning and functional expression of gibberellin 2-oxidases, multifunctional enzymes involved in gibberellin deactivation
Proc. Natl. Acad. Sci. U.S.A. 96 (8), 4698-4703 (1999)
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REFERENCE 2 (bases 1 to 1318)
AUTHORS
Phillips, A.L.
TITLE
Direct Submission
Submitted (18-JAN-1999) Phillips A.L., Plant Sciences, IACR Long Ashton Research Station, Long Ashton Research Station, Bristol, BS41 9AF, UK

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Db 1141 TGTGCTGTCTAGGTTTCAACAGTTGACTCTACTTGACATATATAGAAATGAATAGGT 1200
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Db 1201 TAAAGTGTATATCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1260
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Db 1261 CCCTTTCTCTCAATTTGCAATGGAACGCACTCTAGTTACAAAAAATTTTTTTTTT 1318

RESULT 5
AB181372
LOCUS AB181372 1360 bp mRNA linear PLN 09-JUN-2005
DEFINITION Vigna angularis VaGA2oxA1 mRNA for gibberellin 2-oxidase, complete cds.
ACCESSION AB181372
VERSION AB181372.1 GI:67077811
KEYWORDS Vigna angularis (adzuki bean)
SOURCE Vigna angularis
ORGANISM Vigna angularis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
REFERENCE 1
Park, S., Nakajima, M., Xu, Z., Tomioka, K., Sakane, M. and Yamaguchi, I. Gibberellin 2-oxidases from adzuki bean hypocotyl
Unpublished
REFERENCE 2 (bases 1 to 1360)
Nakajima, M., Xu, Z., Park, S., Tomioka, K., Sakane, M. and Yamaguchi, I. Direct Submission
Submitted (08-JUN-2004) Masatoshi Nakajima, The University of Tokyo, Dept. Appl. Biol. Chem., Fac. of Agriculture, 1-1-1 Yayoi, Bunkyo, Tokyo, 113-8657, Japan
(E-mail: nkjm@agri.ch.a.u-tokyo.ac.jp, Tel: 81-3-5841-5192, Fax: 81-3-5841-8025)
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 84.3%; Score 1110.8; DB 15; Length 1360;
Best Local Similarity 91.6%; Pred. No. 3.7e-281;
Matches 1214; Conservative 0; Mismatches 93; Indels 18; Gaps 3;
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QY 70 GGTGTTCTGCTCAGCGCAGCATTTGAACCAAGTTTCTTCTGTAACCAATTTCAAGTCCAC 129
Db 85 GGTGTTCTGCTCAGCGCAGCATTTGAACCAAGTTTCTTCTGTAACCAATTTCAAGTCCAC 144
QY 130 GCCCTTGTTCAGGGGATTCCTGTGCTGACCTCAGCAACCCCGATGCCAAGATCTCAT 189
Db 145 GCCCTTGTTCAGGGGATTCCTGTGCTGACCTCAGCAACCCCGATGCCAAGATCTCAT 204
QY 190 AGTGAAACCCCTGTAGGGACTTTCGGCTTCTCAAGCTTCTGAACCAATTTGTTCCATTGGA 249
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QY 250 GTTAATGGCCAAATTTAGAAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAA 309
Db 265 GTTAGTGGCCAAATTTAGAAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAA 324
QY 310 AGACAGAGCTGGTCCCGGACCTTTTCGGCTATGGTAGCAAGAGGATTTGGCCCAACCG 369
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QY 370 TGATGTCGGTGGGTGCGAATACCTCTCTCAACCAACCAACCTGATGTTATCTCACCCAA 429
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QY 610 GTTGAACCACTACCCGCTTCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGGTT 669
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QY 730 GCAATCTGCTCAGATGACCTTGGGTTTTCAGTCCACCTGATCAGACTTCCTTTT 789
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QY 850 TAGGGTTTGGCTGACACCAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGCCAGC 909

Db 865 TAGGTTTTGGCTGACACACGAAGTCAAGTTATCAATGATATACCTTTGGAGGACCACG 924
QY 910 GTTGAAGTAAATATAGCACTTTACCTTCAGTGATGTTAAAGGAGAGAGGAGTGTGTA 969
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QY 970 CAAAGAGTTTCAATGGTGTGAATACAAAGAGGCTGCGTACACTTCAAGGCTAGCTGATAA 1029
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QY 1254 TCAACTTCCCTTTCCTCAATTGTCATGGAACGCACTCTAGTTACAAAAAATAAAAA 1313
Db 1285 GCTACTTCCCTTCCCTCTATTGTCAAACTCTAGTTTACNTCTTTTGTGTAAAAAATAAAAA 1344
QY 1314 AAAAA 1318
Db 1345 AAAAA 1349

RESULT 6
CQ899251
LOCUS CQ899251 999 bp DNA linear PAT 08-NOV-2004
DEFINITION Sequence 3 from Patent WO2004092390.
ACCESSION CQ899251
VERSION CQ899251.1 GI:55583091
KEYWORDS Phaseolus coccineus
SOURCE Phaseolus coccineus
ORGANISM Phaseolus coccineus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.
1
Gilbertson, L., Krieger, E., Zhang, W. and Ye, X.
Dna constructs and methods to enhance the production of
commercially viable transgenic plants
Patent: WO 2004092390-A 3 28-OCT-2004;
Monsanto Technology LLC (US)
Location/Qualifiers
1. .999
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FEATURES
source

ORIGIN

Query Match 75.8%; Score 999; DB 6; Length 999;
Best Local Similarity 100.0%; Pred. No. 1e-251;
Matches 999; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 ATGGTTGTTCTGTCTCAGCAGCAGTGAACCAAGTTTCTTCTGTGAACCAATTCAGATCC 127
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QY 128 ACGCCCTTGTTCAGGGGATTCCTGTGTCGACCTCAGCACCCCGATGCCAAGATCTC 187
Db 61 ACGCCCTTGTTCAGGGGATTCCTGTGTCGACCTCAGCACCCCGATGCCAAGATCTC 120

QY 188 ATAGTGAACGCCTGTAGGACTTCGGCTTCTTTCAAGCTTGTGAACCAATGGTGTTCATTTG 247
Db 121 ATAGTGAACGCCTGTAGGACTTCGGCTTCTTTCAAGCTTGTGAACCAATGGTGTTCATTTG 180
QY 248 GAGTTAATGGCCCAATTTAGAAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 307
Db 181 GAGTTAATGGCCCAATTTAGAAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240
QY 308 AAAGACAGAGCTGTGTCCTCCCGACCTTTTCGGCTATGTTAGCAAGAGGATTCGCCCAAC 367
Db 241 AAAGACAGAGCTGTGTCCTCCCGACCTTTTCGGCTATGTTAGCAAGAGGATTCGCCCAAC 300
QY 368 GGTGATGTGGTGGTGGTTCGAATACCTCTCTCAACACCAACCTCTATCTCACCCTC 427
Db 301 GGTGATGTGGTGGTGGTTCGAATACCTCTCTCAACACCAACCTCTATCTCACCCTC 360
QY 428 AAATCACTTTGCAATTTTCGAGAAAAATCTCATATTTTCAGGGCGGTGTGAGAACTAC 487
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QY 548 ATAAGGACAGAGGAATACGTTTAAGCAGGTTGCTGAAGGATGAGAAAAAGTGATTCTGCTTC 607
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RESULT 7
AR528429
LOCUS AR528429 1359 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 62 from patent US 6723897.
ACCESSION AR528429
VERSION AR528429.1 GI:53916494
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1359)
AUTHORS Brown, S.M., Elich, T.D., Heck, G.R., Kishore, G.M., Loguesch, E.W.,


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Db 361 AGATTGAAATCAATTTTGGCGATGATCCCGAGAAAAATTTTCGGTATGCTGTTAATGACTAC 420
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Db 421 GTATCATCATAGAAAGAAATGCTGTGAATTAATTAATTAATTAATTAATTAATTAAT 480
Qy 548 ATAAGCAGAGAAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATCGTGTTC 607
Db 481 ATTACGCCAAAGAACGTTTTCAGCAAGCTCTTGATGATGAACAGAGTGAATCTGTGTTTC 540
Qy 608 AGTTGAACCACTACCCGCTTCCCTGAGTGGCGAGCACTGAA---CGGAAATTTGGTT 564
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Db 958 GATAACAGACTGGTCTGTTGAGAAAAATGCTGCTCCTCAATA 999

RESULT 10
CWA315663
LOCUS CWA315663
DEFINITION Cucurbita maxima partial mRNA for Gibberellin 2-oxidase (ga2ox gene).
ACCESSION AJ315663
VERSION AJ315663.1 GI:32127336
KEYWORDS ga2ox gene; gibberellin 2-oxidase.
SOURCE Cucurbita maxima (winter squash)
ORGANISM Cucurbita maxima
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.

REFERENCE
AUTHORS Frisese, A. and Lange, T.
TITLE Gibberellin biosynthesis in young seedlings of Cucurbita maxima L.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1383)
AUTHORS Lange, T.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-2001) Lange T., Botanical Institute, TU Braunschweig, Mendelssohnstr. 4, D-38106 Braunschweig, GERMANY
COMMENT related entry AJ315662.
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ORIGIN

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Query Match 35.1%; Score 462.2; DB 15; Length 1383;
Best Local Similarity 68.7%; Pred. No. 2.5e-110;
Matches 651; Conservative 0; Mismatches 293; Indels 3; Gaps 1;

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Qy 185 CTCATAGTGAAGCGCTGTAGGACCTTCGCTTCTTCAAGCTTGTGAACCATGTTTCCA 244
Db 124 CTCATGTGCAAGCTGTGGAAGAACTCGGATTCCTTTAAGGTTGTCAACATGTTGCCCC 183
Qy 245 TTGGAGTTAATGGCCAAATTTAGAAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCC 304
Db 184 ATGGAAATTAATCTCTCTCTTGAATCAGATCCACCAAAATCTCTTCCCTCTCTCT 243
Qy 305 GAGAAAGACAGAGCTGTGTCCTCCCGACCTTTTCGGCTATGTGAGCAAGAGGATTTGCCCA 364
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Qy 365 AACGTTGATGTCGGTGGTTCGATACCTCTCTCTCAACACCAACCTGATGTTATCTCA 424
Db 304 AATGGCGATGTGCGTGGGTGGAATATCTCTCTTTGAACACTCATCTCGAATCCAACTCC 363
Qy 425 CCAAAATCACTTTTGCAATTTTCCGAGAAATCCTCATCATTTTCAGGCGCGTGGTGGAGAAC 484
Db 364 GATGGGTTCTCTCAATTTTGGCCCAAGACCCACAAACAACTCCGCTCTCTGTGAACGAT 423
Qy 485 TACATTACAGCAGTGAAGAACATGTCTATGCGGTGTTGGAAATGTATGCGGAGGGGTTG 544
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Solanales; Solanaceae; Nicotiana.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Sakane, M., Nakajima, M. and Yamaguchi, I.
Molecular cloning of GA 2-oxidase in BY-2
Unpublished
2 (bases 1 to 1292)
Sakane, M., Nakajima, M. and Yamaguchi, I.
Direct Submission
Submitted (28-OCT-2003) Masayuki Sakane, University of Tokyo,
Applied Biological Chemistry; Yayoi 1-1-1, Bunkyo-ku, Tokyo
113-0032, Japan [E-mail:m-sakane@agr1.ch.a.u-tokyo.ac.jp,
URL:htcp://pgr1.ch.a.u-tokyo.ac.jp/, Tel:81-3-5841-5158(ex.25158),
Fax:81-3-5841-8025]

FEATURES

Location/Qualifiers

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ORIGIN

Query Match

Best Local Similarity 65.7%; Score 453; DB 15; Length 1292;

Matches 692; Conservative 0; Mismatch 355; Indels 6; Gaps 2;

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DB 68 AGCACTATGTTGGTCTTAACTAAACCTGGCATTTGACATTTCCCATAGTCAAAAACGT 127
QY 121 CAAGTCCAGCCTCTGTTCAAGGGGATTCCTGTGTGACCTCAGCACCCCGATGCCAA 180
DB 128 CAATATCTCTTCAATGGTTCATGATGACCTCTCTAAACCTAACTCTTAA 187
QY 181 GAATCTCATAGTGAACGCTGTAGGACCTTCGGCTTCTTCAAGCTTTGTGAACCATGGTGT 240
DB 188 GAACCTTATTTAAGGCTGTGAAGAAATTTGATTTCTTCAAGTCAATTAACCATAGCT 247
QY 241 TCATTGGAGTTAATGGCCAAATTTAGAAAAGAGGCTCAGGCTCTTTTAAAAAATCTCA 300
DB 248 CCTACGGAATTCATAACTTAACTTGAATCTGAAGCCATCAAAATTTCTCTCTCCCT 307
QY 301 GTCCGAGAAGACAGAGCTGTCCCGCCAGCTTTCCGCTATGTGTAGCAAGAGTTGG 360
DB 308 TTCTGAGAAACAAAAGCTGGGCGAGCTGATCTCTTTGGCTATGGAACAAGAGATTGG 367
QY 361 CCCAAACGGTGTATGTCGGTGTGGTCCAAATACCTCTCTCAACACCAACCTGTATTTAT 420
DB 368 ACCAATGGCGATGTTGGTGGGTGGAATCAATCTCTCTGTCACTCTGAGTTCA 427
QY 421 CTCACCCAATCACTTTGCAATTTCCGAGAAATCTCTCAATTTTCAGGCGGTGTGA 480
DB 428 CTACCAAGTTTGCATCTATATAGTGTAAACCCAGAAACAAATTCGGGCTGCAGTAA 487
QY 481 GAACACTATTACAGAGTGAAGAAATGCTATGCGGTGTTGGAATTCATGTCGCGAGG 540
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QY 541 GTTGGGATAAGGCAGAGGATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTC 600
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RESULT 13

MMY09113

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

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JOURNAL

PUBMED

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	Matches 662; Conservative						Version AR452821.1				
							GI:42684847				
							Keywords				
							Source				
							Unknown.				
							Organism				
							Unclassified.				
							1 (bases 1 to 1352)				
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DEFINITION Sequence 5 from patent US 667502.
ACCESSION AR452817
VERSION AR452817.1 GI:42684843
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1365)
AUTHORS Allen,S.M., Kinney,A.J., Rafalski,J.A., Orozco,E.M. Jr.,
Miao,G.-H., Famodu,O.O., Lee,J.-M., Lohman,K.N., Rendina,A.R.,
Sakai,H., Weng,Z., Caimi,P.G., Fang,Y., Shen,J.B.J., Zoughi,I.L.,
Anderson,S.L., Shi,J., Lu,G., Helentjaris,T.G. and Li,C.P.
TITLE Plant metabolism genes
JOURNAL Patent: US 667502-A 5 13-JAN-2004;
E.I. du Pont de Nemours and Company and Pioneer Hi-Bred
International; Wilmington, DE
FEATURES
source Location/Qualifiers
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/organism="unknown"
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ORIGIN

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Best Local Similarity 65.6%; Pred. No. 1.2e-101;
Matches 664; Conservative 0; Mismatches 333; Indels 15; Gaps 2;

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QY 115 ACCATTCAAGTCCAGCCCTTGTTCACGGGGATTCCTGTGGTGCAGCTTCACGACCCCGA 174
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
9885.961 Million cell updates/sec

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3312346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	999	75.8	999	13	Adt62692 DNA encod
3	893.8	67.8	1359	3	Aaz99471 Soybean g
4	893.8	67.8	1359	6	Aad40261 Soybean G
5	430.8	32.7	1352	12	Adm94213 Soybean D
6	429.2	32.6	1365	12	Adm94205 Soybean D
7	425.8	32.3	1237	3	Aaz55916 Arabidops
8	425.4	32.3	1026	6	Abz13545 Arabidops
9	425.4	32.3	1026	8	Ada67975 Arabidops
10	424.8	32.2	1403	3	Aaz99472 Soybean G
11	424.8	32.2	1403	6	Aad40262 Soybean G
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13	363.6	27.6	1473	12	Adm94207 Wheat Dio
14	356.6	27.1	1324	3	Aac39277 Arabidops
15	356.6	27.1	1316	3	Aaz55915 Arabidops
16	355.6	27.0	1651	14	Aeb67733 Rice geno
17	354	26.9	984	8	Ada70120 Rice gene
18	354	26.9	984	12	Adk00081 Rice cdna
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20	354	26.9	1650	12	Adm94203	Adm94203 Rice Diox	
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22	311	23.6	783	3	Aaz99474	Aaz99474 Cotton gi	
23	311	23.6	783	6	AAD40264	AAD40264 Cotton GA	
24	302.8	23.0	831	13	ADx11608	ADx11608 Plant ful	
25	285	21.6	927	12	ADI45210	ADI45210 Rice isop	
26	273.8	20.8	860	13	ADx13286	ADx13286 Plant ful	
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28	187.2	14.2	1065	8	ADA69812	ADA69812 Rice gene	
29	172.2	13.1	919	13	ADx63586	ADx63586 Plant ful	
30	166	12.6	811	3	Aaz99478	Aaz99478 Maize gib	
31	166	12.6	811	6	AAD40268	AAD40268 Maize GA	
32	161.8	12.3	95769	8	ADA68659	ADA68659 Arabidops	
33	156.2	11.9	504	12	ADI45683	ADI45683 Corn isop	
34	155.6	11.8	403	3	Aaz99473	Aaz99473 Soybean g	
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36	154.8	11.7	406	3	Aaz99475	Aaz99475 Cotton gi	
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c	40	150.4	537	12	ADI45522	ADI45522 Banana is	
41	141	10.7	480	3	AAC50271	AAC50271 Arabidops	
c	42	135.2	10.3	683	3	AAC54605	AAC54605 Arabidops
c	43	133.6	10.1	687	3	AAC53074	AAC53074 Arabidops
44	120	9.1	426	3	Aaz99477	Aaz99477 Maize gib	
45	120	9.1	426	6	AAD40267	AAD40267 Maize GA	

ALIGNMENTS

RESULT 1
AAZ55912
ID AAZ55912 standard; cdna; 1318 BP.
XX
AC AAZ55912;
XX
DT 10-APR-2000 (first entry)
XX
DE Runner bean gibberellin 2-oxidase PCGA2ox1 cdna.
XX
KW Gibberellin 2-oxidase; PCGA2ox1; runner bean; 2-beta-hydroxylation;
KW inactivation; growth inhibition; ss.
XX
OS Phaseolus coccineus.
XX
FH Key Location/Qualifiers
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FT /*tag= a
FT /product= "Gibberellin 2-oxidase PCGA2ox1"
FT /transl_except= (pos:1058..1063, aa:Ala)
XX
PN WO9966029-A2.
XX
PD 23-DEC-1999.
XX
PF 11-JUN-1999; 99WO-GB001857.
XX
PR 12-JUN-1998; 98GB-00012821.
PR 15-JUL-1998; 98GB-00015404.
XX (UYBR-) UNIV BRISTOL.
XX Thomas SG, Hedden P, Phillips AL;
XX WPI; 2000-097742/08.
DR P-PSDB; AAY58597.
XX
PT New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used to produce transgenic plants with improved or altered growth characteristics.
XX
PS Claim 1; Fig 1; 42pp; English.

XX	This sequence represents cDNA encoding a runner bean gibberellin (GA) 2-oxidase, PcsA2ox1. This enzyme is a GA 2-beta-hydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is its only activity.			
CC	Hydroxylation at the 2-beta position of a GA results in a biologically inactive product, and is the most important route for GA metabolism in plants, ensuring that the active hormones do not accumulate in plant tissues. The nucleic acids can be used to transform plants so that gibberellin 2-oxidase can be constitutively over-expressed or otherwise enhanced to reduce the concentration of bioactive GAs in the plants and therefore to inhibit plant growth. Growth inhibition is useful in many agricultural and horticultural applications such as enhancing lodging-resistance and grain yield in cereals, improving seedling quality, reducing the growth of amenity grasses, reducing shoot growth in orchard and ornamental trees, improving tolerance to cold, drought and infection, and increasing yields (by the diversion of assimilates from vegetative to reproductive organs). The nucleic acids may also be used to induce male and/or female sterility (by expression in floral organs), prevent pre-harvest sprouting, reduce shoot growth in hedging plants, inhibit reversibility in the development or germination of seeds and reduce shoot growth in commercial wood species. Antisense constructs of the nucleic acids can also be used to transform plants to reduce the expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set and growth in seedless grapes, citrus fruits and pears), improve skin texture and fruit shape in apples, increase stem length and therefore yield in sugar cane, increase yield and earliness in celery and rhubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species			
XX	SQ Sequence 1318 BP; 358 A; 296 C; 282 G; 382 T; 0 U; 0 Other;			
QY	Query Match	100.0%;	Score 1318;	DB 3; Length 1318;
DB	Best Local Similarity	100.0%;	Pred. No. 0;	
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QY	61	AACAACCATGGTGTGTTCTGCTCAGCCAGCATGTAACCGAGTTTCTCTGTAACCATTT	120	
DB	61	AACAACCATGGTGTGTTCTGCTCAGCCAGCATGTAACCGAGTTTCTCTGTAACCATTT	120	
QY	121	CAAGTCCAGCCCTTGTTCACGGGATCTCTGTGTCGACCTCACGACCCCGATGCCAA	180	
DB	121	CAAGTCCAGCCCTTGTTCACGGGATCTCTGTGTCGACCTCACGACCCCGATGCCAA	180	
QY	181	GAATCTCATAGTGAACCGCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGGT	240	
DB	181	GAATCTCATAGTGAACCGCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGGT	240	
QY	241	TCCATTTGGAGTTAATGGCCAAATTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCA	300	
DB	241	TCCATTTGGAGTTAATGGCCAAATTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCA	300	
QY	301	GTCCGAGAAAGACAGAGCTGGTCCCGCCGACCTTTCCGGCTATGGTAGCAAGAGATTGG	360	
DB	301	GTCCGAGAAAGACAGAGCTGGTCCCGCCGACCTTTCCGGCTATGGTAGCAAGAGATTGG	360	
QY	361	CCCAAAACGGTGATGTCGGTTGGGTGGAATACTCTCTCTCAACACCAACCCCTGATTTAT	420	
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DB	421	CTCACCCTCAATCATTTTTCGAGAAAATCTCATCTATTTTCAGGGCGGTGGTGA	480	
QY	481	GAACCTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGAGGG	540	
DB	481	GAACCTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGAGGG	540	
QY	541	GTTGGGGATAAGCAGAGGAATA CGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTC	600	

PR 09-APR-2003; 2003US-0461459P.
 XX (MONS) MONSANTO TECHNOLOGY LLC.
 PI Gilbertson L, Krieger E, Zhang W, Ye X;
 XX WPI; 2004-758349/74.
 DR
 XX
 XX New DNA plasmid comprising a T-DNA comprising an Agrobacterium Ti plasmid
 PT first border region linked to a transgene linked to an Agrobacterium Ti
 PT plasmid second border region, useful for enhancing production of
 PT transgenic plants.
 XX
 XX Example 1; SEQ ID NO 3; 77pp; English.
 XX
 CC The present invention relates to a DNA plasmid comprising a transfer DNA
 CC (T-DNA) comprising an Agrobacterium Ti plasmid first border region linked
 CC to at least one transgene linked to an Agrobacterium Ti plasmid second
 CC border region, and located in the DNA plasmid outside of the T-DNA is a
 CC plant expression cassette comprising a plant cell non-lethal negative
 CC selectable marker gene linked to a vector backbone DNA. Also disclosed
 CC are a method for enhancing the selection of transgenic plants that do not
 CC contain vector backbone DNA, a method for reducing the copy number of a
 CC transgene in a plant cell, and a transgenic plant produced by the method.
 CC The DNA plasmid comprises the expression cassette comprising a promoter
 CC that functions in plant cells operably linked to a plant cell non-lethal
 CC negative selection marker gene. The promoter is a constitutive promoter.
 CC The promoter expresses the linked non-lethal negative selection marker
 CC gene product in tissue culture during plant regeneration. The plant cell
 CC non-lethal negative selectable marker gene comprises a plant hormone
 CC biosynthetic pathway gene, degradative gene, biosynthetic pathway
 CC substrate-diverting gene or signalling gene, or metabolic interference
 CC gene. The transgene is a plant positive selectable marker gene selected
 CC from antibiotic resistance and herbicide resistance. The transgene
 CC comprises a transgene of agronomic interest. The plant hormone
 CC biosynthetic pathway gene is selected from gibberellic acid pathway
 CC genes, cytokinin pathway genes, auxin pathway genes, ethylene pathway
 CC genes, and abscisic acid pathway genes. The plasmid is useful for
 CC enhancing the production of commercially viable transgenic plants. The
 CC present sequence represents DNA encoding Phaseolus coccineus gibberellin
 CC 2-oxidase. The sequence is used as a non-lethal negative selectable
 CC marker gene.
 XX
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QY 428 AAATCACTTTTCATTTTCCGAGAAAATCCTCATCATTTTCAGGCGGTGGTGAGAACTAC 487
 DB 361 AAATCACTTTTCATTTTCCGAGAAAATCCTCATCATTTTCAGGCGGTGGTGAGAACTAC 420
 QY 488 ATTACAGCAGTGAAGACATCTGTATGCGGTGTGGAAATTCATGCGCGAGGGTTGGGG 547
 DB 421 ATTACAGCAGTGAAGACATCTGTATGCGGTGTGGAAATTCATGCGCGAGGGTTGGGG 480
 QY 548 ATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTCGTGCTTC 607
 DB 481 ATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTCGTGCTTC 540
 QY 608 AGGTTGAACCACTACCCGCCCTTGCCCTGAGTGCAGCACTGAACCGGAATTTGGTTGGG 667
 DB 541 AGGTTGAACCACTACCCGCCCTTGCCCTGAGTGCAGCACTGAACCGGAATTTGGTTGGG 600
 QY 668 TTTGGGAGACACAGACCCACAGATAATTTCTGTCTTAAGATCTAAACAGACATCTGGC 727
 DB 601 TTTGGGAGACACAGACCCACAGATAATTTCTGTCTTAAGATCTAAACAGACATCTGGC 660
 QY 728 TTGCAAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCCTTT 787
 DB 661 TTGCAAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCCTTT 720
 QY 788 TTCAATCAATGTGGTGACGCTCTACAGTAATGACTAATGGAGGTTTAAAAGTGTAAAG 847
 DB 721 TTCAATCAATGTGGTGACGCTCTACAGTAATGACTAATGGAGGTTTAAAAGTGTAAAG 780
 QY 848 CATAGGTTTGGCTGACACAAACGAGTCAAGTTTATCAATGATCTACTTTGGAGGACCA 907
 DB 781 CATAGGTTTGGCTGACACAAACGAGTCAAGTTTATCAATGATCTACTTTGGAGGACCA 840
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 DB 841 GCGTTGAGTGAATAATATAGCACTTTACCTTCAGTGTATGTTAAAAGGAGGAGTGTGTTG 900
 QY 968 TACAAAGAGTTTCAATGTTGTAATATCAAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 1027
 DB 901 TACAAAGAGTTTCAATGTTGTAATATCAAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 960
 QY 1028 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGATTAA 1066
 DB 961 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGATTAA 999

RESULT 3
 AAZ99471
 ID AAZ99471 standard; cDNA; 1359 BP.
 XX
 AC AAZ99471;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE Soybean gibberellic acid 2-oxidase 1 cDNA sequence.
 XX
 KW Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
 KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
 KW seed germination; seedling growth; gibberellin biosynthetic pathway;
 KW transgenic plant; hypocotyl; epicotyl; as.
 XX
 OS Glycine max.
 XX
 FH Key Location/Qualifiers
 FT CDS 102..1103
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 FT /trans_except= (pos: 633..635, aa: Xaa)
 FT /note= "Xaa is an unspecified amino acid"
 XX
 FN WO200009722-A2.
 XX
 PD 24-FEB-2000.
 XX

FT	XX	/note= "Xaa = any amino acid"	
PN	XX	US2002053095-A1.	
XX	PD	02-MAY-2002.	
XX	PF	10-AUG-1999; 99US-00371307.	
XX	PR	10-AUG-1999; 99US-00371307.	
XX	PA	(BROW/) BROWN S M.	
XX	PI	Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;	
PI	PI	Filler KJ, Rao S, Ream JE;	
XX	XX	WPI: 2002-489107/52.	
DR	DR	P-PSDB; AAE24921.	
XX	XX	Control of gibberellin levels in plants useful to avoid unfavorable	
PT	PT	conditions in crops to increase yields, using transgenic plants having	
PT	PT	reduced seed germination and early seedling growth then treatment to	
PT	PT	restore these properties.	
XX	XX	Claim 45; Page 92-93; 155pp; English.	
PS	XX	The invention relates to control of gibberellin (GA) levels in plants.	
XX	CC	The method involves producing transgenic plants having a phenotype of	
CC	CC	reduced seed germination and reduced early seedling growth, then	
CC	CC	restoring seed germination and early seedling growth by treating plants	
CC	CC	with an appropriate compound when conditions are favourable. The method	
CC	CC	is useful to control seed germination and/or early seedling growth in	
CC	CC	agricultural production so that unfavorable environmental conditions	
CC	CC	normally reducing agronomic output can be avoided and yields increased.	
CC	CC	Plants also demonstrate increased uniformity of germination, emergence	
CC	CC	and seedling vigor, so increasing yields at harvest. The method is	
CC	CC	especially useful in crop plants such as e.g. canola, soybean, cotton,	
CC	CC	etc., and is also useful in storage and transport of seeds to reduce	
CC	CC	premature germination which may affect agronomic or food quality of the	
CC	CC	seeds. The present sequence is soybean GA 2-oxidase 1 cDNA	
XX	XX	Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;	
SQ		Query Match 67.8%; Score 893.8; DB 6; Length 1359;	
		Best Local Similarity 84.9%; Pred. No. 3.5e-237;	
		Matches 1069; Conservative 1; Mismatches 158; Indels 31; Gaps 5;	
QY	65	ACCATGGTTGTTCTGCTCAGCCAGCAATGAACCAAGTTTCTCTTGAACCAATTCAG 124	
DB	99	ACCATGGTTGTTCTGCTCAGCCAGCAATGAACCAAGTTTCTCTTGAACCAATTCAG 158	
QY	125	TCCAGGCCCTTGTTCACGGGGATTCCTGTGGTGCACCTCAGCACCACCGCATGCCAAGAT 184	
DB	159	CCACGCCCTTGTTCGGGGGATTCCTGTGGTGCACCTCAGGACCCCGATGCCAAGACC 218	
QY	185	CTCATAGTGAACGCCCTGTAGGACATTCGGCTTCTTCAAGCTTGTGAACCATGGTGTCCA 244	
DB	219	CACATAGTCAATGCTCGCAGGACATTCGGCTTCTTCAAGCTGTGAACCAACGCTGTCG 278	
QY	245	TTGGAGTTAATGGCCAAATTTAGAAACAGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTC 304	
DB	279	TTACAGTTTCATGGCCAAATTTGGAAAAACGAAACCCCTCGGGTTCTTCAAAAAAATCTCAATCC 338	
QY	305	GAGAAAGACAGAGCTGGTCCCGCCAGCTTTGGGCTATGGTAGCAAGAGGATTTGGCCCA 364	
DB	339	GAGAAAGACAGAGCTGGTCCCGCTGACCTTTGGCTACGGACGACGAGGATTTGGCCCT 398	
QY	365	AACGGTGTATCGGTTGGGTGCAATACCTCTCTCAACCAACCAACCCCTGATGTATCTCA 424	
DB	399	AACGGCGATGTCGGTTGGGTGCAATACCTCTCTCAACCAACCAACCCCTGATGTATCTCC 458	
QY	425	CCCAATATCATTTTGCATTTTCCGAGAAATCTCATTCATTCAGGGCGGTGGTGGAGAAC 484	
DB	459	CCCAAGTCAAGTTTCAATTTTCAGAGAAAGGTCTCTCAGAAATTTTCAGGGCGGTGGTGGAGAA 518	

QY	485	TACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAAATGATGCGCGAGGGTTG 544	
DB	519	TACATTAGAGCGGTGAAGAACATGTGCTATGAGGTGTTGGAATGATGCGCGAGGATTG 578	
QY	545	GGGATAAGCGCAGAGCAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAGTGCATTCGTGC 604	
DB	579	GGGATAAGCGCAGAGCAATGTTGTAGTAGGTTGCTGAAGGATGAGAAAGTGCATTCGTGC 638	
QY	605	TTGAGGTTGAACCACTACCGCTTTGCGCTGAGGTGCAAGCACTGAAC---CGGAATTTG 661	
DB	639	TTGAGGTTGAACCACTACCGCTTTGCGCTGAGGTGCAAGCACTGAACCGAAGGATTTG 698	
QY	662	GTGAGGTTGGGAGCACAAGACCCACAGATAATTTCTGCTTAAAGTCTTAACAGCACA 721	
DB	699	GTGAGGTTGGGAGCACAAGACCCACAGATAATTTCTGCTTAAAGTCTTAACAGCACA 758	
QY	722	TCTGCTTGCATCAATCTGCTCAGATGGCACTGGGTTTCAAGTCCCACTCATCAGACT 781	
DB	759	TCAGGCTTGCATCAATCTGCTCAGATGGCACTGGGTTTCTGCTCCCACTCATCAGACT 818	
QY	782	TCCTTTTTCATCAATGTTGGTGACCTCTTACAGGTAAATGACTAAATGGGAGGTTTAAAGT 841	
DB	819	TCCTTTTTCATCAATGTTGGTGACCTCTTACAGGTAAATGACTAAATGGGAGGTTTAAAGT 878	
QY	842	GTAAAGCATAGGTTTGGCTGACACAAGCAAGTCAAGGTATCAATGATCTACTTTTGA 901	
DB	879	GTAAAGCATAGGTTTGGCTGACACAAGTCAAGGTATCAATGATCTACTTTTGA 938	
QY	902	GGACGAGGTTGAGTGAATAATAGCATTTCCTTCAGTGCATGTTTAAAGGAGGAG 961	
DB	939	GGACGAGGTTGAGTGAATAATAGCATTTCCTTCAGTGCATGTTTAAAGGAGGAG 998	
QY	962	TGTTTGTCAAAAGAGTTTCAATGTTGTAATAACAAGAGGCTGCGTACACTTCAAGGCTA 1021	
DB	999	AGTTTGTCAAAAGAGTTTCAATGTTGTAATAACAAGAGGCTGCGTACACTTCAAGGCTA 1058	
QY	1022	GCTGATAATAGGCTTGGCCCTTTCCAGAAATCTGCTGCTGATTAAACCAACACACCTTC 1081	
DB	1059	CGGATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCTGATTAAAGGAGGCAAGTGTGT 1118	
QY	1082	AAA-----TTCCACTCATTTTACGACGCTGTTTATACCCCA-----TTTTCTTCTCTTTT 1132	
DB	1119	CAAAATTTCTACTACTCAATTTTGGCAGCTGTTGTTAGGCCAACTTTTTTATTTTATTT 1178	
QY	1133	TCCTTTCTGCTGCTGCTAGGTTTCAACACAGTTCACCTCTACTTGACATATATAGAAAT 1192	
DB	1179	TTTTTGGGTGTGTATCTAGGTTTCAACACAGTTCACCTTACTTGAGATATATAGAAAT 1238	
QY	1193	GAATAGGT-----TAAGATGTTTATCATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1241	
DB	1239	GAATAGGTGCTTATGCACTTCTTTTAACTCTTGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1298	
QY	1242	TAACAGTGGTCTCAACTTCCCTTTCTCAATGTCATGGAACGCACTCTAGTTACA 1300	
DB	1299	TAATAGT-----CACTACTGCTTCTTATTTATCAATGAAACGCACTCTAGTCACA 1349	

RESULT 5	
ADM94213	
ID	ADM94213 standard; cDNA; 1352 BP.
XX	
AC	ADM94213;
XX	
DT	17-JUN-2004 (first entry)
XX	
DE	Soybean Dioxxygenase cDNA #2.
XX	
DE	Soybean; ss; plant; plant metabolism;
KW	GTP cyclohydrolase II/3, 4-dihydroxy-2-butanone-4-phosphate synthase;
KW	Dioxxygenase; Snt-Kaurene Synthase A; GA-20 oxidase; deaminase;
KW	Gibberellin 3-beta hydroxylase; Riboflavin specific
KW	Ethylene response factor; Acyl-CoA thioesterase II;

KW ABC transporter GCN20-like; P-glycoprotein I; P-glycoprotein 3;
 KW P-glycoprotein ATPGP; P-glycoprotein HVMDR2; ABC transporter;
 KW PMP70 ABC transporter; MRP4 ABC transporter; transgenic.
 OS
 XX Glycine max.

XX US6677502-B1.
 XX 13-JAN-2004.
 XX 12-JUL-2000; 2000US-00614912.
 XX 12-JUL-1999; 99US-0143401P.
 XX 12-JUL-1999; 99US-0143412P.
 XX 30-JUL-1999; 99US-0146650P.
 XX 15-DEC-1999; 99US-0170906P.
 XX 21-DEC-1999; 99US-0172946P.
 XX 21-DEC-1999; 99US-0172959P.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Allen SM, Kinney AJ, Rafalski JA, Orozco EM, Miao G, Famodu OO;
 PI Lee J, Lohman KN, Rendina AR, Sakai H, Weng Z, Cai M, Pang Y;
 PI Shen JB, Zoughi IL, Anderson SL, Shi J, Lu G, Helentjaris TG;
 PI Li CP;
 DR WPI: 2004-088430/09.
 DR P-PSDB; ADM94214.
 XX
 PT New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate
 PT synthase nucleic acid and proteins, useful for creating transgenic plants
 PT where polypeptides are present at higher or lower levels.
 XX
 PS Example 3; SEQ ID NO 13; 186pp; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising a
 CC nucleotide sequence encoding a polypeptide having GTP cyclohydrolase
 CC II/3,4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing as
 CC ADM94266. Also included are a vector comprising the polynucleotide, a
 CC recombinant DNA construct comprising the polynucleotide operably linked
 CC to at least one regulatory sequence, transforming a cell with the
 CC polynucleotide, a cell comprising the recombinant DNA construct,
 CC producing a plant (comprising transforming a plant cell with the
 CC polynucleotide and regenerating a plant from the transformed plant cell),
 CC a plant comprising the recombinant DNA construct and a seed comprising
 CC the recombinant DNA construct. Also disclosed as new are nucleic acid
 CC (cDNA) fragments and assembled contigs encoding plant metabolism proteins
 CC chosen from GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate
 CC synthase, Dioxxygenase, Ent-Kaurene Synthase A, GA-20 oxidase, Gibberellin
 CC 3-beta hydroxylase, Riboflavin specific deaminase, Ethylene response
 CC factor, Acyl-CoA thioesterase II, ABC transporter GCN20-like, P-
 CC glycoprotein I, P-glycoprotein 3, P-glycoprotein ATPGP, P-glycoprotein
 CC HVMDR2, ABC transporter, PMP70 ABC transporter and MRP4 ABC transporter.
 CC The nucleic acid fragments may be used to create transgenic plants where
 CC the polypeptides are present at higher or lower levels than normal or in
 CC cell types or in developmental stages in which they are not normally
 CC found. The polynucleotides can be used as probes for genetically and
 CC physically mapping genes and as markers for traits linked to those genes.
 CC The nucleic acid fragments may be used as restriction fragment length
 CC polymorphism (RFLP). It can also be used to probe Southern blots
 CC containing restriction endonuclease-treated genomic DNAs of a set of
 CC individuals representing parent and progeny of a defined genetic cross.
 CC The nucleic acid fragments may also be used as hybridisation probes
 CC against PCR amplification products generated from the mutation population
 CC using the mutation tag sequence primer in conjunction with an arbitrary
 CC genomic site primer. The peptides can also be used to immunise animals to
 CC produce polyclonal or monoclonal antibodies with specificity for peptides
 CC or proteins comprising the amino acid sequences. Antibodies are useful
 CC for detecting the polypeptides in situ in cells or in vitro in cell
 CC extracts. The present invention encodes a plant metabolism protein (or
 CC fragment).
 XX

SQ Sequence 1352 BP; 439 A; 255 C; 243 G; 415 T; 0 U; 0 Other;
 Query Match 32.7%; Score 430.8; DB 12; Length 1352;
 Best Local Similarity 65.7%; Pred. No. 1.2e-108;
 Matches 665; Conservative 0; Mismatches 332; Indels 15; Gaps 2;
 QY 55 AACAAACAACCAATGGTTGTTCTGTCTCAGCCAGCATTTGAACCAAGTTTTCCTCTCTGAA 114
 DB 146 AACACAAAGAAAATGGTGTGTGTCTCAAGCAACACAGAACATACTCTACATTA 205
 QY 115 ACATTCAAGTCCACGCCCTTGTTCACGGGATTCCTGTGTGCGACTCTCAAGCACCCTGA 174
 DB 206 GAACTGCATGCCAACCAAAATTTTCTTCAACAATTTCCCATAGTGAGACTCTCAAACTGA 265
 QY 175 TGCCAGAAATCTCATAGTGAAGCCCTGTAGGAGCTTTCGGCTTCTTCAAGCTGTGAGACCA 234
 DB 266 TGCAAAGACCCCTTATAGTAGGAGCTTGTGAGAGTTTGGATTCTTCAAAGTCAATCA 325
 QY 235 TGGTGTTCATTTGGAGTTAATGGCCAAATTTAGAAAAACGAGGCCCTCAGGTTCTTTAAAA 294
 DB 326 TGGTGTCTCCATGGAGCTATATCCGAATTTGGAATATGAAGCCCTTCAAATTTCTCTAT 385
 QY 295 ATCTAGTCCGAGAAAGACAGAGCTGGTCCGCCGACCCCTTTCGGCTATGGTAGCAAGAG 354
 DB 386 GTCACCTCAATGAAAGGAAAAAGTAGGACCTCCCAATCCATTTGGGTATGGTAGCAAGAA 445
 QY 355 GATTGGCCCAACCGGTGATGCTGGTGGGTGGAATACCTCCTCAACACCAACCCCTGA 414
 DB 446 AATTGACACAATGGGGAGCTTGGTTGGATTGAGTACCTTCTTCAACACCAATCAAGA 505
 QY 415 TGTATTCTCACCAAAATCACTTTTGGCAATTTTCGAGAAAAATTCCTCATCTTTACGGCGGT 474
 DB 506 ACACAACT-----TCTCTGTTTATGGGAAAAACCCCTGAGAAATTCAGGTGTCT 553
 QY 475 GGTGGAGAACTACATTACAGCAGTGAAGAAATGTGCTATGCGGTGTTGGAAATGTATGCG 534
 DB 554 GTTGAACAGTTACATGTCTTCTGTGAGGAAGATGGCATGTGAGATTCTTGAAGTTGATGGC 613
 QY 535 CGAGGGTTGGGGATAAGCAGAGGAATACGTTTACGAGGTTGCTCAAGAGTGAAGAAAG 594
 DB 614 AGAAGGTTGAAGATTTCAGCAAAAGAGTGTGTTAGCAAGCTTCTAATGGATAAACAAG 673
 QY 595 TGAATTCGTCTTTCAGGTTGAACCACTTACCCGCTTCCCTCGAGGTGCAAGCACTGAACCG 654
 DB 674 TGACTCTATTTTCAGGGTGAATCATTTACCTCTGTTCTCTGAAATGACTCTGAATGATCA 733
 QY 655 GAATTTGGTGGGTTTGGGAGACACAGACCCACAGATAATTTCTGTCTTAAAGATCTAA 714
 DB 734 GAACTTGAATGGGTTTGGGAGAACACACAGACCCACAAATCATCTCTCTGTTAAGATCCAA 793
 QY 715 CAGCACATCTGGCTTGCAAATCTGTCTCACAGATGSCACTTGGGTTTCAGTCCACCTGA 774
 DB 794 CAACCTTCAGGCTTCAGATTATCTTAGAGATGGAATTTGGAATTCAGTCCACACAGA 853
 QY 775 TCAGACTTCTTTTTCATCAATTTTGGTGACGCTCTACAGGTAATGACTTAATGGGAGGTT 834
 DB 854 TGACAAATCTTTTATTAACGTTGGTGTCTCTCTCAGGTTATGCAAAATGGAAGGTT 913
 QY 835 TAAAGTGTAAAGCATAGGGTTTGGCTGACACACAGAAAGTCAAGGTTTCAATGATCTA 894
 DB 914 CCGAAGTGTGAGACACAGAGTGTGGCAAAATGGGTTTCAAGTCCAGGCTTTCATGATTTA 973
 QY 895 CTTTGGAGGACCAAGCGTTTCAGGTGAAATATAGCACCTTTTACCTTCAGTGTGTTAAAGG 954
 DB 974 CTTTGGAGTCCACCTTTGAGTGAGAAAAATAGCAACCATTTATCTCTCTCATG---AAAGG 1030
 QY 955 AGAGGAGTGTGTGTACAAAGAGTTTCAATGGTGTGTAATACAAAGAGGTCGCTACATCTTC 1014
 DB 1031 AAAGAAAGTCTATATAAAGAGTTTACCTGGTTTGGATGACAAAAATCAATCTACGGTTC 1090
 QY 1015 AAGGCTAGCTGATATAGGCTTGCCTTTCAGAAAAATCTGCTGCTGATTA 1066
 DB 1091 AAGATTATCTAAAAAATAGACTTTGAACATTTTGAAGAATTCAGGCTTCGTAA 1142

Db 861 TGCAAAATCCTTTTATTAAAGCTGGTGATCTCTCTCAGGTTATGACAAATGGAAGTT 920
 QY 835 TAAAGGTGTAAGCATAGGTTTGGCTGACACAAAGAGTCAAGGTTATCAATGATCTA 894
 Db 921 CCGAAGTGTAGACACAGAGTGTGGCAATGGGTTCAAGTCCAGGCTTTCAATGATTTA 980
 QY 895 CTTTGAGGACCAAGCCTTGAGTGAATAATAGCACCTTTTACCTTTCAGTGTATTAAGG 954
 Db 981 CTTTGAGGTCACCTTTGAGTGAGAAATAGCACCATTTATCTCTCATG---AAAGG 1037
 QY 955 AGAGGAGTCTTTGTACAAAGATTCACATGGTGTGAATACAGAAAGCTGCGTACACTTC 1014
 Db 1038 AAAAGAAAGTCTATATAAAGAGTTTACCTGGTTTGAGTACAAAAATCAATCTACGGTTC 1097
 QY 1015 AAGGCTAGCTGAATAAGCTTGCCTCCCTTTCCAGAAATCTGCTGCTGATTAA 1066
 Db 1098 AAGATTATCTAAATAATAGACTTGAAACATTTTGAAGAATTCAGCTTCGTAA 1149

RESULT 7
 ID AAZ55916 standard; cDNA; 1237 BP.
 XX AAZ55916;
 XX 10-APR-2000 (first entry)
 DE Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox2 cDNA.
 KW Gibberellin 2-oxidase; AtGA2ox2; 2-beta-hydroxylation; inactivation;
 KW growth inhibition; ss.
 XX Arabidopsis thaliana.

Key Location/Qualifiers
 CDS 109..1134
 FT /*tag= a
 FT /product= "Gibberellin 2-oxidase AtGA2ox2"
 XX WO966029-A2.
 XX 23-DEC-1999.
 XX 11-JUN-1999; 99WO-GB001857.
 XX 12-JUN-1998; 98GB-00012821.
 XX 15-JUL-1998; 98GB-00015404.
 XX (UYBR-) UNIV BRISTOL.
 XX Thomas SG, Hedden P, Phillips AL;
 XX WPI; 2000-097742/08.
 DR P-PSDB; AAV58599.
 XX New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used
 PT to produce transgenic plants with improved or altered growth
 PT characteristics.
 XX Example 3; Fig 7; 42pp; English.

This sequence represents cDNA encoding an Arabidopsis thaliana
 gibberellin (GA) 2-oxidase, PcGA2ox2. This enzyme is a GA 2-beta-
 hydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is
 its only activity. Hydroxylation at the 2-beta position of a GA results
 in a biologically inactive product, and is the most important route for
 GA metabolism in plants, ensuring that the active hormones do not
 accumulate in plant tissues. The nucleic acids can be used to transform
 plants so that gibberellin 2-oxidase can be constitutively over-expressed
 or otherwise enhanced to reduce the concentration of bioactive GAs in the
 plants and therefore to inhibit plant growth. Growth inhibition is useful
 in many agricultural and horticultural applications such as enhancing
 lodging-resistance and grain yield in cereals, improving seedling

CC quality, reducing the growth of amenity grasses, reducing shoot growth in
 CC orchard and ornamental trees, improving tolerance to cold, drought and
 CC infection, and increasing yields (by the diversion of assimilates from
 CC vegetative to reproductive organs). The nucleic acids may also be used to
 CC induce male and/or female sterility (by expression in floral organs),
 CC prevent pre-harvest sprouting, reduce shoot growth in hedging plants,
 CC inhibit reversibility in the development or germination of seeds and
 CC reduce shoot growth in commercial wood species. Antisense constructs of
 CC the nucleic acids can also be used to transform plants to reduce the
 CC expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to
 CC improve fruit set and growth in seedless grapes, citrus fruits and
 CC pears), improve skin texture and fruit shape in apples, increase stem
 CC length and therefore yield in sugar cane, increase yield and earliness in
 CC celery and rhubarb, improve malting yields and quality in cereals
 CC (particularly barley), and increase growth in woody species
 XX
 SQ Sequence 1237 BP; 356 A; 277 C; 280 G; 324 T; 0 U; 0 Other;

Query Match 32.3%; Score 425.8; DB 3; Length 1237;
 Best Local Similarity 66.3%; Pred. No. 2.8e-107;
 Matches 629; Conservative 0; Mismatches 317; Indels 3; Gaps 1;
 QY 146 ATTCTGTGCTGACCTCAGGCACCCCGATGCCAAGAATCTCATAGTGAACGCTTAGG 205
 Db 199 ATCCCGCTGCTCAACCTAGCCGATCCGGAAGCGAAACCCGAATCGTAAAGCCTCGAG 258
 QY 206 GACTTCGGCTTCTCAAGCTTGTGAACCATGTTGCTTCCATTGGAGTTAATGGCAATTTA 265
 Db 259 GAGTTTCGGGTTCTTCAAGTCTGAACCGAGTCCGACCGAATCTATGACTCGGTTA 318
 QY 266 GAAAACGAGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAACAGAGCTGGTCCC 325
 Db 319 GAGCAGGAGGCTATTGGCTTCTTCGGCTTCCTCAGTCTCTTAAAAACCGGCGGTCCA 378
 QY 326 CCGGACCTTTTCGGCTATGCTAGCAGAGAGGATTTGGCCAAAACGCTGATCTGGTTGGTC 385
 Db 379 CCTGAACCGTACGTTTATGGTAAATAACCGATTGGACCAACCGTGACGTTGGTTGGATT 438
 QY 386 GAATACCTCTCTCAACACCAACCTGATTTATCTCACCCCAATCACTTTTGCATTTTC 445
 Db 439 GAGTATCTCTCTCAATGCTAATCTCTCAGCTCTCTCTCTTAAACCTCCGCGCTTTC 498
 QY 446 CGAGAAATCTCTCATCATTTTCAGGGCGGTGGGAGAACTACATTACAGCAGTGAAGAAC 505
 Db 499 CGTCAAAACCCCTCAAAATTTTCGCTGAGTCCGTGGAGAGTACATGAAGAGATTAAAGAA 558
 QY 506 ATGTGCTATGCGGTGTGGAATTTGTCGGGAGGGGTTGGGATAGGACAGGATACG 565
 Db 559 GTGTCGTACAGGTGTGTGGAGATGGTTGCCGAAGAACTAGGGATAGAGCCAGGGACACT 618
 QY 566 TTAAGCAGGTTGCTGAAGGATGAGAAAAGTATTGCTGCTTCAGGTTGAACCACTACCCG 625
 Db 619 CTGAGTAAATGCTGAGAGATGAGAAGAGTACTCTGCTGCTGAGACTAAACCAATATCCG 678
 QY 626 CTTTGGCCCTGAGGTGCAAGCAGCTGAAACCGGAATTTTGGTTGGGTTTGGGGAGCACAGAC 685
 Db 679 GCG---GCGGAGGAGAGCGCGGAGAGATGGTCAAGTGGGGTTTGGGGAACACACAGAC 735
 QY 686 CCACAGATAATTTCTGCTTTAAGATCTAAACAGCAGATCTGGCTTGGCAATCTGCTCTACA 745
 Db 736 CCACAGATAATCTCAGTGTCTAAGATCTAAACACGCGCGGCTCTTCAAAATCTGTGTGAA 795
 QY 746 GATGGCAGTTGGGTTTTCAGTCCCACTGATCAGACTTCTCTTTTTCATCAATGTTGTGAC 805
 Db 796 GATGGAAGTTGGTCCGCTGCTCTCTGATCACTCTTCTTCTTCAATTAATGTTGAGAT 855
 QY 806 GCTCTACAGGTAATGACTAATCGGAGGTTTAAAGTGTAAAGCATAGGTTTGGGTGAC 865
 Db 856 GCTCTTCAGGTTATGACTAAACGGAGGTTCAAGAGTGTAAACACAGGGGCTCTTAGCCGAT 915
 QY 866 ACAACGAGTCAAGGTTATCAATGATCTACTTTGAGGAGCCAGGCTTGATGGAATAATA 925
 Db 916 ACAAGAGATCGAGGATTTCAATGATATATTTTCGGCGGACCGCCATTGAGCCAGAGATC 975

seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.

Claim 45; Page 250; 267pp; English.

The present sequence encodes a gibberellic acid 2-oxidase 2 protein sequence, which is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels. Gibberellic acid levels may be inhibited or controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin biosynthetic pathway sequence, diverts substrate from the pathway, or degrades pathway substrates or products. The methods uses copalyl diphosphate synthase, 3beta-hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a 2beta,3beta-hydroxylase polynucleotides to achieve this. The method is used to control seed germination and seedling growth especially to regulate gene products of gibberellin biosynthetic pathway and restoration of normal seed germination, in transgenic plants. The plants produced are gibberellin deficient, and have shortened hypocotyl and/or epicotyl phenotypes compared to normal plants

Sequence 1403 BP; 440 A; 269 C; 261 G; 433 T; 0 U; 0 Other;

Query Match 32.2%; Score 424.8; DB 3; Length 1403;

Best Local Similarity 66.0%; Pred. No. 5.6e-107;

Matches 669; Conservative 0; Mismatches 327; Indels 18; Gaps 3;

53 ACAACAAACCAACCAACCATGTTGTTCTGTCTCAGCCAGCATTTGAACAGTTTTCCTCTCG 112
 134 AAGCAGCAGAAATAATGTTGCTGTCTCAGCCAGCAACAGACACAGACATCTCTACATC 193
 113 AAACCAATTCAGATCCAGCCCTTGTTCACGGGATTCCTGTGTGACCTCAGCACCCTC 172
 194 AAGAACTACATGCAACGGCATTTCTCTCAACAATTCCTGTGTGACCTCTCAACCA 253
 173 GATGCCAAGATCTCATAGTAGAAGCGCTGTAGGACTTGGCTTCTCAAGCTTGTGAAC 232
 254 GATGCAAGACCCCTCATAGTAGAAGCGCTGTAGGAAATTTGGATTCTTCAAGTCATCAAC 313
 233 CATGGTTTCCATTTGAGTTTAATGGCAATTTAGAAAAAGCGCCCTCAGTTCTTTTAA 292
 314 CATGGTTTCCATTTGAGTTTAATGGCAATTTAGAAAAAGCGCCCTCAGTTCTTTTAA 292
 293 AAATCTCAGTCCGAGAAAGACAGAGCTGTGTCCTCCCGACCTTTCCGGCTATGTAGCAAG 352
 374 ATGCCACTCAATGAGAAGGAAAGTAGGCCCTCCCAACCATATGGGTATGTAGCAAG 433
 353 AGGATTTGGCCCAACCGTGTATGTGCTGTGGTTCGATACCTCTCTCAACACCAACCT 412
 434 AAAATTTGGACAATGGGATGTGTGTTGGGTTGAGTACCTTCTTCAACACCAATCAA 493
 413 GATGTTATCTCACCACCAATCATTGCTTTCCGAGAAATCTCATCATTTTCAGGGCG 472
 494 GAACAACT- - - - -TCTCTGTTATGGCAAAACCGCTGAGAAATTTAGGTGT 541
 473 GTGGTGAGAACTACATTACAGCAGTGAAGAAATGTGCTATGCGGTGTTGGAATTTGATG 532
 542 TTGTTGAACATGATGATCTTCTGTGAGGAAATGCGATGTGAGATCTTGTAGCTGATG 601
 533 GCGGAGGGTTGGGTAAGCGAGAGGAATACGTTAAGCAGGTGCTGAAGGATGAGAA 592
 602 GCAGAGGATTTGAAGATACAAACAAAAATGTGTTAGCAAGCTTCTTATGGATAAGAG 661
 593 AGTGATTCGTGCTTCAGTTGACCACTACCGCTTGCCTGAGTGCAAGCACTGAC 652
 662 AGTGACTCTGTTTATAGGTTGAATCACTACCTGCTTGGCTTGAACCT- - -GTGAATGGT 718
 653 CGGAATTTGGTGGGTTGGGAGCAGACAGACCCACAGATAATTTCTGTCTTAAAGATCT 712
 719 CAACAATGATAGGTTTGGAGACACACGAGCCCAACATCATTTCTTACTTAGTCC 778
 713 AACAGCACATCTGGCTTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAAGTCCACCT 772

779 AACAACTTTCAGGCGCTTCAGATTTTCTTAGAGATGGAACCTGGATTTTCAGTCCACCT 838
 773 GATCAGACTTCCTTTTTCATCAATGTTGGTCAGCTCTACAGGTAACTAAATGGAGG 832
 839 GATCACAATCTTTCTTCATAAATGTTGGTGAATTTCTTCAGGTTATGACCAATGGAAG 898
 833 TTTAAAGTGTAAAGCATAGGTTTGGCTGACACACGAACTCAAGGTTATCAATGATC 892
 899 TTTCAAGTGTGAACACACAGAGTTTGTGCAAAATGGATTTAAGTCTAGACTCTCAATGAT 958
 893 TACTTTGGAGGACCAAGCGTTGAGTGAATAATATAGCACCTTTTACCTTTCAGTGTATTTAAA 952
 959 TACTTTGGAGGTCACCATTTGAGTGAATAATAGTACCATTTCTTCACTATG- - -AAA 1015
 953 GGAGAGGAGTGTGTTGTACAAAGATTCACATGGTGTGAATACAAAGGCTGCGTACACT 1012
 1016 GGAAGAAGAAAGCTTATACAAAGAGTTTACGTGGTTCGAGTATAAAAAATTTAACTATGCT 1075
 1013 TCAAGCTAGCTGATAATAGGCTTGGCCCTTTCCAGAAATCTGCTGATTTAA 1066
 1076 TCAAGATTGGCTGATAATAGGCTTGGACATTTTGGAGAGAAATTTGCTGCTTCATAA 1129

RESULT 11

AAD40262 AAD40262 standard; cDNA; 1403 BP.

XX AAD40262;

DT 22-OCT-2002 (first entry)

XX AC AAD40262;

DE Soybean GA 2-oxidase 2 cDNA.

XX KW Gibberellin; transgenic plant; seed germination; seedling growth;

XX KW transgenic; 2-oxidase 2; enzyme; GA; soybean; gene; ss.

XX OS Glycine max.

XX FH Key Location/Qualifiers

FT CDS 149..1129

FT /*tag= a

FT /product= "GA 2-oxidase 2 protein"

XX US2002053095-A1.

XX 02-MAY-2002.

XX 10-AUG-1999; 99US-00371307.

XX 10-AUG-1999; 99US-00371307.

XX (BROW/) BROWN S M.

XX Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;

XX Filler KJ, Rao S, Ream JE;

XX WPI; 2002-489107/52.

XX P-PSDB; AAB24922.

XX Control of gibberellin levels in plants useful to avoid unfavorable conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to restore these properties.

XX Claim 45; Page 94-95; 155pp; English.

XX The invention relates to control of gibberellin (GA) levels in plants.

XX The method involves producing transgenic plants having a phenotype of reduced seed germination and reduced early seedling growth, then restoring seed germination and early seedling growth by treating plants with an appropriate compound when conditions are favourable. The method is useful to control seed germination and/or early seedling growth in agricultural production so that unfavorable environmental conditions

CC expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to
 CC improve fruit set and growth in seedless grapes, citrus fruits and
 CC pears), improve skin texture and fruit shape in apples, increase stem
 CC length and therefore yield in sugar cane, increase yield and earliness in
 CC celery and rhubarb, improve malting yields and quality in cereals
 CC (particularly barley), and increase growth in woody species
 XX

SQ Sequence 1008 BP; 296 A; 212 C; 232 G; 268 T; 0 U; 0 Other;

Query Match 29.0%; Score 382.8; DB 3; Length 1008;
 Best Local Similarity 64.1%; Pred. No. 2.2e-95;
 Matches 595; Conservative 0; Mismatches 327; Indels 6; Gaps 1;

QY	146	ATTCTGTGGTTCGACCTCAGCACCCGATGCCAAGAATCTCATAGTGAACCCCTGTAGG	205
DB	79	ATCCCTGTTATAGACTTAACCGACTCAGATGCCAAACCCAAATCGTCAAGCATGTGAA	138
QY	206	GACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTTGAGTAAATGCCAATTA	265
DB	139	GAGTTGGGTTCTTCAAGTCTCAACCATGGGTCGACCCGATCTTTTGACTCAGTTG	198
QY	266	GAACACGAGGCTCAGGTTCTTTTAAAAAATCTCAGTCCGAGAAACAGACAGCTGTGCC	325
DB	199	GAGCAGAGCCTCAACTCTTTTGGTCATCTCTCTCAAGACAAAGCGGTCCA	258
QY	326	CCGACCCCTTTCGGCTATGCTAGCAAGAGATGGCCCAACCGGTGANGTCGGTTGGGTC	385
DB	259	CCTGACCCGTTGGTTACGGTACTAAAGGATGGACCCCAATGGTGACCTTGGCTGGCTT	318
QY	386	GAATACCTCTCTCAACCAACCCCTGATGTTATCTCAACCCCAATCATCTTTGCAATTTTC	445
DB	319	GAGTACATCTCTTAACTTAATCTTTTGGCTTGAATCTCTCAACAAACCCGCCATTTTC	378
QY	446	CGAGAAATCCCTCATCTTTCAGGGGGGTGGAGAACTACATTACAGCAGTGAAGAAC	505
DB	379	CGCACACCCCTGCAATTTTCAGAGGGCAGTGGAGATGATTAAGAGATGAAGAGA	438
QY	506	ATGTGCTATGCGGTGTGGAATTTGATGGCGGAGGGTTGGGATAGGCGAGGGAATAGC	565
DB	439	ATGTGAGCAAAATTTCTGGAATTTGTAGAGGAAGAGCTAAAGATAGAGCCAAAGGAGAG	498
QY	566	TTAAGCAGGTGCTGAAGATGAGAAAGTATGTTGCTGCTTCAAGTTGAACACATCCCG	625
DB	499	CTGAGCCGTTTGGTGAAGATGAAGAAAGTATGTTGCTGCTGAGATGAACCAATACCCG	558
QY	626	CCTTGGCCCTGAGTGCAGACACCTGAAACCGGAATTTGGTTGGGTTGGGAGCACACAGAC	685
DB	559	-----GAGAAGAGAGAGACTCGGTCAAGGAGAGAGATTTGGTTGCGTGACACACTGAT	612
QY	686	CCACAGATAATTTCTGCTTTAAGATCTAACAGCACATCTGGCTTGCAAACTCTGTCTACA	745
DB	613	CCACAGTTGATATCACTGCTCAGATCAACAGCACAGAGGGTTTGCAAATCTGTGTCAA	672
QY	746	GATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTTTTCAATCAATGTTGGTGAC	805
DB	673	GATGGAACATGGGTTGATGTTACCTGATCATCTCTCTTCTTCTTCTTCTTCTTCTGAGAT	732
QY	806	GTCTACAGTAACTAATGAGGTTTAAAGTAAAGCATAGGTTTGGTCTGAC	865
DB	733	ACTTTTCAGTGATGACAAACGGAAGATTCAGAGTGTGAACATAGATGGTGAACAT	792
QY	866	ACAAAGAGTCAAGGTTTATCAATGATCTACTTTTGGAGGACCGGTTGAGTGAATAATA	925
DB	793	ACAAAGAGTCAAGGATATCGATGATCTACTTTCGAGGTCCTCTTTCGAGCGAAGATT	852
QY	926	GCACTTTACCTTCAGTGATGTTAAAGAGAGAGGATGTTGTACAAGAGTTACATGG	985
DB	853	GCACCAATATCATGCTTGTGCAAGCAAGATGATTGCTTTTATAATGAGTTTACTTGG	912
QY	986	TCTGATCAAGAGGCTCGGTACATCTTCAAGCTAGCTGATTAATAGGCTTCCCTTTC	1045
DB	913	TCTCAATCAAGATTATCTGCTTACAAAATAAGCTTGGTGACTATAGGCTTGGTCTCTTT	972

QY 1046 CAGAAATCTGCTGCTGATTAACCAAAACA 1073
 DB 973 CAGAAACGACCTCCATTTTCTCTATCCA 1000

RESULT 13

ADM94207
 ID ADM94207 standard; cDNA; 1473 BP.

XX AC ADM94207;
 XX DT 17-JUN-2004 (first entry)
 XX DE Wheat Dioxygenase cDNA #1.

XX KW Wheat; ss; plant; plant metabolism;
 KW GTP cyclohydrolase II/3, 4-dihydroxy-2-butanone-4-phosphate synthase;
 KW Dioxygenase; Ent-Kaurene Synthase A; GA-20 oxidase;
 KW Gibberellin 3-beta hydroxylase; Riboflavin specific deaminase;
 KW Ethylene response factor; Acyl-CoA thioesterase II;
 KW ABC transporter GCN20-like; P-glycoprotein 1; P-glycoprotein 3;
 KW P-glycoprotein ATPGP; P-glycoprotein HVMR2; ABC transporter;
 KW PMP70 ABC transporter; MRP4 ABC transporter; transgenic.

XX OS Triticum aestivum.

XX PN US6677502-B1.

XX PD 13-JAN-2004.

XX PF 12-JUL-2000; 2000US-00614912.

XX PR 12-JUL-1999; 99US-0143401P.

XX PR 12-JUL-1999; 99US-0143412P.

XX PR 30-JUL-1999; 99US-0146550P.

XX PR 15-DEC-1999; 99US-0170908P.

XX PR 21-DEC-1999; 99US-0172946P.

XX PR 21-DEC-1999; 99US-0172959P.

XX PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PI Allen SM, Kinney AJ, Rafalski JA, Orozco EM, Miao G, Fanodu OO;

XX PI Lee J, Lohman KN, Rendina AR, Sakai H, Weng Z, Caimi PG, Fang Y;

XX PI Shen JB, Zoughi IL, Anderson SL, Shi J, Lu G, Helentjaris TG;

XX PI Li CP;

XX WPI; 2004-088430/09.

XX P-PSDB; ADM94208.

XX New isolated GTP cyclohydrolase II/3, 4-dihydroxy-2-butanone-4-phosphate
 synthase nucleic acid and proteins, useful for creating transgenic plants
 where polypeptides are present at higher or lower levels.

XX Example 3; SEQ ID NO 7; 186pp; English.

XX The invention relates to an isolated polynucleotide comprising a
 nucleotide sequence encoding a polypeptide having GTP cyclohydrolase
 II/3, 4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing as
 ADM94266. Also included are a vector comprising the polynucleotide, a
 recombinant DNA construct comprising the polynucleotide operably linked
 to at least one regulatory sequence, transforming a cell with the
 polynucleotide, a cell comprising the recombinant DNA construct,
 producing a plant (comprising transforming a plant cell with the
 polynucleotide and regenerating a plant from the transformed plant cell),
 a plant comprising the recombinant DNA construct and a seed comprising
 the recombinant DNA construct. Also disclosed as new are nucleic acid
 (cDNA) fragments and assembled contigs encoding plant metabolic proteins
 chosen from GTP cyclohydrolase II/3, 4-dihydroxy-2-butanone-4-phosphate
 synthase, Dioxygenase, Ent-Kaurene Synthase A, GA-20 oxidase, Gibberellin
 3-beta hydroxylase, Riboflavin specific deaminase, Ethylene response
 factor, Acyl-CoA thioesterase II, ABC transporter GCN20-like, P-
 glycoprotein 1, P-glycoprotein 3, P-glycoprotein ATPGP, P-glycoprotein

CC HWMDR2, ABC transporter, PMP70 ABC transporter and MRP4 ABC transporter.
 CC The nucleic acid fragments may be used to create transgenic plants where
 CC the polypeptides are present at higher or lower levels than normal or in
 CC cell types or in developmental stages in which they are not normally
 CC found. The polynucleotides can be used as probes for genetically and
 CC physically mapping genes and as markers for traits linked to those genes.
 CC The nucleic acid fragments may be used as restriction fragment length
 CC polymorphism (RFLP). It can also be used to probe Southern blots
 CC containing restriction endonuclease-generated genomic DNAs of a set of
 CC individuals representing parent and progeny of a defined genetic cross.
 CC The nucleic acid fragments may also be used as hybridisation probes
 CC against PCR amplification products generated from the mutation population
 CC using the mutation tag sequence primer in conjunction with an arbitrary
 CC genomic site primer. The peptides can also be used to immunise animals to
 CC produce polyclonal or monoclonal antibodies with specificity for peptides
 CC or proteins comprising the amino acid sequences. Antibodies are useful
 CC for detecting the polypeptides *in situ* in cells or *in vitro* in cell
 CC extracts. The present sequence encodes a plant metabolism protein (or
 CC fragment).
 CC
 CC Sequence 1473 BP; 285 A; 440 C; 468 G; 280 T; 0 U; 0 Other
 CC
 CC

SQ Sequence 1473 BP; 285 A; 440 C; 468 G; 280 T; 0 U; 0 Other;

Query Match 27.6%; Score 363.6; DB 12; Length 1473;
Best Local Similarity 61.3%; Pred. No. 5.6e-90;
Matches 607: Conservative 0; Mismatches 374: Indels 9;

Qy	60	CAACAA	CCATG	TTGTTCTG	TCAGC	CAGCAT	TGAAC	CCAGT	TTTTTCTT	CTCTG	AAACAT	119
Db	119	CAGCCAT	GTGTGTTTCT	CGCCAG	CACGCCCG	CGTCGAT	CATCCCG	TCCTC	ACAGT	CGC	178	
Qy	120	TCAAGT	CCACGCC	CTGTTC	TACGGG	GATTCT	CTGTG	TGTCGAC	CTC	CACG	CACCCG	179
Db	179	CCGACC	CCGGGACT	CTTCT	CCGGCAT	GCCGGT	GTGAC	CTCTC	ACGCC	CTG	CGCGC	238
Qy	180	AGAACT	CTCATAGT	GAA	CGCCTG	TAGG	CACTTC	GGCTTCTT	CAAGT	TTGTG	AAACCAT	239
Db	239	CGCGGG	CCATCG	CCGAC	CGCTG	CAGCG	CTTC	CGGTTCTT	CAAGT	TCGTCA	ACCA	298
Qy	240	TTCCAT	TGGAGT	TAA	TGCGCA	TTTAG	AAAC	GAGG	CCCTC	CAGG	TTCTTT	299
Db	299	TGCCCG	GGGAC	CACGAT	GACAGG	CTCG	AGT	CGGAG	CCGTC	CAGG	TTCTT	358
Qy	300	AGTCCG	AGAA	GACAG	AGCTG	GTCTCC	CCCG	ACCC	TTTC	GGCTAT	GGTAG	359
Db	359	AGGCGG	ACAAG	ACCGCT	CCG	CCCG	CGCTAC	CCCGTTC	GGCTAC	GGCAG	AGCG	418
Qy	360	GCCCAA	ACGGT	GATGT	CGGTT	GGT	CGAAT	CACTCT	CCTC	CAAC	CAAC	419
Db	419	GGCTCA	ATGG	CGACAT	GCGGT	GGCT	CGAGT	CACTG	CTCT	CGCC	GTG	478
Qy	420	TCTCA	CCCAAT	CACTTT	GTGCAT	TTTCC	GAGAAA	TCTCAT	CATTT	CAGGG	CGGTG	479
Db	479	TCTCGG	CGCCTG	CGCCG	CTCGT	CTT	CGC	-----	CGCTCT	CCGGG	CGCGT	529
Qy	480	AGAACT	ACAT	TACAG	CACTG	AGAA	CATGTG	CTATG	CGGTG	TTG	GAATG	539
Db	530	ACGAGT	ACAT	CCGCG	CGGTG	CGG	AGGTG	CGCGGT	GTGAT	GAGG	CGCAT	589
Qy	540	GTTTGG	GAT	AAAG	CAGAG	GAATAC	GTTT	AAGCAG	GTGCTG	AAAGAT	CAGAAA	599
Db	590	GGCTT	GGCAT	TGCG	CGGTG	AG	CGCGCT	GTAG	CGGGAT	TGTTAC	CGGGAG	649
Qy	600	CGTGCT	TT	CAGTT	GAA	CCACT	TAC	CGCCCT	TTGCC	TTGAG	GTGCA	659
Db	650	AGGTGT	TC	CGG	GTGA	ACCA	CTAC	CCGCG	GTGCC	ACGCG	CTG	709
Qy	660	TGTTGG	TTTGG	GAG	GCAC	CAG	ACCA	CCAC	GATAA	TTTCTG	TTTA	719
Db	710	CCA	CGGCTT	CGG	GAG	GCAC	AGG	ACCCG	CACTCAT	CTCG	GTG	769
Qy	720	CAT	CTGG	CTT	CAAA	TCTG	CTC	ACAG	ATGG	CACTT	GGGTTT	779
Db	770	CGT	CGG	CTC	AGAT	CGCG	CTC	AGAA	CGG	CACTG	GTG	829

PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
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PR 01-JUN-1999; 99US-0137222P.
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Query Match		27.1%;	Score 356.6;	DB 3;	Length 1316;
Best Local Similarity		63.2%;	Pred. No. 4.6e-88;		
Matches 586;		Conservative 0;	Mismatches 329;	Indels 12;	Gaps 2;
Qy	132	CCTTGTTCACGGGATTCTCTGTGTCGACCTCAGCCACCCCGATGCCAAGATCTCATAG	191		
Db	78	CCGGTTCCTCTAATCCCGGTTATAGATATGTCTGACCCAGAATCCAAACATGCCCTCG	137		
Qy	192	TGAACGCTGTAGGACTTCGGCTTCTCAAGCTTGTGAACCATGTTCTCCATTGGAGT	251		
Db	138	TGAAGCATGCCAAGACTTCGGCTTCTCAAGTGTCAACCATGGCGTTCCGCAGAGC	197		
Qy	252	TAAATGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAG	311		
Db	198	TAGTCTCTGTTTTAGAACACGAGACCGTGCATTTCTTCTCGTTGCCCAAGTCAGAGAAA	257		
Qy	312	ACAGAGCTGGTCCCGCCGACCTTTCCGGCTATGTAGCAAGAGGATTCGCCCAACGGTG	371		
Db	258	CCCAAGTCG---CAGGTTATCCCTTCGGATACGGGAACAGTAAGATTTGGTCGGAATGGTG	314		
Qy	372	ATGTCGGTTGGGTGCAATACCTCTCCTCAACACCAACCCCTGATGTATCTCACCCAAAT	431		
Db	315	ACGTGGTTGGGTGAGTACTTGTGATGAACGCTAATCAIGATTCCGGTTCGGGTCCAC	374		
Qy	432	CACTTTGCATTTTCCGAGAAATCCTCATCATTTCAGGGCGGTGGTGAGAACTACATTA	491		
Db	375	TATTTCCAAGTCTTCTCAAAAGCCGGGAACTTTTCAGAAAACCAATTTGGAAGAGTACAA	434		
Qy	492	CAGCAGTGAAGAACATGTCTATCGGTGTTGGATTTGATGCGGAGGGGTTGGGGTAA	551		
Db	435	CATCAGTGAGAAAAATGACATTCGATGTTTTGGAGAAAGTACACATGGGCTAGGGTCA	494		
Qy	552	GGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTATTGCTTCAGGT	611		
Db	495	AACCGAGGACACACTTAGCAGCTTGTGTCTGACCAAAACACGACTCGATATTGAGAC	554		
Qy	612	TGAACCACTACCCGCTTGCCCTGAGGTGCAAGCACTGAAC-----CGGAATTTGG	662		
Db	555	TAAATCACTATCCACATGCTCTTAGCAATAAGAAAACCAATGGTGAAGAAATGTA	614		
Qy	663	TTGGGTTTGGGAGACACAGACCCACAGATAATTTCTGTCTTAGATCTAACACACAT	722		
Db	615	TTGGTTTTGGTGAACACACAGATCTCAAAATCATCTGTCTTAAAGATCTAACACACTT	674		
Qy	723	CTGGCTTGCAATCTGTCTACAGATGGCACTTGGTTTTCAGTCCACCTGATCAGACTT	782		
Db	675	CTGGTCTCCAAATTAATCTAAATGATGGCTCATGGATCTGTCTCCTCCGATCACATT	734		
Qy	783	CCTTTTTCATCAATGTGGTGACGCTCTACAGGTAATGACTAATGGAGGTTTAAAAAGTG	842		
Db	735	CCTTCTTCTTCAACGTTGGTGACTCTCTCCAGGTGATGACAAATGGGAGGTTCAAGAGCG	794		
Qy	843	TAAAGCATAGGTTTGGCTGACACACAGAACTCAAGTTATCAATGATCTACTTTGGAG	902		
Db	795	TGAGGCATAGGTTTTTAGCTAACTGTAAAAAATCTAGGGTTTCTATGATTTACTTTCGCTG	854		
Qy	903	GACCAGGTTGAGTGAATAATAGCACCTTTTACCTTCAGTGTATTTAAAGGAGAGGAGT	962		
Db	855	GACCTTCATTGACTCAGAAATCGCTCCGTTGACATGTTTGTATGACATGAGGACGAGA	914		
Qy	963	GTTTGTACAAAGATTTCATGTTGTGAATACAAAGGCTCGGTACACATTCAGGCTTAG	1022		
Db	915	GGTTGTACGAGGATTACTTGGTCTGAATACAAAACTCTACCTACAACTCTAGATTGT	974		
Qy	1023	CTGATAATAGGCTTGCCTTTTCCAGA	1049		
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Job time : 903.539 secs

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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC
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Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	457	34.7	553	AW184969	se84f09.y
2	444.8	33.7	566	BM085298	sa34h07.
3	430	32.6	622	BU549366	GM880016A
4	427.4	32.4	1365	EX814544	Arabidops
5	425.8	32.3	1362	CNSOABST	Arabidops
6	422.6	32.1	1141	CNSO9V5Q	Arabidops
7	417.8	31.7	1363	CNSOABKL	Arabidops
8	386.4	29.3	1339	CNSOABCR	Arabidops
9	378.6	28.7	612	BE802903	Arabidops
10	355.8	27.0	785	AJ803092	Arabidops
11	348.6	26.4	1128	CNSOADMV	Arabidops
12	336.2	25.5	567	BM931076	Arabidops
13	335.4	25.4	594	BI208568	EST526608
14	332.8	25.3	478	AL382874	Arabidops
15	329.2	25.0	893	DN589159	Arabidops
16	323.4	24.5	792	BI935635	Arabidops
17	315.8	24.0	1554	AY104425	Zea mays
18	307.8	23.4	626	CV292693	EST81070
19	307.8	23.4	642	CV292668	EST81045
20	305.8	23.2	438	BP940509	BP940509
21	305.8	23.2	743	BG646259	EST507878
22	305.6	23.2	755	BM690134	BM690134

23	305.6	23.2	776	5	BM692820	BM692820
24	305.6	23.2	779	3	BJ571134	BJ571134
c	305.6	23.2	808	3	BJ575888	BJ575888
25	305.6	23.1	529	2	BG881784	ae889f09.
26	305.6	23.1	663	7	CV292717	EST81094
27	304.2	23.1	753	3	BI968577	GM830005B
c	304.2	22.9	753	3	BI968577	GM830005B
28	301.8	22.7	619	1	AW584268	N210259e
29	298.6	22.7	619	1	AW584268	N210259e
30	298.2	22.6	789	5	BM685035	BM685035
31	297.6	22.6	789	5	BM685035	BM685035
32	297.6	22.6	724	6	CA844444	EA27D12a
c	297.6	22.6	724	6	CA844444	EA27D12a
33	294.6	22.4	517	3	BP074757	BP074757
c	294.6	22.4	517	3	BP074757	BP074757
34	294.6	22.4	520	3	BP074168	BP074168
35	288.6	21.9	847	8	DN982067	SV6_43H10
36	286.6	21.7	789	7	CV470333	43176.1 C
c	286.6	21.7	789	7	CV470333	43176.1 C
37	280.2	21.3	501	3	BP060951	BP060951
38	279.8	21.2	611	1	AW309039	sf94b04.Y
39	278.8	21.2	854	8	DN980660	SV6_28C05
40	278.4	21.1	604	7	CV630114	M85T6013a
41	277.6	21.1	853	7	CV469374	41999.1 C
42	274.4	20.8	738	8	DN501878	V035D04.5
43	273.6	20.8	655	5	BQ404995	GA_Ed007
c	273.6	20.8	800	3	BI970132	GM830009B
c	273	20.7	685	2	BG523146	29-41 Ste

ALIGNMENTS

RESULT 1
AW184969
LOCUS
DEFINITION
se84f09.y1 Gm-c1023 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1023-1410 5' similar to TR:004162 O04162 DIOXYGENASE. ;, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Other ESTs: BU544870 corresponding to Gm-r1088-979 (3')
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert Length: 1472 Std Error: 0.00
High quality sequence stop: 436.
Location/Qualifiers
1. .653
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="T157"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1023-1410"

/tissue type="seed coats of greenhouse grown plants"
/lab_host="DH10B"
/clone_lib="Gm-cl023"
/notes="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
cDNA library was constructed from mRNA isolated from seed
coats (100-200mg) of greenhouse grown plants. The
library was prepared using the Life Technologies
SuperScript cDNA library construction kit. Complementary
DNA was synthesized from mRNA using a poly (dT) sequence
with a Not I restriction site. Sal I linkers adapters
were ligated to the blunt-ended cDNA fragments followed by
Not I digestion. The cDNA fragments were directionally
cloned into the Not I-Sal I restriction site of the
pSPORT1 vector. The ligated cDNA fragments were
transformed into E.coli Electromax DH10B host cells. This
library was constructed by Dr. Lila Vodkin and Dr. Anu
Khanna."

ORIGIN

Query Match 34.7%; Score 457; DB 1; Length 653;
Best Local Similarity 87.2%; Pred. No. 2.7e-111;
Matches 499; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 65 ACCATGGTTGTTCTGCTCAGCAGCATTTGAACAGTCTTTCTCTGAAACCATTTCAAG 124
DB 81 ACCATGGTTGTTCTGCTCAGCAGCATTTGAACAGTCTTTCTCTGAAACCATTTCAAG 140

QY 125 TCCACGCCCTTGTTCAGCGGATTCCTGTGTGACCTCAGCACCCTCCATGCCAAGAT 184
DB 141 CCCACGCCCTTGTTCAGCGGATTCCTGTGTGACCTCAGCACCCTCCATGCCAAGAT 200

QY 185 CTCATAGTGAACCCCTGTAGGACTTCGGCTTCTCAAGCTTGTGAACCATTTGTCTCA 244
DB 201 CACATAGTCAATGCTTCGAGGACTTCGGCTTCTCAAGCTTGTGAACCATTTGTCTCG 260

QY 245 TTGGAGTTAATGGCCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCC 304
DB 261 TTACAGTTTATGGCCCAATTTAGAAAACGAAACCTCGGGTCTTCAAAAAACCTCAATCC 320

QY 305 GAGAAAGACAGACTGGTCCCGGACCTTCGGCTATGTAGCAAGAGATTGGCCCA 364
DB 321 GAGAAAGACAGAGGCTGGTCCCGGACCTTCGGCTATGTAGCAAGAGATTGGCCCT 380

QY 365 AACGGTGATGCGGTTGGGTCGAATACCTCTCTCAACACCAACCTCGATGTTATCTCA 424
DB 381 AACGGCGATGCGGTTGGGTCGAATACCTCTCTCAACACCAACCTCGATGTTATCTCC 440

QY 425 CCCAAATCACTTTGCAATTTCCGAGAAAATTCCTCATCATTTTCAGGCGGTTGGGAGAAC 484
DB 441 CCCAAGTCAAGTTTCAATTTTCAGAAAGGTCCTCAGAAATTTTCANGGCGGTTGGGAGAA 500

QY 485 TACATTACAGCAGTGAAGACATGCTATGCGTGTGGATTTGGATTTGATGGGAGGGTTG 544
DB 501 TACATTAGAGCGGTGAAGAACATGCTATGAGGTGTGGATTTGATGGTGAAGGATTTG 560

QY 545 GGATTAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTCGTGC 604
DB 561 TGGATTAAGCAGTAGGAATGTTGATGATGTTGCTGAACGATGAGAAAGTGAATTTCTTGC 620

QY 605 TTCAGGTTGAACCACTACCGCGCTTGCCTTGA 636
DB 621 TTCAGACNTTACCACCTACCGCGCATTTGCCGA 652

RESULT 2

BM085298
LOCUS saj34h07.y1 Gm-cl066 Glycine max cDNA clone SOYBEAN CLONE ID:
DEFINITION Gm-cl066-4957 5' similar to TR:Q9XG83 Q9XG83 GA 2-OXIDASE. ; mRNA
sequence.
ACCESSION BM085298
VERSION BM085298.1 GI:16995926
KEYWORDS EST.

SOURCE
ORGANISM

Glycine max (soybean)
Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE

1 (bases 1 to 566)

AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corvett, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.

TITLE

Public Soybean EST Project

JOURNAL

Unpublished (1999)

COMMENT

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 426.

FEATURES

source

1..566
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl066-4957"
/tissue_type="Leaf and shoot tip, salt stressed, 2 week
old seedling"
/lab_host="DH10B"
/clone_lib="Gm-cl066"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from unexpanded leaves and the shoot tips of 2 week old
seedling from the cultivar Williams. The 2 week old
seedlings were salt stressed in a solution of 500mM NaCl
for 3 days prior to harvesting. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
Shoemaker."

ORIGIN

Query Match 33.7%; Score 444.8; DB 3; Length 566;
Best Local Similarity 87.9%; Pred. No. 5e-108;
Matches 485; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 65 ACCATGGTTGTTCTGCTCAGCAGCATTTGAACAGTCTTTCTCTGAAACCATTTCAAG 124
DB 15 ACAATGGTTGTTGTTCTCAGCAGCATTTAAACACAGTCTTTCTCTGAAACCATTTCAAG 74

QY 125 TCCAGCCCTTGTTCAGCGGATTCCTGTGTGACCTCAGCACCCTCCATGCCAAGAT 184
DB 75 CCCAGCCCTTGTTCAGCGGATTCCTGTGTGACCTCAGCACCCTCCATGCCAAGAT 134

QY 185 CTCATAGTGAACCCCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATTTGTCTCA 244
DB 135 CACATAGTGAAGCCCTGTAGGAGACTTCGGCTTCTTCAAGCTTGTGAACCATTTGTCTCA 194

QY 245 TTGGAGTTAATGGCCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCC 304

Db 195 TTAGATTTCATGGCCAAATTTGGAAACGAAACCCCTCAGGTTCTTCAAAAACCTCAGTCC 254
 QY 305 GAGAAAGACAGAGCTGGTCCCGCCGACCTTTTCGGCTATGTTAGCAAGAGGATTTGGCCCA 364
 Db 255 GACAAAGACAGGCTGGTCCCGCCGACCTTTTCGGCTACGCGCAGCAAGAGGATTTGGCCCT 314
 QY 365 AACGGTGATGCTGGTGGTGGTGAATACCTTCCTCCACACCAACCCCTGATGTTATCTCA 424
 Db 315 AACGGCGATGCTGGTGGTGGTGGTGAATACCTTCCTCCACACCAACCCCTGACGTCATCTCC 374
 QY 425 CCCAATACCTTTGCAATTTCCGAGAAATCCTCATCTTCCAGGCGGCTGTCGAGAAC 484
 Db 375 CCCAATACCTTTGCAATTTCCGAGAAATCCTCATCTTCCAGGCGGCTGTCGAGAAC 434
 QY 485 TACATTACAGCAGTGAAGAACATGCTATGCTATGCGGTGTTGGAATGATGCGGAGGGTTG 544
 Db 435 TACATTAGAGCGCTGAAGAACATGCTATGCTATGCGGTGTTGGAATGATGCGGAGGGTTG 494
 QY 545 GGGTAAGCAGAGAAATGCTTAAGCAGGTTGCTGAGGATGAGAAAGTGAATTCGTCG 604
 Db 495 GGAATAACTCAGAGAAATGCTTAAGCAGGTTGCTGAGGATGAGAAAGTGAATTCGTCG 554
 QY 605 TTCAGGTTGAAC 616
 Db 555 TTCAGACTTAAC 566

RESULT 3
 BU549366/c
 LOCUS GM880016A20B10 Gm-r1088 Glycine max cDNA clone Gm-r1088-5828 3',
 DEFINITION mRNA sequence.
 ACCESSION BU549366
 VERSION BU549366.1 GI:22932227
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max

REFERENCE 1 (bases 1 to 622)
 AUTHORS Vodkin,L., Shoemaker,R., Keim,P., Retzel,E., Khanna,A., Shealy,R.,
 Clough,S., Thibaud-Nissen,F., Coryell,V., Erpeliding,J., Raph,C.,
 Shoop,E., Stromvik,M., Schweitzer,P., Gong,G. and Liu,L.
 A Functional Genomics Program for Soybean (NSF 9872565) (2002)
 JOURNAL Unpublished (2002)
 COMMENT Other_Ests: BG881784 corresponding to Gm-c1065-2970 (5')
 Contact: Vodkin, L.O., PI, A Functional Genomics Program for
 Soybean (NSF 9872565)
 Lewin, H. A., Director, Keck Center for Comparative and Functional
 Genomics

University of Illinois
 Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
 Tel: (217) 244-6147
 Fax: (217) 333-4582
 Email: l-vodkin@uiuc.edu
 Insert Length: 622 Std Error: 0.00
 Plate: GM880016A20 row: B column: 10
 Seq primer: 5'-TTTTTTTTTTTTTTTTTTT(A/C/G)-3'
 High quality sequence stop: 622.

FEATURES
 source

1. .622
 Location/Qualifiers
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="Gm-r1088-5828"
 /clone_lib="Gm-r1088"

/note="The library Gm-r1088 is a sequence-driven, reracked
 set of 9,216 low redundancy clones selected from cDNA
 libraries from various tissues and stages of development
 of soybean that consists of 2,706 cDNAs from germinating
 cotyledons (source library Gm-c1027); 1,355 cDNAs from

immature seed coats (libraries Gm-c1019 and Gm-c1023); 917
 cDNAs from tissue culture derived somatic embryo8 (source
 libraries Gm-c1036 and Gm-c1075); 3,275 cDNAs from
 germinating seedlings, shoot tips, or leaves exposed to
 various stresses (source libraries Gm-c1064, Gm-c1065,
 Gm-c1066, and Gm-c1067; and Gm-c1068); and 963 cDNAs from
 young leaves exposed to bacterial and fungal pathogens
 (source libraries Gm-c1072, Gm-c1073, and Gm-c1074). The
 5' ESTs of the source clones from the different libraries
 was used to select singletons, or a representative of each
 contig, which were reracked to form library Gm-r1088 and
 the cDNA clones of the reracked Gm-r1088 library were then
 sequenced at the 3' end. The unigene selection and 3'
 sequencing was funded by NSF Plant Genome project #9872565
 (http://soybean.genomics.croscui.uiuc.edu/) as part of
 creation of a low redundancy soybean cDNA set. The source
 cDNA libraries were constructed by the laboratories of
 Lila Vodkin, University of Illinois, Randy Shoemaker, Iowa
 State University, and Paul Keim, Northern Arizona
 University as part of the Public EST project,
 http://129.186.26.94/soybeanest.html. The contig analysis
 to select unique genes was performed by the laboratory of
 Ernest Retzel, Center for Computational Genomics and
 Bioinformatics, University of Minnesota,
 http://web.ahc.umn.edu/biodata/nsfsoy/. Reracking and 3'
 sequencing were conducted by services of the University of
 Illinois Keck Center for Comparative and Functional
 Genomics http://www.biotech.uiuc.edu/keck.htm. Note: The
 corresponding 5' EST from each clone in the Gm-r1088
 library is listed in the 'OTHER EST' field. The detailed
 information on the source library for each clone can also
 be obtained by referring to the Genome Systems clone ID of
 the original cDNA library that is also listed under 'OTHER
 EST'."

ORIGIN

Query Match 32.6%; Score 430; DB 5; Length 622;
 Best Local Similarity 84.1%; Pred. No. 4.9e-104;
 Matches 522; Conservative 0; Mismatches 88; Indels 11; Gaps 3;

QY 554 CAGAGGAATAGCTTAAAGCAGGTTGCTGAAGGATGAGAAAGTATTGCGCTTCAGGTTG 613
 Db 621 CAGAGGAATGCTTGAGTAGGTTGCTGAAGGATGAGAGAGTATTCTGCTTCAGACTT 562
 QY 614 AACCACTACCCGCTTGCCCTGAGGTGCAAGCACTGAA---CCGGAATTTGGTGGGTTT 670
 Db 561 AACCNNNACCCGCTATGCCAGAGGTGCAAGCATTGAACGGCAGAAATTTGGTGGGTTT 502
 QY 671 GGGGAGCAGACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGCTTG 730
 Db 501 GGAGAGCAGACAGACCCACAGATAATTTCTGTCTTTGAGATCTTAACAGCACCTCAGGCTG 442
 QY 731 CAAATCTGCTCACAGATGGCAGCTTTGGGTTTCAGTCCACCTGATCAGACTTCTTTTTC 790
 Db 441 CAAATCTGCTCACAGATGGCAGCTTTGGGTTTCAGTCCACCTGATCAGACTTCTTTTTC 382
 QY 791 ATCAATGTTTGGTGACGCTCTACAGGTAATGACTAATGGAGGTTTAAAAGTGTAAAGCAT 850
 Db 381 ATCAATGTTTGGTGACACTCTACAGGTGATGACTAATGGAGGTTTAAAAGTGTAAAGCAT 322
 QY 851 AGGGTTTGGCTGACACAAAGCAAGTCAAGTTATCAATGATCTACTTTGGAGGACCCAGG 910
 Db 321 AGAGTTTGGCTGACCCCAACCAAGTCAAGTTTGTCAATGATCTACTTTGGAGGACCCAGC 262
 QY 911 TTGAGTGAATATAGCACCTTTTACCTTCAGTGATGTTTAAAGGAGGAGAGTGTGTTGATC 970
 Db 261 TTGAGTGAATATAGCACCTTTTACCTTCATGTTTAAAGGAGGAGAGTGTGTTGATC 202
 QY 971 AAAGAGTTTCACATGCTGTGAATACAAAGAGGCTGGGTACACTTCAAGGCTAGCTGATAAT 1030
 Db 201 AAAGAGTTTCACATGCTGTGAATACAAAGAGGCTGGGTATCGCTCAAGGCTAGCGGATAAT 142
 QY 1031 AGGCTTGCCCTTTCCAGAAATCTGCTGCTGATTAAACCAACACACACCTTCAAA-----T 1085

Db 141 AGGCTCGCTCCTTTTGGAGAAATCTGCTGATTAAGAGTCAAGTGTGTCAAAATTTT 82
QY 1086 TCCACTCATTTTAGCGAGGTGTTATTACCCCAATTTT---CTTCTCTTTTCTTTTCCTG 1142
Db 81 ACTGCTCAATTTTGGCAGGTATTGTTAGGGAACCTTTTTCATATATATATATATTTTGG 22
QY 1143 TGTCTCTCTAGGTTTCAACA 1163
Db 21 TTGTATCTAGGTTTCAACA 1

RESULT 4

CNSOAC6N 1365 bp mRNA linear HTC 06-FEB-2004
LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
DEFINITION GSLTFB7ZE01 of Flowers and buds of strain col-0 of Arabidopsis
thaliana (thale cress).

ACCESSION

VERSION BX814544

KEYWORDS HTc; GSLT cDNA.

SOURCE

ORGANISM Arabidopsis thaliana (thale cress)

REFERENCE

AUTHORS Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.

TITLE Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome

JOURNAL

REFERENCE Unpublished

AUTHORS 2 (bases 1 to 1365)

TITLE Genoscope.

JOURNAL Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

COMMENT - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen)

full-length libraries construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli

V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,

Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis

genome released by MIPS (Munich Information center for Protein

Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_Full

length

http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis.

Location/Qualifiers

1. .1365

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/db_xref="taxon:3702"

/clone="GSLTFB7ZE01"

/tissue_type="Flowers and buds"

/ecotype="Col-0"

/plasmid="pCMVSPORT_6"

1. .1365

/gene="Atlg30040"

gene

1. .1365

/gene="Atlg30040"

ORIGIN

Query Match 32.4%; Score 427.4; DB 4; Length 1365;

Best Local Similarity 66.4%; Pred. No. 2.9e-103;

Matches 630; Conservative 0; Mismatches 316; Indels 3; Gaps 1;

QY 146 ATTCTGTGTGACCTCAGCACCCGATGCCAAGATCTATAGTGAACGCTGTAGG 205

Db 195 ATCCCCGTGTC AACCTAGCCGATCCGGAAGCGAAACCGAATCGTAAAGCCTCGAG 254

QY 206 GACTTCGGCTTCTTCAAGCTTGTGAACCATGTTGTTCATTGGAGTTAATGGCAATTTA 265
Db 255 GAGTTTCGGGTTCTTCAAGGTCTGTAAACACGAGTCCGACCCGACTCATGACTCGGTTA 314
QY 266 GAAAAAGAGGCGCTCAGGTTCTTTAAAAATCTAGTCCGAGAAAAGACAGAGCTGTGCC 325
Db 315 GAGCAGGAGGCTATTGGCTTCTTCGGCTTGCCTCAGTCTCTTTAAAAACCGGGCGGTCCA 374
QY 326 CCGGACCTTTTCGGCTATGTTAGCAGAGGATTGGCCCAACGGTGATCTCGTTGGTGC 385
Db 375 CCTGAACCGTACGCTTATGGTAATAACGGATTGGACCAACCGGTGACCTTGGTTGGATT 434
QY 386 GAATACCTCTCTCAACACCAACCTGATGTTATCTCAACCACCAATTCATTTGTCATTTTC 445
Db 435 GAGTATCTCTCTCTCAATGCTAATCTCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 494
QY 446 CGAGAAAAATCCTCATCATTTTCAGGGCGGTGGTGGAGAACTACATTACAGCAGTGAAGAAC 505
Db 495 CGTCAAAACCCCTCAAAATTTTCGCTGAGTCGTTGGAGGAGTACATGAAGGAGATTAGGAA 554
QY 506 ATGTGCTATGCGGTGTTGGAATTTGATGGCGGAGGGTGGGGATAGAGCAGAGGANTACG 565
Db 555 GTGTGCTACAAGGTGTTGGAGATGGTTCGCCGAAGAACTAGGGATAGAGCCNAGGGACAT 614
QY 566 TTAAGCAGGTTGCTGAAGGATGAGAAAGTGAATTCGTCTTCAGGTTGAACCACTACCCCG 625
Db 615 CTGAGTAAATCTCTGAGAGATGAGAGAGTGAATCTGTGCTGAGACTAAACCATATTCGG 674
QY 626 CTTGCCCTGAGTGCAGACTGAACCGGAATTTGGTTGGTGGTGGGAGCAGACAGAC 685
Db 675 GCG---GCGGAGGAAGAGGCGGAGAGAGTGTGAAGTGGGGTGGGGGAAACACACAGAC 731
QY 686 CCACAGATAATTTCTGCTTAAGATCTAACACGACATCTGGCTTGCAAATCTGTCTCACA 745
Db 732 CCACAGATAATCTCAGTGTCTAAGATCTAATAACACGCGGGGTCTTCAAACTCTGTGAAA 791
QY 746 GATGGCAGTTCGGTTTTCAGTCCACCTGATCAGACTTCCTTTTTCATCAATGTTGTGTGAC 805
Db 792 GATGGAAGTTGGTTCGTCTCTCTCTGATCACTCTTCTTCTTCTTCTTCTTCTTCTTCT 851
QY 806 GCTCTACAGGTAATGAATAAGCGAGGTTTAAAGTGTAAAGCATAGGCTTTTGGCTGAC 865
Db 852 GCTCTTCAGGTTATGACTAAACGGAGGTTTCAAGAGTGTATAACACACAGGCTCTTAGCCGAT 911
QY 866 ACACGAGAGTCAAGTTATCAATGATCTACTTTTGAGGACAGCGCTTGATGAAATATA 925
Db 912 ACAAGGAGATCGAGGATTTCAATGATATATTTTCGGCGGACCGCCATTGAGCCAGAGATC 971
QY 926 GCACCTTTTACCTTCAGTGAATGTTAAAGGAGAGGAGTGTTCGTACAAAGAGTTTCACATCG 985
Db 972 GCACCATTCGCAATGCTTGTCTCTGAGCAGAGATGATGGCTTTTACAAAGATTCATCTGG 1031
QY 986 TGTGAATAACAAGAGGCTCGTACACTTCAAGGCTAGCTGATGATTAAGGCTTCCCTTTTC 1045
Db 1032 TCTCAATACAAATCTTCTGCTTACAAAGTCTAAGCTTGGTGTATATAGACTTGGTCTCTTT 1091
QY 1046 CAGAAATCTGCTGCTGATTAACCAACACACCCCTTCAAAATTCACATCAT 1094
Db 1092 GAGAAACCAACCTCTTGTCAATCATAAACCCCTTGTATGAGAGTAGTGCAT 1140

RESULT 5

CNSOABSJ

LOCUS

DEFINITION

Arabidopsis thaliana Full-length cDNA Complete sequence from clone

GSLTFB7ZE01 of Hormone Treated Callus of strain col-0 of

Arabidopsis thaliana (thale cress).

ACCESSION BX816963

VERSION HTc; GSLT cDNA.

KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana

CNSOABSJ 1362 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTFB7ZE01 of Hormone Treated Callus of strain col-0 of
Arabidopsis thaliana (thale cress).

ACCESSION BX816963

VERSION HTc; GSLT cDNA.

KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana

URGV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis
 genome released by MIPS (Munich Information center for Protein
 Sequences). 5 prime and 3 prime are assembled with Phrap.
 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full
 length
 http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis.

FEATURES
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 1. .1141
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 /clone="GSLTFB20ZB08"
 /tissue_type="Flowers and buds"
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 1. .1141
 /gene="Atlg30040"

gene

ORIGIN
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 Best Local Similarity 66.1%; Pred. No. 5.4e-102;
 Matches 627; Conservative 0; Mismatches 319; Indels 3; Gaps 1;

QY 146 ATTCTGTGTCGACCTCAGCACCACCGCATGCCAAGAATCTCATAGTGAACCGCTGTAGG 205
 DB 165 ATCCCGTCGTCAACCTAGCCGATCGGAAGCGMAAACCCGAATCGTAAAGCGCTGCGAG 224
 QY 206 GACTTCGGCTTCTTCAAGCTTGTGAACCAATGTTTCCATTTGAGTTAATGCCAATTTA 265
 DB 225 GAGTTTCGGGTTCTTCAAGTCGTAAACCAACCGAGTCCGACCGAATCATGACTCGGTTA 284
 QY 266 GAAACGAGCGCCTCAGGTTCTTTAAAAAATCTCAGTCGAGAAACACAGAGCTGTGCC 325
 DB 285 GAGCAGAGGCTAATGCTCTTTCGGCTTTCGCTCAGTCTCTTAAACCGCGCGGTCCA 344
 QY 326 CCCGACCTTTTCGGCTATGTAGCAAGAGAGATTGGCCCAACCGTGTGATGTCGGTTGGGTC 385
 DB 345 CTTGAACCGTACGGTTATGTTAATAAACGATTTGGACCAACCGTGACGTTGTTGGATT 404
 QY 386 GAATACCTCTCTCAACACCAACCTGATGTTATCTCACCACATCACTTTGCAATTTTC 445
 DB 405 GAGTATCTCTCTCAATGCTAATCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 464
 QY 446 CGAGAAATCTCTCATATTTAGGGGGTGTGGAGAACTACATACAGCAGTGAAGAAC 505
 DB 465 CGTCAACCCCTCAATTTTCGTGAGTCGTGGAGAGTACATGAGAGATTAGGAA 524
 QY 506 ATGTGCTATGCGGTGTGGAATTTGATGGCGGAGGGTTGGGGATAGGAGGAGGATACG 565
 DB 525 GTGTCTACAGGTGTGGAGATGGTTGCCGAAGAACTAGGGATAGAGCAAGGACACT 584
 QY 566 TTAAGCAGGTTGCTGAAGATGAGAAAGTATGTTGCTTCAAGTTGACCACTACCCG 625
 DB 585 CTGAGTAAATGCTGAGATGAGAGAGTGAATCTGTCGCTGAGACTAAACCACTATTCG 644
 QY 626 CTTGCGCTGAGTGAAGCACTGAACCGGAATTTTGTGGTTCGGGAGACACAGAC 685
 DB 645 GCG---GCGGAGAGAGCGGAGAGATGTTGAGGTGGGTTTGGGAAACACAGAC 701
 QY 686 CCACAGATAATTTCTGCTTAAGATCTAACAGCACAATCTGGCTTGCAAAATCTGTCTACA 745
 DB 702 CCACAGATAATCTCAGTGTAGATCTAATAACACGCGGGTCTTCAATCTGTGTGAA 761
 QY 746 GATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTTTTTCATCAATGTTGTGAC 805
 DB 762 GATGGAAGTTGGTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 821
 QY 806 GCTCTACAGTAAATGATGAGGAGTTTAAAGGTAAAGCATAGGGTTTGGCTGAC 865
 DB 822 GCTCTTCAGGTTATGACTACGGGAGGTTCAAGAGTGTAAACACAGGCTCTTAGCCGAT 881
 QY 866 ACAACGAAGTCAAGGTTATCAATGATCTACTTTTGGAGGACCGGTTGATGAAATATA 925

882 ACAAGGAGATCGAGGATTTCAATGATATATTTCGGCGGACCGCATTTGAGCCAGAGATC 941
 QY 926 GCACCTTTTACCTTCACTGATGTTTAAAGGAGAGGAGTGTTCGTACAAAGAGTTTCATCG 985
 DB 942 GCACCATTCGCCATGCTTGTCTCCCTGAGCAGAGATGATGCTTTTACAAAGATTCATCG 1001
 QY 986 TGTGAATCAAGAGAGGTCGCTACACTTCAAGGCTAGCTGATAATAGGCTTCCCTTC 1045
 DB 1002 TCTCAATACAAATCTTCTGCTTACAAGTCTAAGCTTGGTGAATATAGACTTGGTCTCT 1061
 QY 1046 CAGAAATCTGCTGCTGATTAACCAACACACACCTTCAAAATTCACATCAT 1094
 DB 1062 GAGAAACCAACCTCTTCTCAATCATAAACCTTGTATGAAGTAGTCAT 1110

RESULT 7
 CNSOABKL 1363 bp mRNA linear HTC 06-FEB-2004
 LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
 DEFINITION GSLTPGH20ZC07 of Hormone Treated Callus of strain col-0 of
 Arabidopsis thaliana (thale cress).
 ACCESSION BX815974.1 GI:42471555
 VERSION HTC; GSLT_cDNA.
 KEYWORDS Arabidopsis thaliana (thale cress)
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 REFERENCE 1 (bases 1 to 1363)
 AUTHORS Castelli, V., Aury, J.M., Jallion, O., Wincker, P., Clepet, C.,
 Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
 Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
 TITLE Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:
 A Combined Approach to Evaluate and Improve Arabidopsis Genome
 Annotation
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1363)
 AUTHORS Genoscope.
 JOURNAL Direct Submission
 TITLE Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT The sequences are based on single pass reads.
 Life Technologies (a division of Invitrogen) members carried out
 full-length libraries construction : Temple G.
 Genoscope members carried out sequencing and annotation : Castelli
 V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C.,
 Schachter V., Weissenbach J., Salanoubat M.
 URGV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis
 genome released by MIPS (Munich Information center for Protein
 Sequences). 5 prime and 3 prime are assembled with Phrap.
 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full
 length
 http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis.

FEATURES
 source
 1. .1363
 /organism="Arabidopsis thaliana"
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 /db_xref="taxon:3702"
 /clone="GSLTPGH20ZC07"
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 /ecotype="Col-0"
 /plasmid="pCMVSPORT_6"
 1. .1363
 /gene="Atlg30040"

gene

ORIGIN
 Query Match 31.7%; Score 417.8; DB 4; Length 1363;
 Best Local Similarity 65.0%; Pred. No. 1.1e-100;
 Matches 624; Conservative 0; Mismatches 322; Indels 3; Gaps 1;

[illegible]

RESULT 8	CNS0AC3R	1339 bp	mrna	linear	HTC 06-FEB-2004
LOCUS	CNS0AC3R				
DEFINITION	Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB702F11 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).				
ACCESSION	BX814383				

Db 493 CGTCAAAACCCCTCAAAATTTTCCTGAGTCCGTGGAGAGGTACATGAAGAGAGATTAAAGAA 552

QY 506 ATGTGCTATGCGGTGTGGAATGATGCGGAGCGGTTCGGGATAGGACAGAGGAATACG 565

Db 553 GTGTCTGTACAGGTGTGGAGATGGTTCCGAAGAACTAGGATAGAGCAAGGGACACT 612

QY 566 TTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTCGTGCTTCAGGTTGAACCACTACCCG 625

Db 613 CTGAGTAAATGCTGAGAGATGAGAAGAGTACTGCTGCTGAGACTAAACCACTATCCG 672

QY 626 CTTGGCCCTGAGTGAAGACTGAACCGGAATTTGGTTGGGTTTGGGAGACACAGAC 685

Db 673 GC---GCGGAGGAGAGCGGAGAGATGGTGAAGTGGGGTTTGGGGAACACACAGAC 729

QY 686 CCACAGATATTTCTGCTTAAGATCTAACAGCACACTCGGCTTGCAAAATCTGCTCACA 745

Db 730 CCACAGATATCTCAGTGTAGATCTAATAACACGCGGGTCTTCAAAATCTGTGTGAA 789

QY 746 GATGGCACTTGGGTTTCAGTCCACCTGATCAGACTTCTCTTTTCATCAATGTTGGTGAC 805

Db 790 GATGGAAGTTGGTCTGCTGCTCCTCTGATCACTCTTCTTCTTCAATGTTGGAGAT 849

QY 806 GCTCTACAGTAATGACTAATGGAGGTTTAAAGTGTAAAGATAGGGTTTGGCTGAC 865

Db 850 GCTCTTCAGGTTATGACTAAACGGGAGGTTCAAGAGTGTAAACACACAGGGTCTTAGCCGAT 909

QY 866 ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCGCTTGAGTGAATAATA 925

Db 910 ACAGGAGATCGAGGATTTCAATGATATATTTTCGGCGGACCGCAATGAGCAGAAGATC 969

QY 926 GCACCTTTTACCTT---CAGTGTATGTTAAAGAGGAGGAGTGTGTTGTACAAAGATTTCACA 982

Db 970 GCACCAATTGCCATTGCTTGTCCCTGAGCAAGATGATTTGTGCTTTACAAAGATTCACT 1029

QY 983 TGGTGTGAATACAAAGAGCGTGGTACA 1010

Db 1030 TGGTCTCAATACAAATCTTCTGCTTACA 1057

RESULT 9

BE802903

LOCUS

DEFINITION

sr46c09.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1051-1097 5' similar to TR:064692 O64692 PUTATIVE GA4 PROTEIN.

! mRNA sequence.

ACCESSION

BE802903

VERSION

BE802903.1 GI:10234015

KEYWORDS

EST.

SOURCE

Glycine max (soybean)

ORGANISM

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE

1 (bases 1 to 612)

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corvett, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, J., Person, B., Swaller, T., Gibbons, M., Pope, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

CONTACT: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD

57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)

High quality sequence stop: 413.

Location/Qualifiers

1..612

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Corolla"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1051-1097"

/tissue_type="floral meristematic mRNA"

/lab_host="DH10B"

/clone_lib="Gm-c1051"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from floral meristematic mRNA provided by Dr. Halina Knap of Clemson University. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dI) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN

Query Match 28.7%; Score 378.6; DB 2; Length 612;

Best Local Similarity 88.4%; Pred. No. 3.2e-90;

Matches 411; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 65 ACCATGGTTGTTCTGTCTCAGCCAGCATTTGAACCAAGTTTTTCTCTCTGAAACCAATTCAG 124

Db 148 ACCATGGTTGTTCTGTCTCAGCCAGCATTTAAACCAAGTTTTTCTCTCTGAAACCAATTCAG 207

QY 125 TCACGCCCTTGTTCACGGGGATTCCTGTGGTGCACCTCAGCACCCCATGCGAAGAT 184

Db 208 CCCACGCCCTTGTTCGGGGGATTCCTGTGGTGCACCTCAGCACCCCATGCGAAGAT 267

QY 185 CTCATAGTGAACGCGCTGTAGGACTTCGGGCTTCTTCAAGCTTGTGAACCAATTCAGTTC 244

Db 268 CACATAGTCATGCTGTGAGGACTTCGGGCTTCTTCAAGCTGTGACCAAGGATTCG 327

QY 245 TTGGAGTTAATGCGCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCC 304

Db 328 TTACAGTTTCATGCGCAATTTGGAAAAGAAACCCCTCGGGTTCTTCAAAAAACCTCAATCC 387

QY 305 GAGAAAGACAGAGCTGGTCCCGGACCTTCGGCTATGGTAGCAGAGGATTCGCCCA 364

Db 388 GAGAAAGACAGAGCTGGTCCCGGACCTTCGGCTATGGTAGCAGAGGATTCGCCCT 447

QY 365 AACGGTGTGTCGGTTGGGTGCAATACCTCCTCCTCAACACCAACCTCATGTTATCTCA 424

Db 448 AACGGGATGTCGGTTGGGTGCAATACCTCCTCCTCAACACCAACCTCATGTTATCTCC 507

QY 425 CCCAAATCACTTTGCAATTTCCGAGAAAAATCCTCATATTTCAGGCGGTTGGGAGAAC 484

Db 508 CCCAAGTCACAGTTCATTTTCAGAGAACTCTCAGAAATTTTCATGGCGGTGGGAGGAA 567

QY 485 TCATTACAGCAGTGAAGACATGCTATGCGGTGTTGGAATTG 529

Db 568 TACATTAGAGCGGTGAACACATGTGCTATGACGTGGTGGAAATTG 612

RESULT 10

AJ803092

LOCUS

DEFINITION

AJ803092 Antirrhinum majus whole plant Antirrhinum majus cDNA clone O18 5.05 o18, mRNA sequence.

ACCESSION

AJ803092

VERSION

AJ803092.1 GI:51118420

KEYWORDS

EST.

SOURCE

Antirrhinum majus (snapdragon)

ORGANISM

Antirrhinum majus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Lamiales; Plantaginaceae; Antirrhineae; Antirrhinum.

1 (bases 1 to 785)

Bey M., Stueber K., Fellenberg K., Schwarz-Sommer Z., Sommer H.,

Saedler H. and Zachgo S.

Characterization of Antirrhinum Petal Development and

Identification of Target Genes of the Class B MADS Box Gene

DEFICIENS

Plant Cell 16 (12), 3197-3215 (2004)

15539471

Contact: Schwarz-Sommer Z

Molekulare Pflanzengenetik

MPI fuer Zuechtungsforschung

Carl-von-Linne Weg 10, D-50829, Germany.

Location/Qualifiers

1..785

/organism="Antirrhinum majus"

/mol_type="mRNA"

/db_xref="taxon:4151"

/clone="018.5.05.018"

/tissue_type="whole plant"

/clone_lib="Antirrhinum majus whole plant"

ORIGIN

Query Match 27.0%; Score 355.8; DB 1; Length 785;

Best Local Similarity 68.4%; Pred. No. 4.5e-84;

Matches 508; Conservative 0; Mismatches 232; Indels 3; Gaps 1;

QY 302 TCCGAAAGACAGAGCTGGTCCCCGACCCCTTCGGCTATGGTAGCAAGAGGATTGGC 361

DB 20 TCTGAAAGGAGAAACAGGGACCCCTGACCCCTTTTGGCTATGGAATGAATAATTGA 79

QY 362 CCAGAGGTGATCGGTGGTCCGAATACCTCCCTCAACCAACCACTCATCTATC 421

DB 80 CCAATGGCGATGGGATGGGTGGAATACCTTGTCTTAACCACTAAATCTGATCTCAT 139

QY 422 TCACCAAAATCACTTTGCAATTTCCGAGAAAATCTCTCATCACTTCAGGCGGTGGAG 481

DB 140 TACAGAAATTTGCATCGTTTGGTGAAGCTGCAGAAATTCAGGTGATATGAT 199

QY 482 AACTACATPACAGCTGGAAGAACATGCTATGCGGTGTTGGAATGATGCGAGGG 541

DB 200 GATTATGTTCTCGAGTAAAGAAATGGCGTGTGAGATCTTGAATGTTGCTGATGAA 259

QY 542 TTGGGATPAGCAGAGGATACGTTAAGCAGGTTGCTGAAGCATGAGAAAGTATCG 601

DB 260 CTTAAGATTCAACAAGGAAACGCTTTAGCAAACTTTTAATGGATGAACAGAGTGACTCT 319

QY 602 TCGTTTCAGTTCAACCACTACCGCTTCGCCCTGAGGTGCAAGCACTGAACCGGAATTG 661

DB 320 GTTTTCAGCTAAATCACTATCCACATGCCCGAATTTCAAGATCCAC---ACTTA 376

QY 662 GTTGGTTTGGGAGCACAAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACA 721

DB 377 ATCGGTTTGGTGAACATACTACCGCAAAATAATATCGTTTGTAGATCCAAACACT 436

QY 722 TCTGGCTTCAAAATCTGTCTCAGATGCCACTTGGGTTTCAGTCCACCTGATCAGACT 781

DB 437 TCGGGTCTTCAAAATTTGTTGAAGATGGGAATTTGGAATTTCTATCCCACTGATCAAA 496

QY 782 TCCCTTTTCATCAATGTTGGTCAAGCTCTACAGGTAAATGCAATGGGAGGTTTAAAGT 841

DB 497 TCTTTCTTCAATATGTTGGTCACTACGAGGTATGCAATGGCAGGTTTAAAGT 556

QY 842 GTAAGCATAGGGTTTGGCTGACACCAAGAGTCAAGGTATCAATGATCTACTTTTGA 901

DB 557 GTAAGCAGAGGGTGTGGCCACAGCTCAAAACCAAGACTTTCAATGATATATTTTGA 616

QY 902 GGACGAGCGTTGAGTGAATAATAGCACCTTTACCTTTCAGTATGTTTAAAGGAGGAG 961

DB 617 GGACCAACCAATTAAGTGAAAGATAGTCTCCATTTGCCTTTCAGTACTAATGAAGGAGAGAC 676

QY 962 TGTGTGTAACAAGAGTTCCATGTTGTAATACAAGAGGTCGCTACACTTCAAGGCTA 1021

DB 677 AGCTTGTACAAGGAATTTACTTGGTTTGAGTACAAAAAATCTGTTATATAATCAAGGCTGG 736

QY 1022 GCTGATATAGCTTGGCCCTTT 1044

DB 737 GCTGATATAGTGGTCTGTT 759

RESULT 11

CNSOADM

LOCUS

DEFINITION

Arabidopsis thaliana Full-length cDNA Complete sequence from clone

GSUTFB56ZG10 of Flowers and buds of strain col-0 of Arabidopsis

thaliana (thale cress).

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

Castelli V., Aury J.M., Jaillon O., Wincker P., Clepet C.,

Menard M., Cruaud C., Quetier F., Scarpelli C., Schachter V.,

Temple G., Caboche M., Weissenbach J. and Salanoubat M.

Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome

Annotation

Unpublished

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : segre@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out

full-length libraries construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli

V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,

URV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis

genome released by MIPS (Munich Information center for Protein

Sequences). 5 prime and 3 prime are assembled with Phrap.

length

http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

FEATURES

source

1..1128

/organism="Arabidopsis thaliana"

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/db_xref="taxon:3702"

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/tissue_type="Flowers and buds"

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/plasmid="pCMVSPORT 6"

complement(1..1128)

/gene="At1g78440"

ORIGIN

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Best Local Similarity 62.7%; Pred. No. 4.2e-82;

Matches 581; Conservative 0; Mismatches 334; Indels 12; Gaps 2;

QY 132 CCTTCTTCCAGGGATTCTCTGTTGTCGACCTCACCCCGATCCAGAAATCTCATAG 191

DB 84 CCGGGTCTCTCTAATCCCGTTATAGATATGTCGACCCAGAAATCCAAACATGCCCTCG 143

QY 192 TGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTGGAGT 251

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Db 144 TGAAGAGTCGGAAGACTTCGGCTCTCAAGGTGATCAACCATGCGCTTTCGCGAGAGC 203
QY 252 TAAATGCCAATTATAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCGAGAAAG 311
Db 204 TAGTCTCTCTTTTAAACAACGGAACGTCGATTTCTCTCGTTGCCAGCTCAGAAAAA 263
QY 312 ACAGAGCTGGTCCCGCCGACCTTTTCGGCTATGTTAGCAAGAGGATTTGGCCCAAGGGT 371
Db 264 CCAAGTCG---CAGGTTATCCCTTCGGATACGGACAGTAGATGTTGTCGGAATGGTG 320
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Db 321 ACGTGGTTGGGTGAGTACTTGTGATGAACGCTAATCATGATTCGGTTCGGGTCCAC 380
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QY 492 CAGCAGTGAAGAACATGCTATGCGGTCTTGAATTTGATGGCGAGGGGTTGGGGATAA 551
Db 441 CATCAGTGAGAAAATGCAATTCGATGTTTGGAGAGATCACAGATGGGCTAGGGATCA 500
QY 552 GGCAGAGGAATAGTTTAAGCAGAGTTGCTGAAGGATGAGAAAAGTGAATGCTGCTTCAGGT 611
Db 501 AACCGAGGAACACACTTAGCAAGCTGTATCTGACCAAAACACGAGTCTGATTTGAGAC 560
QY 612 TGAACCACTACCGGCTTCGCTGAGGTGCAAGCACTGAAC-----CGGAATTTGG 662
Db 561 TTAATCACTATCCACCATGCTCTTAGCAATTAAGAAAACCAATGGTGTGAAGAATGCA 620
QY 663 TTGGGTTTCGGGAGCACAGACCCACAGATAATTTCTCTTAAGATCTTAACAGCAGAT 722
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QY 723 CTGGCTTGCAAAATCTGCTCACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTT 782
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QY 783 CTTTTCATCAATGTTGGTGAAGCTCTACAGTAATGATCTAATGGAGGTTTAAAGTG 842
Db 741 CTTCTCTTCAACGTTGGTGAAGCTCTCCAGGTGATGACAAATGGGAGGTTCAAGAGCG 800
QY 843 TAAAGCATAGGTTTGGCTGACACAAAGAGTCAAGGTTATCAATGATCTACTTTGGAG 902
Db 801 TGAGGCATAGGTTTGGTCTCACTGTAAGAAATCTAGGGTTTCTATCAITTTACTTCGCTG 860
QY 903 GACCAGCTTGAGTGAATAATATAGCACTTTTACCTTCAGTGATGTTTAAAGGAGAGGAGT 962
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QY 963 GTTTGTACAAAGTTTCATGATGTTGAATATACAGAAAGGCTGGTACATCTCAAGGCTAG 1022
Db 921 GGTGTGACAGGAGTTTACTTGGTCTGAATACAAAACCTTACCTACAACCTCTAGATTGT 980
QY 1023 CTCATATAGGCTTGCCCTTTCCACA 1049
Db 981 CTGATAATAGGCTTCAACAATTCCGAAA 1007
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RESULT 12
BM893076
LOCUS
DEFINITION
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  samslf05.y1 Gm-c1069 Glycine max cDNA clone SOYBEAN CLONE ID:
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  sequence.
ACCESSION
  BM893076
VERSION
  BM893076.1 GI:19348544
KEYWORDS
  EST.
SOURCE
  Glycine max (soybean)
  Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 567)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stop: 435.
Location/Qualifiers
1. 567
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/tissue="SOYBEAN CLONE ID: Gm-c1069-2961"
/clone_type="Degenerating cotyledons, 9-10 day old
etiolated seedling"
/lab_host="DH10B"
/clone_lib="Gm-c1069"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from degenerating cotyledons of 9-10 day old etiolated
seedlings for the cultivar Williams. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (GibcoBRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker."
```

ORIGIN

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Query Match 25.5%; Score 336.2; DB 3; Length 567;
Best Local Similarity 88.4%; Pred. No. 7.7e-79;
Matches 365; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 65 ACCATGGTTGTTCTGTCTCAGCCAGCATTTGAACCCAGTTTTCCTTCTGAAACCATTCAG 124
Db 154 ACAATGGTTGTTTGTCTCAGCCAGCATTTAAACCACTTTTCTTCTGAAACATCGAG 213
QY 125 TCCACGCCCTTGTTCACOGGGATTCCTGTGGTGCACCTCACGACCCCCGATGCCAAGAT 184
Db 214 CCCACGCCCTGTTCTCCGGGATTCGGTGGTGCACCTCACGACCCCCGATGCCAAGACC 273
QY 185 CTCATAGTGAACGCTGTAGGACACTTCGGCTTCTTCAAGCTTGTGACCATGGTGTCCA 244
Db 274 CACATAGTGAAGCCCTGCGAGGACTTCGGCTTCTTCAAGCTCGTGAACCAACCGGTGTCCA 333
QY 245 TTGGAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCC 304
Db 334 TTAGAGTTTCATGCCCAATTTGAAAACGAAAACCTCAGGTTCTTCAAAAACCTCAGTCC 393
QY 305 GAGAAAGACAGAGCTGGTCCCGCCCGACCTTTTGGCTATGGTAGCAAGAGGATTTGCCCA 364
Db 394 GACAAAGACAGGCTGGTCCCGCTGATCCTTTTGGCTAGCGCAGCAAGAGGATTTGCCCT 453
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FEATURES source

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QY 365 AACGGTGATGTCGGTTGGGTGGAATACCTCTCTCTCAACACCAACCCCTGATGTATCTCA 424
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Db 454 AACGGCGATGTCGGGTGGGTGGAATACCTCTCTCTCAACACCAACCCCTGACGTCTCC 513
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QY 425 CCCAATCACTTTGCAATTTCCGAGAAATCTCATCTTTGAGGCGGTGT 477
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Db 514 CCCAAGTCACAGTTCAATTTCCGAGAAAGTCCTCAGAAATTTGAGGCGGTGTGT 566
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RESULT 13
B1208568
LOCUS B1208568 694 bp mRNA linear EST 11-JUL-2001
DEFINITION EST126608 cTOS Lycopersicon esculentum cDNA clone cTOS17020 5' end,
        mRNA sequence.
ACCESSION B1208568
VERSION B1208568.1 GI:14686292
KEYWORDS EST.
SOURCE Lycopersicon esculentum (Solanum lycopersicum)
ORGANISM Lycopersicon esculentum
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
        asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 694)
AUTHORS van der Hoeven,R., Sun,H., Bezzerides,J., Cho,J., Utterback,R.,
        Roming,C. and Tanksley,S.
TITLE Generation of ESTs from Tomato Suspension Cultures
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
        Clemson University Genomics Institute
        100 Jordan Hall, Clemson, SC 29634, USA
        Email: http://www.genome.clemson.edu/orders/index.html.

FEATURES
    source
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            /cultivar="TA496, B6203"
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            /tissue_type="suspension cultures"
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            /clone_lib="cTOS"
            /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
            XhoI; Suspension cultures of L.esculentum E6203 were grown
            in Murashige and Skoog based medium, supplemented with 1%
            coconut milk (filter sterilized and added after
            autoclaving), 2% saccharose, and 1mg/ml 2,4D (pH5.8).
            Fresh medium was added every 7 days, and cultures were
            grown at 25 C, with 12hrs of light and continuous
            shaking."

ORIGIN
Query Match 25.4%; Score 335.4; DB 2; Length 694;
Best Local Similarity 69.6%; Pred. No. 1.3e-78;
Matches 485; Conservative 0; Mismatches 206; Indels 6; Gaps 2;

QY 336 TCGGCTATGCTAGCAAGAGATTGGCCCAACGGTGATGCGTGTGGGTGCAATCCTCC 395
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QY 396 TCCTCAACACCAACCTCGATGTTATCTCACCACCAATCCTTTGCAATTTCCGAGAAATC 455
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Db 61 TCCTTTCAACAAATTCGAATTCATACCAGAAATTCGATCTGATTAGGTGTCAATC 120
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QY 456 CTCATCATTTTCAGGGCGGTGGTGGAGAACTACATTCACAGAGTGAAGAACATGTGCTATG 515
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QY 516 CGGTGTTGCAATTTGATGGCGGGGGTGGGATAGGCGAGGATACGTTAAGCAGGT 575
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Db 181 AGATTCTGAAAAGTTGGCGGGAGGGATTAAGATTCAACCGAGAAATGTTTGGAGTAAGC 240
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QY 636 AGGTCAAGACACTGAA---CGGAAATTTGGTTGGGTTGGGGAGCACACAGACCCACAGA 692
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QY 693 TAAATTTCTGTCTTAAGATCTAACAGCACATCTGGCTTGCAAAATCTGTCTCAGATGGCA 752
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Db 361 TCATGTCGATTTTAAGATCCAAACACTTCCTGGTCTTCAAAATTTTACTCAAAAATGGCA 420
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QY 933 TACCTTCAGTGATGTTAAAGGAGAGGAGTGTGTTGTACAAAGAGTTCATGCTGTGAAT 992
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Db 658 ACCAAAGTCAGTTACCAAGACTAGACTAGCTGATAA 694
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RESULT 14
AL382874
LOCUS AL382874 478 bp mRNA linear EST 03-AUG-2000
DEFINITION M1BC10E02F1 M1BC Medicago truncatula cDNA clone M1BC10E02 T3, mRNA
        sequence.
ACCESSION AL382874
VERSION AL382874.1 GI:9682625
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
        rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
        Medicago.
REFERENCE 1 (bases 1 to 478)
AUTHORS Journeel,E.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O.,
        Niebel,A., Carreau,V., Chatagnier,O., Kahn,D.,
        Gianinazzi-Pearson,V. and Gamas,P.
TITLE Medicago truncatula ESTs from endomycorrhizal roots
JOURNAL Unpublished (2000)
COMMENT Contact: Genoscope
        Genoscope - Centre National de Sequencage
        2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
        Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
        Contact : Pascal Gamas and Etienne-Pascal Journeel, Laboratoire de
        Biologie Moleculaire des Relations Plantes-Microorganismes,
        CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
        Mt-est@toulouse.inra.fr Website :
        http://sequence.toulouse.inra.fr/Mtruncatula.html).
        Location/Qualifiers
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                /clone_lib="M1BC"

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/notes="Vector: pBluescript pSK; Site 1: EcoRI; Site 2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 C. before transplanting into a 1/3 Epsilone soil : 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LP48). The plants were watered every day and twice a week with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAseit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note : EST may be of fungal origin."

ORIGIN

Query Match 25.3%; Score 332.8; DB 1; Length 478;
Best Local Similarity 83.0%; Pred. No. 6.1e-78;
Matches 395; Conservative 0; Mismatches 72; Indels 9; Gaps 1;
QY 557 AGGAATACGTTAAGCAGGTTGCTGAAGGATGACAAAAGTGATTCGTGCTTCAGGTTGAAC 616
DB 3 AGAATGTTTAAGCAGGTTATTGAAGATGAGAAAGTGATTCGTTTCAAAATTAAC 62
QY 617 CACTACCCGCTTGCCTCAGGTGCAAGCA-----CTGAACCGGAATTTGGTTGG 667
DB 63 CATTACCCACCGTGCCTGAGGTGCAACAGCAGCATTTGAATGGAAGGAATTTGCTTGG 122
QY 668 TTTGGGGAGCACACAGACCCACAGATAATTTCTGCTTAAGATCTTAACAGCACATCGGC 727
DB 123 TTTGGGGAGCATACAGACCCACCAAGTCATTTCTGCTTGAGATCTAATAGCACATCAAGA 182
QY 728 TTCAAAATCTGCTCAGAGATGCACCTTGGGTTTCAAGTCCACCTCATCAGACTTCCTTT 787
DB 183 CTGCAAAATCTGCTCAGATGGAACCTTGGGTTTCAAGTCCACCTCATCAGACTTCCTTT 242
QY 788 TTCAATCAATGTTGGTGACGCTTACAGGTAATGACTAAATGGGAGGTTTAAAGTGTAAAG 847
DB 243 TTCAATCAATGTTGGTGATACCTTTCAGGTATTCAGTAAATGGTGGTAAAGTGTAAAG 302
QY 848 CATAGGTTTGGCTGACACCAAGTCAGGTTATCAATGATCTACTTTTGGAGGACCA 907
DB 303 CATAGGTTTGGCTGACACCAAAAGTCAAGGTTGTCGATGATATCTTTGGAGGACCA 362
QY 908 GCCTTCAGTGAAATATAGCACCTTTACCTTCAGTGTATGTTAAAGGAGGAGTGTTG 967
DB 363 CCCTTGAGTGAAAGATAGTGCCCTTACCTTCCTTAAATGTTAAAGAGAGAAAGTTTG 422
QY 968 TACAAAGAGTTTCATGGTGTGAATACAAAGAGCGTCGCTACACTTCAAGGCTAGC 1023
DB 423 TACAAAGAGTTTACGTTGGTGGAGTACAAAGAGCAATGTACAATTCAGGCTGGC 478

RESULT 15
DN589159
LOCUS

DEFINITION 50141.1 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
50141.5', mRNA sequence.
DN589159

ACCESSION DN589159.1 GI:61239615
VERSION
KEYWORDS
SOURCE

ORGANISM Solanum tuberosum (potato)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 893)

REFERENCE Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Lague,M., De

TITLE
JOURNAL
COMMENT

Koeber,D., Audy,P., Goyer,C., Li,X.-Q., Wang-Pruski,G. and Regan,S.
Generation of ESTs from late blight-challenged potato tubers
Unpublished (2005)
Contact: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflinn@biatlantech.nb.ca
Seq primer: T3.

FEATURES
source

Location/Qualifiers
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/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/clone="50141"
/tissue_type="Tubers"
/lab_host="XL10-Gold"
/note="Vector: pBluescript II SK(+); Site 1: EcoRI;
Site 2: XhoI; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were incubated 1 minute to allow inoculum
absorption. The infection area was outlined for future
collection reference. Surface slices were sampled from the
tubers at 1 day, 5 days, 7 days, 11 days and 14 days
post-infection. All samples were pooled and used for RNA
isolation and library construction. A normalized library
was constructed following a modified protocol of Bonaldo
et al. (1996. Genome Research 6: 791-806)."

ORIGIN

Query Match 25.0%; Score 329.2; DB 8; Length 893;
Best Local Similarity 67.6%; Pred. No. 6.5e-77;
Matches 495; Conservative 0; Mismatches 228; Indels 9; Gaps 2;
QY 329 GACCCCTTCGGCTATGGTAGCAGAGGATTGCCCAACCGGTGATGTCGGTTGGGTCGAA 388
DB 3 GACCCCTTCGGCTATGGTAATGAGAAATGACCTAATGGTGATGTTGGTTGGGTTGAA 62
QY 389 TACCTCTCTCAACACCAACCCCTGATGTTATCTACCCAAATCACTTTGGCAATTTCCGA 448
DB 63 TACATTTCTTTGTCAACAAATTTCTGAGTTCAATTTACCAAAATTTTGCATCTATTTGGGT 122
QY 449 GAAATCTCTCATCATTTTCAGGGCGGTGGGAGAACTACATTACAGCTGAGACATG 508
DB 123 GTCAATCCAAAAGATATAAGAGATGCTGTGAATGATTTATGTATTAGCAATGAAGAAATG 182
QY 509 TGCTATGCGGTGTTGGAATTTGATGGCGGAGGGGTTGGGATTAAGGCAGAGGAATACGTTA 568
DB 183 GCTTGAGATCTTTGAAATGTTAGCAGAGGANTTAAATTCATCCAAGAAATGTTATTT 242
QY 569 AGCAGGTTGCTGAAGGATGAGAAAAGTGTATCGTGCTTCAGGTTGAACCACTACCCGCT 628
DB 243 AGTAAGCTTTTAAATGGATGAAAAAGTATTCACTTTTATAGGCTAAATCATTTACCTCCA 302
QY 629 TGCCTCTGAGG-----TGCAAGCACTGAACCGGAATTTGGTTGGGTTTGGGGAGCACACA 682
DB 303 TGTCTCTGATGAATTTCAAGAAATATAATGGAAGAAATTTAAATTTGGATTTGGTGAACATCT 362
QY 683 GACCCACAGATAATTTCTGCTCTTAAGATCTAACAGCACATCTGGCTTGCATAATCTGCTC 742
DB 363 GATCCACAATTTATTTCTTTTATAGATCCAATAACACTCTTGGACTTCAAATTCACATT 422
QY 743 ACAGATGGCACTTGGGTTTTCAGTCCACCTGATCAGACTTCCTTTTTCATCAATGTTGGT 802
DB 423 GTTGATGGCAATTTGGATTTCTGTCCCACTGATCAAAATTTCAATTTCTTCATCAATGTTGT 482
QY 803 GAGCTCTACAGTAAATGACTAATGGAGGTTTAAAGGTTAAAGCATAGGTTTGGCT 862
DB 483 GATTCTTCAGCGTGTATGACAAATGGGAGGTTTAAAGAGTGTAAACATAGAGTTTGGCC 542

Qy	863	GACACAA	CGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCGTTGAGTGA	AAAT	922
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Qy	923	ATAGCACCTTTACCTTCAGTGATGTTAA	AGGAG---AGGAGTGT	TTGTACA	AGGTTTC 979
Db	603	ATAGCACCAATTGTCATCTATTAA	TAAAGGGGATCAAGACAGCTTTGTACA	AAAGAA	TTT 662
Qy	980	ACATGGTGTGAATACAAG	AGGCTGCCTACACTTCAAGGCTAGCTGATATAATAGGCTTGCC		1039
Db	663	ACATGGTTTGAGTACAA	AAATTCAGCATATAATCTAGATTGGCTGATATAATAGGTTGGTC		722
Qy	1040	CCTTCCAGAA			1051
Db	723	CTATTGAGAA			734

Search completed: December 28, 2005, 00:38:43
Job time : 6016.88 secs

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Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	1318	100.0	1318	3	US-09-719-108-1	Sequence 1, Appl
2	893.8	67.8	1359	3	US-09-371-307-62	Sequence 62, Appl
3	430.8	32.7	1352	3	US-09-614-912-13	Sequence 13, Appl
4	429.2	32.6	1365	3	US-09-614-912-5	Sequence 5, Appl
5	425.8	32.3	1237	3	US-09-719-108-7	Sequence 7, Appl
6	424.8	32.2	1403	3	US-09-371-307-64	Sequence 64, Appl
7	382.8	29.0	1008	3	US-09-719-108-9	Sequence 9, Appl
8	363.6	27.6	1473	3	US-09-614-912-7	Sequence 7, Appl
9	356.6	27.1	1318	3	US-09-719-108-5	Sequence 5, Appl
10	354	26.9	1650	3	US-09-614-912-3	Sequence 3, Appl
11	315.8	24.0	1555	3	US-09-614-912-1	Sequence 1, Appl
12	311	23.6	783	3	US-09-371-307-67	Sequence 67, Appl
13	166	12.6	811	3	US-09-371-307-71	Sequence 71, Appl
14	155.6	11.8	403	3	US-09-371-307-66	Sequence 66, Appl
15	154.8	11.7	406	3	US-08-371-307-68	Sequence 68, Appl
16	152.4	11.6	966	3	US-09-371-307-70	Sequence 70, Appl
17	120	9.1	426	3	US-09-371-307-58	Sequence 58, Appl
18	113.6	8.6	450	3	US-09-614-912-9	Sequence 9, Appl
19	103	7.8	210	3	US-09-719-108-3	Sequence 3, Appl
20	101	7.7	199	3	US-09-719-108-4	Sequence 4, Appl
21	80	6.1	535	3	US-09-614-912-15	Sequence 15, Appl
22	75.8	5.8	618	3	US-09-614-912-11	Sequence 11, Appl
23	72.4	5.5	723	3	US-09-371-307-56	Sequence 56, Appl
24	72.4	5.5	4170	3	US-09-371-307-57	Sequence 57, Appl

[illegible]

```

US-09-371-307-62
; Sequence 62, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: WOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Glycine max
US-09-371-307-62

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Query Match	67.8%	Score	893.8	DB 3	Length	1359
Best Local Similarity	84.9%	Pred. No.	1.5e-255			
Matches 1069	Conservative	1	Mismatches	158	Indels	31
					Gaps	5

Qy	65	ACCAATGGTTGTTCTGTCTCAGCGACGATGAAACGAGTTTTTCTCTCTGAAACCATTCACG	124
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Qy	125	TCCACGCCCTTGTTTCA CGGGGATTCCTGTGTGCACTCAGCACCCCGATGCCAAGAT	184
Db	159	CCCAAGCCCTTGTTCCGGGGATTCCTGTGTGCACTCAGCACCCCGATGCCAAGACC	218
Qy	185	CTCATAGTGAACGGCTGTGAGGACCTTGGGCTTCTTCAAGCTTGTGAAACATGGTGTTC	244
Db	219	CACATAGTCAATGCTGTGAGGACCTTGGGCTTCTTCAAGCTGTGAACACAGCGTGTCCG	278
Qy	245	TTGAGGTTAATGGCCCAATTTAGAAAAACGAGCGCCCTCAGTCTCTTTAAAAAATCTCAGTCC	304
Db	279	TTACAGTTTCATGGCCCAATTTGAAAAACGAAACCTTCGGGTCTCTTCAAAAAACCTCAATCC	338
Qy	305	GAGAAAGACAGAGCTGTGTCCTCCCGACCTTTTCGGCTATGTGAGCAAGAGGATTCGCCCA	364
Db	339	GAGAAAGACAGGGCTGTGTCCTCCCTTGACCTTTTGGCTACGGCAGCAAGAGGATTCGCCCT	398
Qy	365	AACGGTGATGTCGGTTGGGTGGAATPACCTCTCTCTCAACACCAACCCCTGATGTTATCTCA	424
Db	399	AACGGCGATGTGCGTTGGGTGGAATPACCTCTCTCTCAACACCAACCCCTGATGTTATCTCC	458
Qy	425	CCCAAAATCACTTTGCATTTTCCGAGAAAACTCTCATCATTTTCAGGCGCGTGTGAGAAC	484
Db	459	CCCAAGTCCAGTTTCATTTTCAGAGAAAGGTCTCTAGAAATTTTCAGGCGCGTGTGAGGAA	518
Qy	485	TACATTACAGCAGTGAAGAAACATGTGCTATCGGTGTTTGGAAATTCATGTCGAGAGGGTTG	544
Db	519	TACATTAGAGCGGTGAAGAAACATGTGCTATGAGGTGTTTGGAAATTCATGTCGAGGATTCG	578
Qy	545	GGGATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGGTCG	604
Db	579	GGGATAAGGCAGAGGAATGCTTGAAGTGGTGTGTAAGGATGAGAAAAGTGATTCGGTCG	638
Qy	605	TTCAGGTTTGAACCACTACCCGCCCTTGCCTCAGGTGCAAGCACTCAAC --- CGGAATTTTG	661
Db	639	TTCAGATTAACTACTACCCGCCCATGCCCGAGGTGCAAGCAATGAAACGAGGAATTTTG	698
Qy	662	GTTCGGTTTGGGAGCACAAGACCCACAGATAATTTCTGTCTTAAAGTCTTAAACAGCAACA	721
Db	699	GTTCGATTTTGAGAGCACAAGACCCACAGATAATTTCTGTCTTAAAGTCTTAAACAGCACC	758

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QY 722 TCTGGCTTCCAAATCTGTCTCAGATGCGACTTGGGTTTTCAGTCCCACTGATCAGACT 781
Db 759 TCAGGCTTCCAAATCTGTCTCAGATGCGACTTGGGTTTTCAGTCCCACTGATCAGACT 818
QY 782 TCTTTTTCATCAATGCTGGTACGCTCTACAGGTAATGACTAAATGGGAGGTTTAAAGT 841
Db 819 TCTTTTTCATCAATGCTGGTACGCTCTCTCAGGTAATGACTAAATGGGAGGTTTAAAGT 878
QY 842 GTAAGCATAGGTTTGGCTGACACCAAGCAAGTCAAGGTTATCAATGATCTACTTTTGA 901
Db 879 GTAAGCATAGGTTTGGCTGACCAAGCAAGTCAAGGTTATCAATGATCTACTTTTGA 938
QY 902 GGACGAGCTTGGTCAAAATATAGACCTTTACCTTTAGTGTATGATGATGATGAGGAG 961
Db 939 GGACCACTTGTGTGAAAGATAGCACCTTTACCTTTACCTTTACCTTTACCTTTACCTTT 998
QY 962 TGTGTTGTAAGAGATTACATGCTGTAATACAGAGGCTGCTGATCACTTTCAAGGCTA 1021
Db 999 AGTTTCTCAAGAGATTACATGCTGTAATACAGAGGCTGCTGATCACTTTCAAGGCTA 1058
QY 1022 GCTGATAATAGGTTGCTGCTTTCAGAAATCTGCTGCTGATTAACCAACACACCTTTC 1081
Db 1059 GCGGATAATAGACTCGGCTTTCAGAAATCTGCTGCTGATTAAGGAGGCAAGTGCT 1118
QY 1082 AAA-----TTCACACTTTTACGACGCTGTTATTAACCCAA-----TTTCTTTTCTTTT 1132
Db 1119 CAAATTTCTACTACTCAATTTTGGCAGCTGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1178
QY 1133 TCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1192
Db 1179 TTTTGGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1238
QY 1193 GAATAGT-----TAAGATGTTTATCATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1241
Db 1239 GAATAGTGGTTTATGCTACTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1298
QY 1242 TAAAGTGGTCTCAACTTCCCTTTCTCAATGCTCAATGCTCAATGCTCAATGCTCAATGCTCA 1300
Db 1299 TAATAGT-----CACTACTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1349
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RESULT 3

US-09-614-912-13

Sequence 13, Application US/09614912

Patent No. 6677502

GENERAL INFORMATION:

APPLICANT: Allen, Steve

APPLICANT: Rafalski, Antoni

APPLICANT: Orozco, Buddy

APPLICANT: Miao, Gou-Hau

APPLICANT: Famodu, Omolayo O.

APPLICANT: Lee, Jian Ming

APPLICANT: Sakai, Hajime

APPLICANT: Weng, Zude

APPLICANT: Caimi, Perry G

APPLICANT: Anderson, Shawn

TITLE OF INVENTION: Plant Metabolism Genes

FILE REFERENCE: B01378 US NA

CURRENT APPLICATION NUMBER: US/09/614,912

CURRENT FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: 60/143,401

PRIOR FILING DATE: 1999-07-12

PRIOR APPLICATION NUMBER: 60/143,412

PRIOR FILING DATE: 1999-07-12

PRIOR APPLICATION NUMBER: 60/146,650

PRIOR FILING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: 60/170,906

PRIOR FILING DATE: 1999-12-15

PRIOR APPLICATION NUMBER: 60/172,959

PRIOR FILING DATE: 1999-12-21

PRIOR APPLICATION NUMBER: 60/172,946

PRIOR FILING DATE: 1999-12-21

NUMBER OF SEQ ID NOS: 204

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 13

; LENGTH: 1352

; TYPE: DNA

; ORGANISM: Glycine max

US-09-614-912-13

Query Match 32.7%; Score 430.8; DB 3; Length 1352;

Best Local Similarity 65.7%; Pred. No. 1.2e-117;

Matches 665; Conservative 0; Mismatches 332; Indels 15; Gaps 2;

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QY 55 AACAAACAACCACTGGTGTCTCTCAGCCAGCAATTGAACCAAGTTTCTTCTCTCTGAA 114
Db 146 AACAAACAAGAAAATGGTGTCTCTCAAAGCAACAACAGAAACAATACTCTACATTA 205
QY 115 ACCATTCAAGTCCACGCCCTTGTTCACGGGATTCCTGTGTCGACCTCACGACCCCGA 174
Db 206 GAACTGCAATGCAACCAAAATTTCTCAACAATTCCTCATAGTGGACCTCTCCAACTGA 265
QY 175 TGCCAAAGAAATCTCATAGTGAAGCCCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGA 234
Db 266 TGCAAAAGACCTTATAGTGAAGGCTTGTGAGGATTTGGATTTCTTCAAAGTCATCA 325
QY 235 TGGTCTTCCATTTGGAGTTAATGGCCAAATTAGAAAACGAGGCCCTCAGGTTCTTAA 294
Db 326 TGGTCTTCCATTTGGAGCTATATCCGAATTTGGAATATGAAGCCTTCAAATTTCTT 385
QY 295 ATCTCAGTCCGAGAAAGACAGAGCTGGTCCCCCGACCCCTTTCGGCTATGGTAGCA 354
Db 386 GTCACTCAATGAAAGAAAGTAGGACCTCCCAATTCATTTGGGTATGGTAGCAAGAA 445
QY 355 GATTGCCCAACCGTGTATGCTGGTGGTGAATACCTCTCTCAACACCAACCTCTGA 414
Db 446 AATTGACACAAATGGGACGTTGGTGGATTTGAGTACCTTCTTCTCAACACCAATCA 505
QY 415 TGTATCTCAACCAATCACITTTGCAATTTCCGAGAAATCTCATCTTTCAGGGCGGT 474
Db 506 ACACAAC-----TCTCTGTTATGGGAAAAACCCCTGAGAAATTCAGGTGCT 553
QY 475 GGTGAGAACTACATTACAGCAGTGAAGAAATGCTGCTATGCGGTGTTGGAATTTGAT 534
Db 554 GTTGAACAGTTACATGCTCTCTGTGAGGAAGATGGCATGTGAGATTTCTTGAGTGC 613
QY 535 GGAGGGTTGGGATTAAGGACAGAGAAATACGTTAAGCAGGTTGCTGAAGATGAGAAA 594
Db 614 AGAAGGTTGAAGATTCAGCAAAAGGATGTGTTAGCAAGCTTCTAATGGAATAAAG 673
QY 595 TGATTCGTCTTCAAGTTGAACCACTACCCGCTTCCCTGAGGTGCAAGCACTGAACCG 654
Db 674 TGACTCTATTTTCAGGGTGAATTCATTACCTGCTTGTCTGAAATGACTCTGAAATGA 733
QY 655 GAATTTGGTGGTGGTGGGAGCACACAGCCACAGATAATTTCTGCTTAAAGATCTAA 714
Db 734 GAACTTGAATGGGTTTGGAGAACACACAGCCACCAATCATCTCTCTGTTAAGATCCA 793
QY 715 CAGCACATCTGGCTTCCAAATCTGTCTCAGATGGCACTTGGGTTTCAGTCCCACTGA 774
Db 794 CAACACTTCAGGCTTCCAGATTTATCTTAGAGATGGAATTTGATTTTCACTCCACCA 853
QY 775 TCAGACTCTCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAG 834
Db 854 TGACAAATCTCTTTTATTAACGTTGGTGAATTTCTCTTCAAGGTTATGACAAATGG 913
QY 835 TAAAGATGTAAAGCATAGGTTTTCGCTGACACAACAGGATCAAGGTTATCAATGATCT 894
Db 914 CCGAAGTGTGAGACACAGAGTGTGGCAATTTGGGTTTCAAGTCCAGGCTTCAATGAT 973
QY 895 CTTTGGAGGACAGCGTTGAGTGAATAATAGCACCTTTTACCTTCAGTGAATGTTAA 954
Db 974 CTTTGGAGGTCACCTTTGAGTGAGAAAATAGCACCAATTTATCTCTCTCATG---AA 1030
QY 955 AGAGGAGTGTGTTGTAACAAGAGTTCAATGTTGTAATACAAGAGGCTGCGTACACTTC 1014
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Db 1031 AAAAGAAAGTCTATATAAAGAGTTTACCTGGTTTGGAGTACAAAAAATCAATCTACGGTTC 1090
QY 1015 AAGGCTAGCTGATATAGAGTTGCCCTTTCCAGAAATCTGCTGCTGATTA 1066
Db 1091 AAGATTATCTAAAAATAGACTTTGAACATTTTGAAGAATTTGCAGCTTCGTAA 1142

RESULT 4

US-09-614-912-5
; Sequence 5, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Calimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Glycine max
US-09-614-912-5

Query Match 32.6%; Score 429.2; DB 3; Length 1365;
Best Local Similarity 65.6%; Pred. No. 3.7e-117;
Matches 664; Conservative 0; Mismatches 333; Indels 15; Gaps 2;

QY 55 AACAAACACACCATGGTTGTTCTGCTCAGCCAGCATTTGAACAGTTTCTCTGAA 114
Db 153 AACAAACAGAAAATGGTGTGTGTTCCAAAGCAACACAGAAACAATCTCTACATTA 212
QY 115 ACCATTCAAGTCCACGCCCTTGTTCAGGGGATTCCTGTGTCGACTCAAGCACCACCGA 174
Db 213 GAATGCTGATCCAAACCAATTTCTTCAACAAATCCATAGTGAGACTCTCAGAACTGA 272
QY 175 TGCAAGAAATCTCATAGTGAACGCCCTGTAGGGACTTTCGGCTTCTTCAAGCTTGTGAACCA 234
Db 273 TGCAAGAGCCCTTATAGTGAAGCTTGTGAGGAGTTTGGATTCTTCAAGTCAATCA 332
QY 235 TGGTGTTCATTTGAGTTAATGGCCAAATTTAGAAACAGAGCCCTCAGGTTCTTTAAAAA 294
Db 333 TGGTGTCTCATGGAAGCTATATCCGAAATTTGGAATATGAAGCCTTCAAAATTTCTCTAT 392
QY 295 ATCTCAGTCCGAGAAAGACAGAGCTGTCTCCCGCCCTTTCGGCTATGTAGTGAAGAG 354
Db 393 GTCACCTCAATGAAGAAAGAAAGTAGGACCTCCCAATCCATTTGGGTATGTAGCAAGAA 452
QY 355 GATTGGCCCAACAGGTTGATGTCGGTTGGGTGCGAATACCTCTCTCAACACCAACCTGA 414
Db 453 AATTGGACACAATAGGAGCGTTGGTTGGATTGAGTACCTTCTTCTCAACCAATCAAGA 512

QY 415 TGTATCTCACCCCAATCACTTTTGCATTTTCCGAGAAATCTCTCATCTTTTCAGGCGGT 474
Db 513 ACACACT-----TCTCTGTTATGCGCAAAACCCCTGAGAAATTCAGGTGCT 560
QY 475 GGTGAGAACTACATTTACAGCAGTAGTGAAGAAATGTGCTATGCGGTGTTGGAATTTGATGC 534
Db 561 GTTGAACAGTTACATGTTCTTGTGAGGAAGATGCGATGTGAGATTCTTGTAGTTGATGC 620
QY 535 GGAGGGTTGGGGATTAAGCAGAGGAATACGTTTACGAGGTTGCTGAAGGATGAGAAAG 594
Db 621 AGAAGGGTTGAAGATTCAGCAAAAGGATGTGTTAGCAAGCTTCTAAATGGATAAACAAG 680
QY 595 TGATTCTGCTTTCAGGTTGAACCACTACCCGCTTTCCTGAGGTGCAAGCAAGCACTGAACCG 654
Db 681 TGACTCTATTTTCAGGGTGAATCATTTACCTGCTGTCTCTGAAATGACTCTCAATGATCA 740
QY 655 GAATTTGGTTGGGTTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAAGATCTAA 714
Db 741 GAATTTGATTGGGTTTGGAGAACACACAGACCCACAAATCATCTCTCTTAAAGATCCAA 800
QY 715 CAGCAGATCTGGCTTGCATAATCTGCTCAGATGCGACTTGGGTTTTCAGTCCACCTGA 774
Db 801 CAACACTTCAGGCTTTCAGATTATCTTAGAGATGGAAATTCGATTTTCAGTCCACCGA 860
QY 775 TCAGACTTCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAAATGGGAGGTT 834
Db 861 TGACAAATCCTTTTATTAACGTTGGTGATTTCTCTTCAAGTTATGACAAATGGGAGGTT 920
QY 835 TAAAAGTGTAAAGCATAGGTTTGGCTGACACAAAGAGTCAAGGTTTCAATGATCTA 894
Db 921 CCGAAGTGTGACACACAGAGTGTGCAAAATGGTTTCAAGTCCAGGCTTTCATGATTTA 980
QY 895 CTTTGAGGACACAGGTTGAGTGAATAATATAGCACTTTACCTTTCAGTGTATGTTAAAG 954
Db 981 CTTTGAGGTCACCTTTTGAGTGAGAAAAATAGCACCATTATCTCTCTCATG---AAAGG 1037
QY 955 AGAGGAGTGTGTTACAAAGAGTTACATGTTGTGAATACAAAGAGGTCGCTGATCTTTC 1014
Db 1038 AAAAGAAAGTCTATATAAAGAGTTTACCTGGTTTGGAGTACAAAAAATCAATCTACGGTTC 1097
QY 1015 AAGGCTAGCTGATATAATAGGCTTGGCCCTTTCCAGAAATCTGCTGCTGATTA 1066
Db 1098 AGATTATCTAAAAATAGACTTTGAACATTTTGAAGAAATTCGAGCTTCGTAA 1149

RESULT 5

US-09-719-108-7
; Sequence 7, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/09/719,108
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-719-108-7

Query Match

32.3%; Score 425.8; DB 3; Length 1237;

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Best Local Similarity 66.3%; Pred. No. 3.6e-116;
Matches 629; Conservative 0; Mismatches 317; Indels 3; Gaps 1;

QY 146 ATTCTGTGTGCTGACCTCAAGCAGCCGATGCAAGAAATCTCATAGTGAACCCCTGTAGG 205
Db 199 ATCCCGCTGCTCAACTAGCCGATCGGAGCGAAACCCGATCGTAAGCCCTGCGAG 258
QY 206 GATCTCGGCTTCTCAAGCTTGTGAACCATGGTGTTCATTTGAGTTAATGAGCCCAATTA 265
Db 259 GAGTTTCGGGTTCTTCAAGGTCGTAACCAACGAGTCCGACCCGAACTCATGACTCGGTTA 318
QY 266 GAAACGAGGCGCTCAGGTTCTTTAAATAATCTCAGTCCGAGAAAGACAGAGCTGGTCC 325
Db 319 GAGCAGGAGGCTATTTGGCTTCTTCGGCTTCCTCAGTCTCTTAAATAACCGGCGCGTCCA 378
QY 326 CCGGACCCCTTTCGGCTATGATGAGCAAGAGATTTGGCCAAACGGTGTGCTGGTGGGTC 385
Db 379 CTGAAACCGTACGGTTATGTTAATAACCGATTTGACCAACGGTGTGCTGGTGGAT 438
QY 386 GAATACCTCTCTCAACACCAACCCCTGATTTATCTCAACCAATCACTTTGCAATTTTC 445
Db 439 GAGTATCTCTCTCAATGCTAATCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 498
QY 446 CGAGAAATCTCATATTTCAAGGCGGTGGTGGAGAACTACATTTACAGCAGTGAAGAC 505
Db 499 CGTCAACCCCTCAAAATTTCCGTGAGTCGGTGGAGAGTACATGAAGGAGATTAAAGAA 558
QY 506 ATGTGCTATGCGGTGTGGAAATTTGATGGCGGAGGGTGGGGAATAAGGCAGAGGAATACG 565
Db 559 GTGTGCTACAGGTGTGGAGATGTTGCCGAAGAACTAGGATAGAGCAAGGAGCACT 618
QY 566 TTAAGCAGGTTGCTGAAGGATGAGAAAGTGTGCTGCTCAGGTTGAACACACTACCG 625
Db 619 CTGAGTAAATCTCAGAGATGAGAAGAGTGTGCTGCTGAGACTAAACCATTTATCG 678
QY 626 CTTGCGCTGAGTGAAGCACTGAACCGGAATTTGGTGGTGGTGGGAGGACACAGAC 685
Db 679 GCG---GGGAGGAGAGGCGGAGAAGAATGGTGAAGGTGGGGTGGGGAACACACAGAC 735
QY 686 CCACAGATAATTTCTGCTTAAGATCTACACACATCTGGCTGCAATCTGCTCTACA 745
Db 736 CCACAGATAATCTCAGTGTGAAGATCTAATAACCGCGGCTCTCAATCTGTGTGAA 795
QY 746 GATGCGACTTGGGTTTCAGTCCCACTGATCAGACTTCTTTTTCATCAATGTTGGTGAC 805
Db 796 GATGGAAGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 855
QY 806 GCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAAGCTAAGCATAGGTTTGGCTGAC 865
Db 856 GCTCTTCAAGTTATGACTAAACGGGAGGTTCAAGAGGTGTTAAACACAGGGTCTTAGCCGAT 915
QY 866 ACAACGAGTCAAGGTTATCAATGATCTACTTTGGAGGACAGCGTTGAGTGAAATATA 925
Db 916 ACAGAGATCAAGGATTTCAATGATATAATTTCCGGGAGCCGCTTAGGCGAGAGATC 975
QY 926 GCACCTTTACCTTCAAGTGTAAAGAGGAGGAGTGTGTTGACAAAGAGTTCACTAGG 985
Db 976 GCACCATTTGCCATGCTTCTGCTGAGCAAGATGATGGCTTTTACAAAGAAATCACTTGG 1035
QY 986 TGTGAATCAAGAGGCTGCGTACACTTCAAGGCTAGCTGATTAAGCTTGGCTTCCCGCTTC 1045
Db 1036 TCTCAATACAAATCTTCTGCTTCAAGTCTAAGCTTGGTGTATATAGACTTGGTCTCTTT 1095
QY 1046 CAGAAATCTGCTGCTGATTAACCAACACACACCCCTCAATTCACATCCAT 1094
Db 1096 GAGAAACAACTCTTCTCAATCATAAACCCCTTGTATGAGAGTAGTGCAT 1144

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RESULT 6

US-09-371-307-64
; Sequence 64, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:

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; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Pillier, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Rao, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: M08T:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Glycine max
; US-09-371-307-64

Query Match      32.2%; Score 424.8; DB 3; Length 1403;
Best Local Similarity 66.0%; Pred. No. 7.7e-116;
Matches 569; Conservative 0; Mismatches 327; Indels 18; Gaps 3;

QY 53 ACAACAACAACAACATGGTTGTTCTGTCTCAGCCAGCATTTGAACAGTTTTCCTCTG 112
Db 134 AAAGCAGCAGAGAAATGGTGTGCTGTCGAAGGCAACAACAGAAACAATACTCTACATC 193
QY 113 AAACCATTCAGTCCAGCCCTTGTTCACGGGGATTCCTGTGTCAGCTCAGCACCCC 172
Db 194 AAGAACTACATGCCAACGGCAATTCCTCAACAAATTCCTGAGTGGAGCTCTCCAAACCA 253
QY 173 GATGCAAGAAATCTCATAGTGAACCGCTGTAGGGAGCTTCGGCTTCTCAAGCTTGTGAAC 232
Db 254 GATGCAAGACCTCATAGTGAAGGCTTGTGAGNAATTTGAGTCTTCAAGTCAATCAAC 313
QY 233 CATGTTGTTCCATTTGGAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAA 292
Db 314 CATGTTGTTCCATTTGGAAATATATCCCAAATTTGGAATCTGAAGCCCTCAAGTCTTCTCT 373
QY 293 AAATCTCAGTCGAGAAAGACAGAGCTGGTCCCCCGAGCCCTTCGGCTATGTTAGTAGCA 352
Db 374 ATGCCACTCAATGAGAGGAAAGATAGGCCCTCCCAACCATATGGGTATGTTAGTAGCAAG 433
QY 353 AGGATTTGCCCAACCGGTGATGTCGGTTGGGTGCGAATACCTCCTCAACACCAACCCCT 412
Db 434 AAATTTGACACAAATGGGGATGTTGGTTGGTTGAGTACCTTCTTCTCAACACCAATCAA 493
QY 413 GATGTTATCTCAACCCAAATCACTTTTGCAATTTTCCGAGAAAATTCCTCATCATTTTCAGGGCG 472
Db 494 GAACACAACT-----TCTCTGTTTATGGCAAAAACGCTGAGAAAATTTAGGTGT 541
QY 473 GTGGTGGAGAACTACATTTACAGCAGTGAAGACATGCTGCTATGCGGTGTTGGAATGTAG 532
Db 542 TTGTTGAACAGTTACATGCTTCTTGTGAGGAAAATGGCAATGTGAGATTTCTTGAGCTGATG 601
QY 533 GCGGAGGGGTTGGGATTAAGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAA 592
Db 602 GCAGAGAGATTTGAGATACAAAAAATGTTTATGAGAGCTTCTTATGATTAAGAG 661
QY 593 AGTGAATTCGTGCTCAGGTTGAACCACTACCGCCCTTCCTCCCTGAGGTGCAAGCACTGAAC 652
Db 662 AGTGACTCTGTTTTTAGGGTGAATCACTACCTGCTTCCCTGAACTT---GTGAATGCT 718
QY 653 CGGAATTTGGTGGGTTGGGGAGCACAAGACCCCAAGATAATTTCTGTCTTAAGATCT 712
Db 719 CAAACATGATAGGGTTGGGAGAACACACGAGCCCAACAAATCAATTTCTTACTTAGGTCC 778
QY 713 AACAGCACATCTGGCTTCAAAATCTGCTCAAGATGACACTTGGGTTTTCAGTCCACCT 772
Db 779 AACAACTTTCAGGCCCTTCAAGATTTTCTTAGAGATGGAATCTGGAATTCAGTCCACCT 838

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; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 1473
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-614-912-7

Query Match      27.6%; Score 363.6; DB 3; Length 1473;
Best Local Similarity 61.3%; Pred. No. 1.4e-97;
Matches 607; Conservative 0; Mismatches 374; Indels 9; Gaps 1;

QY 60 CAACACCAATGGTGTGTTCTCTCAGCCAGCAATGAAACCAAGTTTTTCTTCTTGAACCAAT 119
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Db 119 CAGCCATGTTGTTCTCGCCAGCACGCCCGCTCGATCACATCCGCTCTCAGTCGC 178

QY 120 TCAAGTCCAGCCGCTTGTTCAGGGGATTCCTGTGTGTCAGCTCAGCACCCCGGATGCCA 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 CCGACCCCGGGACTACTTCTCGGCATCGCGTGTGTCAGCTCTCCAGCCCTGGCGGC 238

QY 180 AGAATCTCATAGTAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTG 239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 239 CGGGGCCATCGCCGACGGTGGAGCGCTTCGGGTCTTCAAGCTGTGCAACACGGGG 298

QY 240 TTCCATTGGAGTTAATGGCCAAATTTAGAAAAAGAGCCCTCAGGTTCTTTAAAAAATCTC 299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 299 TGCCCGCGACGATGGACAGCTCGAGTCGGAGGCCGTCAAGTTCTTCTCGCTGCCG 358

QY 300 AGTCGAGAAAGACAGAGCTGTGTCGCCCGACCCCTTTCGGCTATGTTAGCAAGAGATTG 359
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 359 AGCGCCGACAGACCCCTCCGGCCCGGCCCTACCCGTTCCGCTACGGCAGCAAGCGCATG 418

QY 360 GCCCAACGCTGATGTCGGTGGTGGATACCTCTCTCAACACCAACCCCTGATGTTA 419
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 419 GGTCAATGGACATGGGGTGCTCGAGTACTCTCTCTGGCGTGGACTCGCGTCCG 478

QY 420 TCTCAACCAATACACTTTGTCATTTTCCGAGAAAAATCCTCATCATTTTCAGGGGGTGGTG 479
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 479 TCTCCGGCGCTCGCGCGTCCGCTCTCGG-----CGTCTTCCGGCGCGCTCA 529

QY 480 AGAATACATTCAGCAGTGAAGAACATGTGCTATCGCGTGTGGATGTGTCGGGAGG 539
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 530 ACGAGTACATCGCGCGTGCAGAGTGGCGGTGCGGTGATGAGGCGATGCGCGAGG 589

QY 540 GGTGGGATAGGCAGAGATACGTTAAGCAGGTTCTGAGGATGAGAAAGTATT 599
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 590 GGTGGGATAGGCAGAGATACGTTAAGCAGGTTCTGAGGATGAGAAAGTATT 649

QY 600 CGTGTCTCAGGTTGAACCACTACCCGCTTGCCTGAGGTGCAAGCACTGAACCCGGAATT 659
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 650 AGTGTTCGGGTGAACCACTACCCGCTGCAACGCGCTGCAGGGCTGGGTCAGGG 709

QY 660 TGGTTCGGTTTGGGAGCACAAGACCCACAGATAATTTCTGCTTAAAGATCTAACAGCA 719
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 710 CCACCGGCTTCGGGAGCACAAGACCCGCTCATCTCCGCTGCTGCGCTCCACGGCA 769

QY 720 CATCTGCTTGAATCTGCTCAGATGGCACTTGGGTTTCAGTCCCACTGATCAGA 779
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 770 CGTCCGCGCTGCAGATCGCGCTCCAGAACGGGCGAGTGGGTGTCGCTCGACCCG 829

QY 780 CTTTCCTTTTTCATCAATGTGTGTGAGCTCTACAGGTAAATGACTAATGGGAGGTTTAAAA 839
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 830 ACGCTTCTTCTGCAACGTGCGGACTCGTTGCAAGTGTGACCAACGGGAGGTTCAAGA 889

QY 840 GTGTAAGCATAGGTTTTGGTGTGACACAAACGAAGTCAAGGTTATCAATGATCTACTTTG 899
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 890 GCGTGAAGCACAGGTTGGTGGCCAAACAGCCTAAAGTCTAGGGTTTCCATGATCTACTTTG 949

QY 900 GAGGACCGGTTGAGTGAATAATAGCACTTTTACCTTCAGTGTGTTTAAAGAGGAGG 959
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 950 GAGGGCCAGCGATGACACAGAGGATTTGCACCAATTCGCCGACGCTGTGGGCGGGAGAGC 1009
```

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QY 960 AGTGTTCCTACAAGAGATTCAATGCTGTGAATACAAGAGGCTCGGTACACTTCAAGGC 1019
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1010 AGAGCCTGTACAAGGACTTCAATGGGGCGAGTACAAGAGGCTCGGTACACTTCAAGGC 1069

QY 1020 TAGCTGATAATAGGCTTCCCTTTCCAGA 1049
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1070 TCGGGACACAGGCTGGCTAGTTCCACA 1099

RESULT 9
US-09-719-108-5
; Sequence 5, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/09/719,108
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1243, 1265)
; OTHER INFORMATION: unidentified residue
US-09-719-108-5

Query Match      27.1%; Score 356.6; DB 3; Length 1318;
Best Local Similarity 63.2%; Pred. No. 1.5e-95;
Matches 586; Conservative 0; Mismatches 329; Indels 12; Gaps 2;

QY 132 CTTCTTTCACGGGGATCTCTGTGTGCGACCTCACGCCGCCGATGCCAAGAAATCTCATAG 191
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 78 CCGGCTTCTCTAATCCGGTTATAGATATGCTGACCCAGAAATCCAAACATGCCCTCG 137

QY 192 TGAACCGCTGTAGGACTTCGCTTCTCAAGCTTGTGNAACCATGGTGTTCATTGGAGT 251
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 138 TGAAGCATGCGAAGACTTCGCTTCTTCAAGGTGATCAACCATGGCGTTTCCGCAGAGC 197

QY 252 TAATGCCCAATTTAGAAAAAGAGGCCCTCAGGTTCTTTTAAAAAATCTCAGTCCGAGAAAAG 311
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 198 TAGTCTCTGTTTTAGAACACAGAGACCGTGGATTTCTTCTGTTGCCCAAGTCAGAGAAA 257

QY 312 ACAGAGCTGTGTCCTCCCGACCCCTTTCGGCTATGTTAGCAAGAGGATGTCGCAACCGTG 371
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 258 CCCAAGTCG---CAGGTTATCCCTTCGGATACGGGAACAGTAAGATTGTCGGAATGGTG 314

QY 372 ATGTCGGTTGGGTGGAATACCTCTCTCCCAACCAACCCCTGATGTTATCTCACCCAAAT 431
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 315 ACGTGGTTGGGTGAGTACTTGTGATGAAACGCTAATCATGATTCGGGTTCGGGTCCAC 374

QY 432 CACTTTGCAATTTCCGAGAGAAATCTCATATTTTCAAGGCGGTGGTGGAGAACTACATTA 491
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 375 TATTTCCAAAGTCTTCTCAAAAGCCCGGGAACCTTTCAGAAACGCAATGGAGAGTACAAA 434

QY 492 CAGCAGTGAAGAACATGTGCTATGGCGTGTTCGAAATTTGATGGCGAGGGGTGGGGATAA 551
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 435 CATCAGTGAGAAAAATGACATTCGATGTTTTGAGAGAGATCACAGATGGCTAGGGATCA 494

QY 552 GGCAGAGGAATACGTTAAGCAGGTTGCTGAAAGGATGAGAAAAAGTGAATTCGTGCTTCAGGT 611
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```



```
RESULT 11
US-09-614-912-1
; Sequence 1, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Cai, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1555
; TYPE: DNA
; ORGANISM: Zea mays
US-09-614-912-1

Query Match      24.0%; Score 315.8; DB 3; Length 1555;
Best Local Similarity 58.9%; Pred. No. 2.4e-83;
Matches 586; Conservative 0; Mismatches 397; Indels 12; Gaps 2;

QY 59 ACAACCAACCATGTTCTGTCTCAGCCAGCAATGAACACAGTTTTCCTCTCTGAAACCA 118
    |||||
DB 112 ACAGCATGTTGGTCTCCCAAACCGCTCTGTCGACACATCCCGTCTCTGGGTCC 171
    |||||

QY 119 TTCAAGTCCACGCCCTTTTCACGGGATTCCTGTGGTGCACCTCACGCCACCCCGATGCC 178
    |||||
DB 172 CCGGGCCCCCAGGACACAGCTTCTCGGGAGTGCCTGCTGCTGACCTGTCCAGCCACCGCGG 231
    |||||

QY 179 AGAATCTCATAGTGAACGCTGTAGGACTTCGGCTTCTCAAGCTTGTGAACCATGTT 238
    |||||
DB 232 CGCGGGCGCATGTCGACGCCCTGCGAGCGCTTCGGGTCTTCAAGTCTGTCACCAACCGC 291
    |||||

QY 239 GTTTCATTCGAGTTAATGCGCAATTTAGAAAACGAGGCCCTCAGGTCTCTTTAAAAATCT 298
    |||||
DB 292 GTGGCGGGCCACCATGACAGGGCCGAGTCCGAGGCCGTCAAGTTCTTCGCGCAGGGG 351
    |||||

QY 299 CAGTCCGAGAAAGACAGAGCTGGTCCCCCGACCCCTTTTCGGCTATGTTAGCAAGAGGATT 358
    |||||
DB 352 CAGGCGGACAAGACCGCGCGGGCGCGGTACCCGTTCCGGGTACGGCAGCAAGCGGATC 411
    |||||

QY 359 GGCCCAACCGGTGATGTCGGTGGGTGGAATACCTCTCTCAACACCAACCCCTGATGTT 418
    |||||
DB 412 GGGCTCAATGGCGACATGGGGTGGGTTCGAGTACCTCTCTCGCGGTGCACGCCGCTCG 471
    |||||

QY 419 ATCTCACCACCAATCACTTTTGCAATTTTCGAGAAATCCTCATCATTTTCAGGCGGTGGT 478
    |||||
DB 472 CTCCTCGAGCGCTGCCCGGTGCCCTCCAGC-----CGCGTTCGGAGCGCGCTG 522
    |||||

QY 479 GAGAACTACATTACAGCAGTGAAGAACATGTCTATGCGGTGTTGGAATTGATGCGGAG 538
    |||||
```

```
RESULT 12
US-09-371-307-67
; Sequence 67, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Filler, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOST:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 67
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (726)
; OTHER INFORMATION: n = a, c, g, or t
US-09-371-307-67

Query Match      23.6%; Score 311; DB 3; Length 783;
Best Local Similarity 70.1%; Pred. No. 4.4e-82;
Matches 441; Conservative 0; Mismatches 170; Indels 18; Gaps 1;
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QY 458 CATCATTTTCAGGCGGTGGAGAACTACATTACAGCAGTGAAGAACATGTGCTATGCG 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 52 CAAACTTTGAGGGTGGCTTTGATATATATATCAAAATCAGTAAGAAATGGCTGTGAG 111

QY 518 GTGTTGGAATTTAGTGGCGAGGGTGGGATGAAGCAGAGGAATACGTTAAGCAGGTTG 577
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 112 ATACTTTGAAATGATGCTGATGGTTGAAGATACAACCCAGGAATGTGTTGAGCAAGCTG 171

QY 578 CTGAAGGATGAGAAATGATTCGTCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 637
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 172 TTGATGGATGAAGAGAGTGAATCTGTTTTCAGGGTGAATCATTTACCCACCATGCCCCAT 231

QY 638 GTGCAAGCACTG-----AACCGGAATTTGGTTCGGTTCGGTTCGGTTCGGTTCGG 679
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 232 GTTCAACCTTTGAGTGGTAATGCAATGCAATGGGATGTGATTTGATGTAACAC 291

QY 680 ACAGACCCACAGATAATTTCTGCTTAAGATCTAACAGCACATCTCGGCTTGCATAATCTGT 739
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 292 ACTGATCCACAAATTTATCTCAGTGTGAGATCTAACACACATCTCTGCTCTTCAAAATCTCT 351

QY 740 CTCACAGATGGCACTTTGGGTTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 799
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 352 CTAAGAGAGGAAGCTGGATTTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 411

QY 800 GGTGACGCTCTACAGGTAAATGACTAAATGGAGGTTTAAAGTGAAGCATAGGTTTGG 859
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 412 GGTGATCTCTTACAGTAAATGACCAATGGAGGTTTAAAGTGAAGCATAGGTTAGTG 471

QY 860 GCTGACACAAACGAAGTCAAGGTTTATCAATGATCTACTTTGGAGGACCGGTTGAGTGAA 919
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 472 ACCAACAGTGTGAATCAAGGCTATCAATGATTTATTTTGGTGGACCAACCATTTGAGTGAG 531

QY 920 AATATAGCACCTTTACCTTCAGTGTATGTTAAAGAGAGAGAGGTTTGTACAAAGAGTTTC 979
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 532 AAAATAGCACCTTTGGCCATCTTTGATGAGAGGTTGATCAAAAGCTTTATATAAGAAATTT 591

QY 980 ACATGCTGTGAATACAAAGAGGCTGGGTACACTTCAAGGCTAGCTGATTAATAGGCTTGCC 1039
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 592 ACTTGGTTCGAGTACAAGAAATCTGCTTATTAATTCAGATTCGACAGTAATAGGCTCATTT 651

QY 1040 CCTTTCCAGAAATCTGCTGCTGAATTAACC 1068
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 652 CACTTTGAAAAAATGCTGCTTCTTAATC 680

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RESULT 13

US-09-371-307-71

; Sequence 71, Application US/09371307A

; Patent No. 6723897

; GENERAL INFORMATION:

; APPLICANT: Brown, Sherri M.

; APPLICANT: Heck, Gregory R.

; APPLICANT: Piller, Kenneth J.

; APPLICANT: Kishore, Ganesh M.

; APPLICANT: Elich, Tedd D.

; APPLICANT: Logusch, Eugene W.

; APPLICANT: Rao, Sudabathula

; APPLICANT: Ream, Joel E.

; APPLICANT: Logusch, Sherry J.

; TITLE OF INVENTION: Methods for controlling gibberellin levels

; FILE REFERENCE: MOBT:216

; CURRENT APPLICATION NUMBER: US/09/371,307A

; CURRENT FILING DATE: 1999-08-10

; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 71

; LENGTH: 811

; TYPE: DNA

; ORGANISM: Zea mays

US-09-371-307-71

Query Match 12.6%; Score 166; DB 3; Length 811;

Best Local Similarity 55.8%; Pred. No. 7e-39;

Matches 316; Conservative 0; Mismatches 250; Indels 0; Gaps 0;

```

QY 485 TACATTTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTTGATGCGGAGGGTTG 544
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2 TACACGTTGCCGTGCGGCGATGCGGTGCGGCGTCTGAGCTGATGCGGAGGGGCTG 61

QY 545 GGGATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAAGTGAATTCGTGC 604
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 GGCATCGCGCGCGCGCGCGGCGCGGCGGTGCTGGCGGCGTGGTGGCGCGCGGACAGC 121

QY 605 TTCAGTTTGAACACATACACCGGCTTGCCTGAGGTGCAAGCACTGAACCGGAATTTGGTT 664
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 GACTGCATCTCGGCGTGAACCACTACCGCGCGCGCGCGCTCAACCCCAAGCTCACG 181

QY 665 GGGTTGGGGAGCACACAGACCCACAGATAAATTTCTGCTTAAGATCTAACAGCACATCT 724
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 GGGTTGGCGGAGCACACACCGACCCGCGAGATCATCTCGGTCTCCGCGCCCAACCGCACCTCC 241

QY 725 GCGTTGCAAACTGTCTCACAGATGGCACTTGGGTTTTCAGTCCCACTGATCAGACTTCC 784
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 GGCCTGGAGATCGCGTGGGAGCGGCGCTGGGCTCCGTCCGCGCCCGACGCGGACGCC 301

QY 785 TTTTTCATCAATGTTGGTCAACCTCTACAGGTAATGACTAAATGGGAGGTTTAAAAGTGA 844
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 TTCTTCGTCAACGTGCGCGCACACCTGTCAGGTGTTGACGAACGCGGAGGTTTCAGGAGCGTG 361

QY 845 AAGCATAGGTTTGGTGCACACAGCAAGTCAAGGTTTCAATCAATGATCTACTTTGGAGGA 904
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 AGGCACAGGTTGGTGAACAGCGAGAGTCCCGGTTTCCATGGTCTTCTTCGCGCGGC 421

QY 905 CCAGCGTTGAGTGAATAATATAGCACCTTTTACCTTTCAGTGTATTTAAAAGAGAGGAGTGT 964
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 CCGCGCGCGCGAGAGGCTGGCGCGCTCCGAGCTCTGGGCGACGCGCGCGGAGC 481

QY 965 TTGTACAAAGAGTTTCAATGTTGAATACAAAGAGGTCGCTACACTTCAAGGCTAGCT 1024
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 482 CGGTACCGGAGCTTTCACCTGAGCGAGTTTCAAGACCAAGCGGTTGCGAGGACCGAGCTCGCG 541

QY 1025 GATATAGGCTTGGCCCTTTCCAGAA 1050
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 542 GAAGACCGCTGTCCGCTTCGAGAA 567

```

RESULT 14

US-09-371-307-66

; Sequence 66, Application US/09371307A

; Patent No. 6723897

; GENERAL INFORMATION:

; APPLICANT: Brown, Sherri M.

; APPLICANT: Heck, Gregory R.

; APPLICANT: Piller, Kenneth J.

; APPLICANT: Kishore, Ganesh M.

; APPLICANT: Elich, Tedd D.

; APPLICANT: Logusch, Eugene W.

; APPLICANT: Rao, Sudabathula

; APPLICANT: Ream, Joel E.

; APPLICANT: Logusch, Sherry J.

; TITLE OF INVENTION: Methods for controlling gibberellin levels

; FILE REFERENCE: MOBT:216

; CURRENT APPLICATION NUMBER: US/09/371,307A

; CURRENT FILING DATE: 1999-08-10

; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 66

; LENGTH: 403

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (178)

; OTHER INFORMATION: n = a, c, g, or t

US-09-371-307-66

Query Match 11.8%; Score 155.6; DB 3; Length 403;
Best Local Similarity 63.2%; Pred. No. 5.8e-36;
Matches 261; Conservative 0; Mismatches 140; Indels 12; Gaps 1;

QY 284 TTCCTTAAATAATCTCAGTCGCGAGAAACACAGAGCTGGTCCCCCGACCCCTTCGGCTAT 343
DB 2 TTCCTTCTCTATGTCACTCAATGAAAGGAAAGTAGGACCTCCCAATCCCATTTGGGTAT 61

QY 344 GTAGCAAGAGATTGGCCCAACCGGTGATGTCGGTGGGTGCGAATAGCTCTCTCTCAAC 403
DB 62 GTAGCAAGAAATTTGGACACATGGGACGTTGGTTGGATTGATACCTTCTTCTCAAC 121

QY 404 ACCAACCTGTATGTTCCTCAACCAATCATTTCGATTTTCCGAGAAATCCTCATCAT 463
DB 122 ACCAATCAAGAACCACT-----TCTCTGTTTATGGCAAAACCCCTGAGAAA 169

QY 464 TTCAGGCGGTGGTGAGAACTACATTACAGCAGTGAAGAACATGTGTCGCGTGTG 523
DB 170 TTCAGGTGCTGTTGAACAGTTTACATGCTTCTGTGAGGAAAGATGGCATGTGAGATTCTT 229

QY 524 GAATTTGATGGCGAGGGTGGGATAAGGCGAGAGGAATACGTTAAGCAGGTTGCTGAAG 583
DB 230 GAGTTGATGGCAGAGGGTTGAAGATTCAGCAAGAGGATGTTTAGCAGCTTCTAATG 289

QY 584 GATGAGAAAGTGATTCGTGTTTCAAGTTGAACCACTACCCGCTTGGCCCTGAGGTGCAA 643
DB 290 GATAAACAAAGTGACTTATTTTTCAGGTTGAATCATTTAGCGTCTTGTCTGMAATGACT 349

QY 644 GCAGTGAACCGGAATTTGGTGGTGGGAGGACACAGACCCACAGATAAT 696
DB 350 CTGAATGATCAGAACTTGAATTTGGGTTTGGAGAAACACAGACCCCAAAATCAT 402

RESULT 15

US-09-371-307-68
; Sequence 68, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Filler, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (306)
; OTHER INFORMATION: n = a, c, g, or t
US-09-371-307-68

Query Match 11.7%; Score 154.8; DB 3; Length 406;
Best Local Similarity 66.6%; Pred. No. 1e-35;
Matches 279; Conservative 0; Mismatches 113; Indels 27; Gaps 3;

QY 314 AGAGCTGTGTCCTCCCGACCTTTTCGGCTATGTAGCAGGATGGCCCAACCGTGAT 373
DB 2 AAACAGGACAAACCCCGCTTATGGCTATGTAATAAAGGATTGGACCAAAATGGTAT 61

QY 374 GTCGGTTGGTTCGAATACCTCTCTCAACCAACCCCTGATGTTATCTCACCCAAATCA 433

DB 62 GTTGGTTGGTGGAAATATCTTCTCTCACAAACCAACCAAG-----ACCCGAATCT 111
QY 434 CTTTGCATTTTCCGAGAAATCTCTCATCATTTTCAGGCGGTGGTGGAGAACTACATTACA 493
DB 112 CTTTGGAACT-----GAAACCCAGAGAGTTTCAGGATTGCTTTGGATAATTATATGCA 166

QY 494 GCAGTGAAGAACATGTGCTATGCGGTGTGGAATTGATGGCGGAGGGTTGGGGATAAGG 553
DB 167 GCAGTGAAGAAATGGCATGTGAGATACCTTGAATGTAGCTGATGGGCTAAAGGTTTCAG 226

QY 554 CAGAGGAATACGTTAAGCAGGTTGCTGAAGATGAGAAAGTGAATTCGTGCTTCAGGTTG 613
DB 227 CCAAGAAATGTGTTAAGTAAAGCTGATGATGGATGAACAGAGTGACTCTGTTTTCAGGCTG 286

QY 614 AACCACTACCCGCTTGGCCCTGAGG-----TGCAAGCACTCAACCCGGAATTTG 661
DB 287 AACCACTACCCCTCGTGCNAGAGGTGGTTCAAGTCCCTTGAATGGACGAGTAAATGTG 346

QY 662 GTTGGGTTTGGGAGACACACAGACCCACAGATAATTTCTGTCTTAAGATCTAAACAGCAC 720
DB 347 ATTGGATTGGGTGAACACACACTGACCCCAAAATCATTTTCAGTCTTAAGATCCAAACAC 405

Search completed: December 28, 2005, 00:46:40
Job time : 272.271 secs

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OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 17:51:22 ; Search time 1238.83 Seconds
(without alignments)
8797.858 Million cell updates/sec

Title: US-10-670-454-1
Perfect score: 1318
Sequence: 1 gttctctctctaccctgt.....CaaaaaAAAAAAAAAAAA 1318

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

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Maximum Match 100%
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1318	100.0	1318	8	US-10-670-454-1	Sequence 1, Appli
2	999	75.8	999	8	US-10-821-711-3	Sequence 3, Appli
3	893.8	67.8	1359	3	US-09-371-307-62	Sequence 62, Appl
4	893.8	67.8	1359	6	US-10-401-321-62	Sequence 7, Appli
5	425.8	32.3	1237	8	US-10-670-454-7	Sequence 1350, Ap
6	425.4	32.3	1026	3	US-09-938-842A-1350	Sequence 1350, Ap
7	425.4	32.3	1026	3	US-09-938-842A-1350	Sequence 64, Appl
8	424.8	32.2	1403	3	US-09-371-307-64	Sequence 64, Appl
9	424.8	32.2	1403	6	US-10-401-321-64	Sequence 21951, A
10	397.6	30.2	1390	7	US-10-424-599-21951	Sequence 9, Appli
11	382.8	29.0	1008	8	US-10-670-454-9	Sequence 5, Appli
12	356.6	27.1	1318	7	US-10-670-454-5	Sequence 3, Appli
13	354	26.9	984	7	US-10-392-325-3	Sequence 78659, A
14	354	26.9	1260	7	US-10-437-963-78659	Sequence 69575, A
15	315.8	24.0	1611	8	US-10-425-115-69575	Sequence 67, Appl
16	311	23.6	783	3	US-09-371-307-67	Sequence 6183, Ap
17	311	23.6	783	6	US-10-401-321-67	Sequence 141, App
18	302.8	23.0	831	7	US-10-425-114-6183	Sequence 9278, Ap
19	285	21.6	927	6	US-10-259-194A-141	Sequence 129307,
20	279.2	21.2	591	7	US-10-424-599-9278	Sequence 7861, Ap
21	273.8	20.8	860	7	US-10-424-599-129307	Sequence 16086, A
22	273.8	20.8	860	7	US-10-425-114-7861	
23	203.2	15.4	1008	7	US-10-437-963-16086	

24	201.8	15.3	847	8	US-10-425-115-159585	Sequence 159585,
25	188.6	14.3	1322	7	US-10-425-114-4257	Sequence 4257, Ap
26	188	14.3	1327	8	US-10-425-115-103352	Sequence 103352,
27	187.2	14.2	1271	7	US-10-437-963-1288	Sequence 1288, Ap
28	185	14.0	415	7	US-10-424-599-128562	Sequence 128562,
29	182.4	13.8	608	7	US-10-424-599-101563	Sequence 101563,
30	172.2	13.1	919	7	US-10-425-114-34429	Sequence 34429, A
31	169.8	12.9	802	8	US-10-425-115-177171	Sequence 177171,
32	166	12.6	811	3	US-09-371-307-71	Sequence 71, Appl
33	166	12.6	811	6	US-10-401-321-71	Sequence 71, Appl
34	156.2	11.9	504	6	US-10-259-194A-614	Sequence 614, App
35	155.6	11.8	403	3	US-09-371-307-66	Sequence 66, Appl
36	155.6	11.8	403	6	US-10-401-321-66	Sequence 66, Appl
37	154.8	11.7	406	3	US-09-371-307-68	Sequence 68, Appl
38	154.8	11.7	406	6	US-10-401-321-68	Sequence 58, Appl
39	152.4	11.6	966	3	US-09-371-307-58	Sequence 58, Appl
40	152.4	11.6	966	6	US-10-401-321-58	Sequence 453, App
41	150.4	11.4	537	6	US-10-259-194A-453	Sequence 6780, A
42	146.4	11.1	322	7	US-10-424-599-6780	Sequence 20123, A
43	140.4	10.7	2478	7	US-10-437-963-20123	Sequence 42166, A
44	133.8	10.2	457	7	US-10-424-599-42166	Sequence 108868,
45	127.4	9.7	597	7	US-10-424-599-108868	

ALIGNMENTS

RESULT 1
US-10-670-454-1
; Sequence 1, Application US/10670454
; Publication No. US20040229357A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/10/670,454
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Phaseolus coccineus

Query Match 100.0%; Score 1318; DB 8; Length 1318;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	121	CAAGTCCACGCCCTTGTTCACGGGATTCCTGTGTCGACCTCAGGCACCCCGATGCCAA 180
QY	181	GAATCTCATAGTGAACGGCTGTAGGACATTCGGCTTCTTCAAGCTTGTGAACCATGGTGT 240

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Db 241 TCCATTGGAGTTAATGSCCAATTTAAGAACGAGGCCCTCAGGTTCTTTAAAGAAATCTCA 300
Qy 301 GTCCGAGAAAGACAGAGCTGGTCCCCCGACCCCTTTCGGCTATGGTAGCAAGAGATTGG 360
Db 301 GTCCGAGAAAGACAGAGCTGGTCCCCCGACCCCTTTCGGCTATGGTAGCAAGAGATTGG 360
Qy 361 CCCAAACGGTGATGTCGGTTGGTGGTGAATACCTCTCTCAACACCAACCCCTGATGTTAT 420
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Qy 421 CTCACCAATACATTTTGCATTTTCGAGAAATCTCATCTATTTTCAGGCGCGTGTGGA 480
Db 421 CTCACCAATACATTTTGCATTTTCGAGAAATCTCATCTATTTTCAGGCGCGTGTGGA 480
Qy 481 GAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAAATTTGATGCGGAGGG 540
Db 481 GAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAAATTTGATGCGGAGGG 540
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Qy 601 GTGCTTCAGGTTGAACCACTACCCGCTTGCCCTGAGGTCAGCACTGAACCGGAATTT 660
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Qy 661 GGTGGGTTTGGGAGCACACAGACCCACAGATAATTTCTGCTTAAGATCTAAACAGCAC 720
Db 661 GGTGGGTTTGGGAGCACACAGACCCACAGATAATTTCTGCTTAAGATCTAAACAGCAC 720
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Db 721 ATCTGGCTGCAAAATCTGTCTACAGATGCACTTGGGTTTCACTCCACCTGATCAGAC 780
Qy 781 TTCCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACCTAAATGGGAGGTTTAAAG 840
Db 781 TTCCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACCTAAATGGGAGGTTTAAAG 840
Qy 841 TGTAAAGCATAGGTTTGGCTGACACAAAGAGTCAAGGTTATCAATGATCTACTTTGG 900
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Qy 1261 CCCTTTCTCAATTTGTAATGGAACCGAACTCTAGTTTACAAAGAAAGAAAGAAAGAA 1318
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RESULT 2

US-10-821-711-3
; Sequence 3, Application US/10821711
; Publication NO. US20040237142A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Larry A
; APPLICANT: Krieger, Blysia K
; APPLICANT: Ye, Xudong
; APPLICANT: Zhang, Wanggen
; TITLE OF INVENTION: DNA CONSTRUCTS AND METHODS TO ENHANCE THE PRODUCTION OF
; FILE REFERENCE: 38-21(52967)B
; CURRENT APPLICATION NUMBER: US/10/821,711
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: 60/461,459
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 3
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Phaseolus coccineus
US-10-821-711-3

Query Match 75.8%; Score 999; DB 8; Length 999;
Best Local Similarity 100.0%; Pred. No. 2.1e-281;
Matches 999; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 128 AGCCCTTGTTCACGGGGATTCCTGTGTGTCGACCTCAGCAGCCCGATGCCAGATCTC 187
Db 61 AGCCCTTGTTCACGGGGATTCCTGTGTGTCGACCTCAGCAGCCCGATGCCAGATCTC 120
Qy 188 ATAGTGAAACGCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATCGTGTTCATTTG 247
Db 121 ATAGTGAAACGCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATCGTGTTCATTTG 180
Qy 248 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 307
Db 181 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240
Qy 308 AAAGACAGAGCTGTGCCCCCGACCCCTTTCGGCTATGGTAGCAAGAGGATTCGCCCAAC 367
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Qy 368 GGTGATGTCGGTTGGTTCGAATACTCTCTCAACACCAACCCCTGATGTTATCTCACCC 427
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Qy 428 AAATCACTTTGATTTTCGAGAAATCTCTCATATTTTCAGGCGGTGTGGAGAACTAC 487
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RESULT 3
US-09-371-307-62
; Sequence 62, Application US/09371307A
; Patent No. US20020053095A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Glycine max
US-09-371-307-62

Query Match 67.8%; Score 893.8; DB 3; Length 1359;
Best Local Similarity 84.9%; Pred. No. 1.7e-250;
Matches 1069; Conservative 1; Mismatches 158; Indels 31; Gaps 5;

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DB 159 CCACGCCCTTGTTCGGGGGAATTCCTGTGTGCGACTTCACGCAACCCCGATGCCAAGAC 218
QY 185 CTCATAGTCAACGCGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTTGTCCA 244
DB 219 CACATAGTCAATGCTTCGCGGGAATTCGGCTTCTTCAAGCTTGTGAACCATGTTGTCCG 278
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RESULT 4

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US-10-401-321-62
; Sequence 62, Application US/10401321
; Publication No. US20030233679A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
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QY 365 AACCGTGTATGTGGTTCGAATACCTCTCTCAACACCAACCTCTGAATGTATCTCA 424
DB 399 AACGCGATGTGGTTCGAATACCTCTCTCAACACCAACCTCTGAATGTATCTCTCC 458
QY 425 CCATAATCATTGATTTTCGAGAAAATCTCTCATCATTTTCAGGCGGCTGTGAGAAC 484
DB 459 CCCAAGTCACTAGTTTCAATTTTCAGAGAAGGTCTCTCAGAAATTTTCAGGCGGCTGTGAGGAA 518
QY 485 TACATTACAGCAGTGAAGAATGTGTATGCGGTGTTGGAATTCATGTCGCGAGGGTTG 544
DB 519 TACATTAGAGCGGTGAAGAACATGTCTATGAGGTGTTGGAATTCATGTCGCGAGGGATG 578
QY 545 GGGATAAGCGCAGAGGAATACGTTAAGCAGGTTGCTGAAGAGGATGAGAAAAGTGAATTCGTGC 604
DB 579 GGGATAACGACAGAGGAATGTGTGTAGTAGTGTGCTGAAGGATGAGAGAGTGTATCTTGC 638
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DB 879 GTAAAGCATAGAGTTTTCGCTGACCCCAACCAAGTCAAGGTTGCAATGATCTACTTCTGA 938
QY 902 GGACCAAGGCTTGAAGTGAATAATAGCACCTTTTACCTTTCAGTGTATTTAAAGGAGAGAG 961
DB 939 GGACCAACCTTGTGTGAAGATAGCACCTTTTACCTTTCATCTCATGTAAAGGAGAGAG 998
QY 962 TGTGTTTCAAGAGTTTCAATGTTGTAATACAAAGGCTGCTGATCACTTCAAGGCTA 1021
DB 999 AGTTTCTCAAAAGTTTCAATGTTGGGAATAACAAAGAGGCTGCTGATCGCGTCAAGGCTA 1058
QY 1022 GCTGATAATAGCTTGGCCCTTCCAGAAATCTGCTGATTAACCAACACACCCCTTC 1081
DB 1059 GCGGATAATAGACTCGGCCCTTTTGAAGAAATCTGCTGATTAAGGAGGCAAGTGTGT 1118
QY 1082 AAA-----TTCACATCATTTTACGCACTGTTTATTTACCCCAA-----TTTTCTTCTCTTT 1132
DB 1119 CAAATTTCTACTACTCAATTTTGGCAGTGTGTTAGGCAACTTTTATTTTATTTT 1178
QY 1133 TCTTTTCTGCTGTCTGTAGGTTTCAACAGTGTCACTTCTGATCATATATAGAAAAT 1192
DB 1179 TTTTGGGTGTGTGTATCTAGGTTCCAAACAGTGTGACTTACTTGAATATATAGAAAAT 1238
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DB 1239 GAATAGGTTGCTTATGCACTTCCCTTTTAAATCTGTTCTTTTCTTTTCTTTTGAATG 1298
QY 1242 TAAACAGTGGTCTCAACTTCCCTTTTCAATGTTCAATGGAACGCAACTCTAGTTTACA 1300
DB 1299 TAAATAGT-----CACTACTGCGCTTCTATTTATCAATGAACGCAACTCTAGTTACA 1349
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QY 206 GACTTCGGCTTCTTCAAGCTTGTAACCAAGTGTTCCTAATGGAGTTAATGCCAATTTA 265
Db 259 GAGTTCGGGTTCTTCAAGGTCGTAAACACGAGTCCGACCCGAACTCATGACTCGGTTA 318
QY 266 GAAACGAGCCCTCAGGTTCTTTAAATAATCTCAGTCCGAGAAAGACAGAGCTGGTCC 325
Db 319 GAGCAGAGGCTATTGGCTTCTTCCGCTTGCCTCAGTCTCTTAAACACGGGCCCGTCCA 378
QY 326 CCCGACCCCTTTCGGCTATGTAAGCAAGAGATTGGCCCAACGGTGAATGCGTGGGTC 385
Db 379 CCGAACCGTATGCTATGTAATAAACGATTGGACCAACGCTGACGTTGGTGGATT 438
QY 386 GAATACCTCCTCCTCAACACCAACCTGATGTTATCTCAACCAATCATCTTGGCAATTTTC 445
Db 439 GAGTATCTCCTCCTCAATCTCAATCTCAGCTCTCCTCTCTCTTAAACACCTCCGCCGCTTTTC 498
QY 446 CGAGAAATCCCTCATCTTTCAGGCGGTTGGGAGACTACATTAACGACGTGAAGAAC 505
Db 499 CGTCAACCCCTCAATTTTCCGTGAGTCGGTGGAGGAGTACATGAAGAGATTAAAGAA 558
QY 506 ATGTGCTATGCGGTGTGGAATTTGATGGCGGAGGGGTTGGGATAGGCAGAGGAATACG 565
Db 559 GTGTGCTCAAGGTTGAGATGTTGCGGAAGAACTAGGATAGAGCAAGGACACT 618
QY 566 TTAAGCAGGTTGCTGAAGATGAGAAAGTATGTTGCTTTCAGGTTGAACCACTACCCG 625
Db 619 CTGAGTAAATGCTGAGAGATGAGAAGAGTACTCGTGCCTGAGACTAAACCATATACG 678
QY 626 CTTGGCCTGAGGTGCAACGACTGAACCGAATTTGGTGGGTTGGGAGCAGACGAC 685
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Db 736 CCACAGATAATCTCAGTGTCTAGATCTAATTAACACGGCGGCTCTCAAAATCTGTGTGAA 795
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QY 806 GCTCTACAGTAACTAATGGAGGTTTAAAGTGAAGCATAGGTTTGGCTGAC 865
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QY 1046 CAGAAATCTGCTGATTAATCAACCAACACCCCTTCAAAATTCACCTCAT 1094
Db 1096 GAGAAACAACCTTCTTCAATCATATAAAACCCCTTGTATGAGAGTAGTGCAT 1144
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RESULT 6

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US-09-938-842A-1350
; Sequence 1350, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Haiper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
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; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1350
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-1350

Query Match      32.3%; Score 425.4; DB 3; Length 1026;
Best Local Similarity 66.8%; Pred. No. 2.8e-113;
Matches 622; Conservative 0; Mismatches 306; Indels 3; Gaps 1;

QY 146 ATTCTGTGGTCGACCTCAACGACCCCGATGCAAGAAATCTCATATAGTGAAACGCTGTAGG 205
Db 91 ATCCCGTCGTCAACCTAGCCGATCCGGAAGCGAAACCCGAAATCGTAAAGCTTCCGAG 150
QY 206 GACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTTGGAGTTAATGGCCAAATTA 265
Db 151 GAGTTCCGGGTTCTTCAAGGTCGTAAACCAACGAGGTCGACCCGAACTCATGACTCGGTTA 210
QY 266 GAAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAGACAGAGCTGGTCCC 325
Db 211 GAGCAGAGGCTATTGGGCTTCTTCGGCTTGCCTCAGTCTCTTAAAAACCGGCCCGTCCA 270
QY 326 CCAGACCCCTTTCCGCTATGCTAGCAAGAGATTGGCCCAACCGGTGATGTCGGTTGGGTC 385
Db 271 CCTGAACCGTACGGTTATGGTAAATAACGAGTTGGACCAACCGGTGACGTTGGTGGATT 330
QY 386 GAATACCTCCTCCTCAACCAACCCCTGATGTTATCTCACCACCAATCATCTTTCGCAATTTTC 445
Db 331 GAGTATCTCCTCCTCAATGCTAATCCTCAGCTCTCCTCTCTTAAAAACCTCCGCCGCTTTTC 390
QY 446 CGAGAAATCTCTCATCTTTCAGGCGGTGGTGGAGAACTACATTAACAGAGTGAAGAAC 505
Db 391 CGTCAACCCCTCAAAATTTTCGTGAGTCCGTGGAGGAGTACATGAGGAGATTAAAGAA 450
QY 506 ATGTGCTATGCGGTGTGGAATTTGATGGCGGAGGGTTGGGATAGGCAGAGGAATACG 565
Db 451 GTGTGCTACAAGGTCGTGGAGATGTTGCGGAAGAACTAGGATAGAGCAAGGACACT 510
QY 566 TTAAGCAGGTTGCTGAAGATGAGAAAGTGAATTCGTGCTTCAGGTTGACCACTACCCG 625
Db 511 CTGAGTAAATGCTCAGAGATGAGAAAGATGACTCGTGCCTGAGACTAAACCATTTATCCG 570
QY 626 CTTGCCCTGAGTCAAGCACTGAACCGGAATTTGGTGGGTTGGGAGGACACACAGAC 685
Db 571 GC---GGCGGAGGAAGAGCGGAGAGAGATGTTGAAGGTGGGGTTTGGGGACACACAGAC 627
QY 686 CCACAGATAATTTCTGCTTAAAGATCTAACACGACATCTGGCTTGCAAATCTGTCTCACA 745
Db 628 CCACAGATAATCTCAGTCTAAGATCTAATAACCGGGGCTTTCAAAATCTGTGTGAAA 687
QY 746 GATGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTCTTTTTCATCAATGTTGGTGAC 805
Db 688 GATGGAAGTTGGTTCGCTGCTCCTCTCATCATCTCTTCTTCTTCAATGTTGGAGAT 747
QY 806 GCTCTACAGGTAATGACTAATGGGAGGTTTAAAGGTAAACCATAGGCTTTTGGCTGAC 865
Db 748 GCTCTTCAAGTTATGACTAAACGGGAGGTTCAAGAGTGTAAACACAGGCTCTTAGCCGAT 807
QY 866 ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAAGCGTTGAGTGAATAATA 925
Db 808 ACAAGGAGATCGAGGATTTCAATGATATATTTCGGCGGACCCGCAATTGAGCCAGAGATC 867
QY 926 GCACCTTTACCTTCACTGATGTTTAAAGAGAGGAGTGTGTTGTACAAAGATTCAATCG 985
```

Db 868 GCACATTGCCATCGCTTGTCTCGAGCAAGATGATGGCTTTACAAAAGATTCACCTGG 927

Qy 986 TGTGATACAGAGAGCGCTGGTACACTTCAAGCTAGCTGATTAATAGGCTTGCCTTTTC 1045

Db 928 TCTCAATACAAATCTTCTGCTTACAAAGTCTAAGCTTGGTGAATTATAGACTTGGTCTCTTT 987

Qy 1046 CAGAAATCTGCTGCTGATTAACCAACACAC 1076

Db 988 GAGAAACACCTCTTCTCAATCATAAACCC 1018

RESULT 7

US-09-938-842A-1350

; Sequence 1350, Application US/09938842A

; Publication No. US20040009476A9

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; FILE REFERENCE: SAME, AND METHODS OF USE

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 1350

; LENGTH: 1026

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-1350

Query Match 32.3%; Score 425.4; DB 3; Length 1026;

Best Local Similarity 66.8%; Pred. No. 2.9e-113;

Matches 622; Conservative 0; Mismatches 306; Indels 3; Gaps 1;

Qy 146 ATTCTGTGTGCTGACCTCAGCACACCCGATCGCAAGATCTCATAGTGAACGCTCTAGG 205

Db 91 ATCCCGCTGTCAACTAGCCGATCGGAGCGAAGAACCCGATCTGAAGCGCTCGAG 150

Qy 206 GACTTCGGCTTCTCAAGCTTGTGAACCATGTTGTTCCATTGAGTTAATGCGCAATTTA 265

Db 151 GAGTTGGGTTCTTCAAGGTCGTAACACCGAGTCCGACCGAACTCATGACTCGGTTA 210

Qy 266 GAAACGCGCCCTCAGGTTCTTTAAAAATCTCAGTCCGAGAAACAGACGCTGGTCCC 325

Db 211 GAGCAGGAGCTATTGGCTTCTTTCGGCTTGCCTCAGTCTTTAAAAACCGGCGGTCCA 270

Qy 326 CCGACCCCTTTCGGCTATGTTAGCAAGAGATTGGCCCAACCGTGATGTCGGTTGGGTC 385

Db 271 CTTGAACCGTAGCGTTATGTTAATAACCGATTGGACCAACCGTGACGTTGGTTGATT 330

Qy 386 GAATACCTCTCTCTCAACCAACACCTGATGTTATCTCAACCAATCATTCTGCAATTTTC 445

Db 331 GAGTATCTCTCTCTCAATGTAATCTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 390

Qy 446 CGAAGAAATCTCTCATTTTCAGGCGGTGGTGAGAACTACATTACAGCAGTGAAGAAC 505

Db 391 CGTCAAAACCCCTCAAAATTTTCGTTGAGTCCGTTGGGAGGTACATGAAGGAGATTAAGGAA 450

Qy 506 ATGTGCTATCGGTGTGGAATTTGATGGCGAGGGTGGGGATAAGGCAGAGGAATACG 565

Db 451 GTGCTGACAGGTGTGGAGATGTTGCGGAGAACTAGGATAGAGCCAGGACACT 510

Qy 566 TTAAGCAGGTTGCTGAAGATGAGAAAGTATTCGTGCTTCAAGTTGAACCACTACCCG 625

Db 511 CTGAGTAAAAATGCTGAGAGATGAGAGAGTGAAGTCTGCTGCTGAGACTTAAACCATTTACG 570

Qy 626 CTTGGCCTGAGTGCAGACACTGAACCGGAATTTTGGTGGTGGGAGCACACAGAC 685

Db 571 GC---GGCGGAGAGAGCGCGGAGAGATGTTGAAGTGGGTTTGGGGAACACACAGAC 627

Qy 686 CCACAGATAAATTTCTGTTTAAAGATCTAACACACATCTGGCTTCAAAATCTGTCTACA 745

Db 628 CCACAGATAAATCTCAGTGTCTAAGATCTAATAACACCGGGGGTCTTCAAAATCTGTGAAA 687

Qy 746 GATGCACCTTGGGTTTTCAGTCCACCTGATCAGACTTCTCTTTTTCATCAATCTTGGTGAC 805

Db 688 GATGGAAGTTGGTTCGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 747

Qy 806 GCTCTACAGGTAATGACTAATCGGAGGTTTAAAGTGTAAAGCATAGGCTTTTGGCTGAC 865

Db 748 GCTCTTTCAGGTTATGACTAAGCGGAGGTTCAAGAGTGTAAACACAGGCTTTCAGCCGAT 807

Qy 866 ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAAGCTTGTAGTGAATAATA 925

Db 808 ACAAGGAGATCAGGATTTTCAATGATATATTTCCGCGGACCGCATTTGAGCCAGAGATC 867

Qy 926 GCACCTTTACCTTCAGTGTATGTTAAAGGAGAGGAGTGTTCACAAAAGTTCACATGG 985

Db 868 GCACCATTTGCCATGCTTGTCCCTGAGCAAGATGATTTGGCTTTTACAAAGATTTCACTGG 927

Qy 986 TGTGAATACAAAGAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGGCCCTTTTC 1045

Db 928 TCTCAATACAAATCTTCTGCTTCAAGTCTAAGCTTGGTGTGATTTAGACTTGGTCTCTTT 987

Qy 1046 CAGAAATCTGCTGCTGATTAACCAACACAC 1076

Db 988 GAGAAACACCTCTTCTCAATCATAAACCC 1018

RESULT 8

US-09-371-307-64

; Sequence 64, Application US/093711307A

; Patent No. US20020053095A1

; GENERAL INFORMATION:

; APPLICANT: Brown, Sherri M.

; APPLICANT: Heck, Gregory R.

; APPLICANT: Piller, Kenneth J.

; APPLICANT: Kishore, Ganesh M.

; APPLICANT: Elich, Tedd D.

; APPLICANT: Logusch, Eugene W.

; APPLICANT: Rao, Sudabathula

; APPLICANT: Ream, Joel E.

; APPLICANT: Logusch, Sherry J.

; TITLE OF INVENTION: Methods for controlling gibberellin levels

; FILE REFERENCE: MOBT:216

; CURRENT APPLICATION NUMBER: US/09/371,307A

; CURRENT FILING DATE: 1999-08-10

; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 64

; LENGTH: 1403

; TYPE: DNA

; ORGANISM: Glycine max

US-09-371-307-64

Query Match 32.2%; Score 424.8; DB 3; Length 1403;

Best Local Similarity 66.0%; Pred. No. 5e-113;

Matches 669; Conservative 0; Mismatches 327; Indels 18; Gaps 3;

Qy 53 ACAACAAACAAACCAATGTTGTTCTGCTCAGCCAGCAATGAACCAAGTTTTCCTTCTG 112

Db 134 AAAGCAGCAAGAAAAATGTTGTTGCTTCAAGGCAACCAACAACTACTCTACATC 193

Qy 113 AAACCAATTCAGTCCAGCCCTTGTTCAGGGGATTCCTGTCGACCTCAGCACCC 172

Db 194 AAGAACTATATGCCAACGGCAATTCCTCAACAAATTCCTGATGGACCTCTCAAAACCA 253

Qy 173 GATGCCAAGATCTCATAGTGAACGCCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAAC 232

206 GACTTCGGCTTCTTCAAGCTTGTGAACCATGTGTTCATTTGGAGTTAATGGCCCAATTAA 265
 Db |||||
 139 GAGTTTGGGTTCTTCAAGTCTCAACCATGGGTCCGACCCGATCTTTTGACTCAGTTG 198
 Qy |||||
 266 GAAACGAGGCTCAGGTTCTTTAAATACTCAGTCCGAGAAAGACAGAGCTGTCCTC 325
 Db |||||
 199 GAGCAGAGCCATCACTTCTTTGGTCTCTCTCAAGACAAAGCGGTCA 258
 Qy |||||
 326 CCCGACCTTTCGGCTATGTAGTGAAGGATGGCCCAACCGTGATGTGGTTGGGTC 385
 Db |||||
 259 CCGACCGTTGGTTACGGTACTAAAGGATGGACCCCAATGGTGACCTTGGCTGGCTT 318
 Qy |||||
 386 GAATACCTCTCTCAACCAACCTGATGTATCTCAACCAATCACTTTGCAATTTTC 445
 Db |||||
 319 GAGTACATCTCTTAATCTTTTGGCTTGAAGTCTCAACCAACCAACCGCCATTTTC 378
 Qy |||||
 446 CCAGAAATCTCTCATCTTCAAGCGGTGGGAGAACTACATTTACAGCAGTGAAGAAC 505
 Db |||||
 379 CGGCACACCTTGGCAATTTTCAGAGGCGAGTGGAGAGTACATTTAAGAGATGAAGAGA 438
 Qy |||||
 506 ATGTGCTATGCGGTGTGGAAATGTATGGCGGAGGGTGGGGATAGAGGAGGAAATACG 565
 Db |||||
 439 ATGTCGACCAATTTCTGGAATGTGTAGAGGAGAGCTAAAGATAGAGCCAAAGGAGAG 498
 Qy |||||
 566 TTAAGCAGGTTCTGAAGATGAGAAAGTATGTGTCTTCAAGTTGAACCACTACCGG 625
 Db |||||
 499 CTGAGCGGTTTGGTGAAGTGAAGAAAGTATGTGTCTGAGAAATGAACCATTTACCG 558
 Qy |||||
 626 CTTGCCCTGAGTGCAGCAGTCAACCGGAATTTGGTTGGGTTGGGGGACACACAGAC 685
 Db |||||
 559 -----GAGAAGAGAGACTCCGGTCAAGGAGAGATTTGGGTTCGGTGAGCAGACTGAT 612
 Qy |||||
 686 CCACAGATAATTTCTTAAAGATCTAACAGCACATCTGGCTTGCAAACTGTCTCACA 745
 Db |||||
 613 CCACAGTTGATATCACTGCTCAGATCAACAGCACAGAGGGTTTGCATACTGTCTCAA 672
 Qy |||||
 746 GATGCACCTTGGGTTTCACTGCTCAGTCACTTCTTTTCACTCAATGTTGGTGAC 805
 Db |||||
 673 GATGGAACATGGGTTGATGTTACACCTGATCATCTCTTCTTCTTCTTCTCGAGAT 732
 Qy |||||
 806 GCTCTACAGGTAATGACTAATGGAGGTTTAAAGTGAAGCATAGGTTTGGCTGAC 865
 Db |||||
 733 ACTCTTCAAGTGTATGACAAACGGAAGATCAAGAGTGTGAACATAGAGTGTGACAAAT 792
 Qy |||||
 866 ACAACGAAGTCAAGGTTATCAATGATCTACTTTTGGAGGACAGCGTTGAGTGAAATATA 925
 Db |||||
 793 ACAAGAGTCAAGGATATCGATGATCTACTTTCGAGGTCCTCTTGGAGCGAGAGATT 852
 Qy |||||
 926 GCACCTTTACCTTCACTGATGATTTAAAGGAGAGGAGTGTGTGTACAAGAGTTCACTGG 985
 Db |||||
 853 GCACCAATATCATGCTTGTGCGAAAGCAAGATGATTTGCTTTTATAATGAGTTTACTTGG 912
 Qy |||||
 986 TGTGAATACAAGAGGCTCGGTACACTTCAAGGCTAGCTGATTAATAGGCTTCCCTTTC 1045
 Db |||||
 913 TCTCAATACAAGTATCTGCTTACAAACGTAAGCTTGGTGATGATAGGCTTCTCTTT 972
 Qy |||||
 1046 CAGAAATCTGCTGATTAACCAACA 1073
 Db |||||
 973 GAGAAACGACCTCCATTTTCTCTATCCA 1000

RESULT 12
 US-10-670-454-5
 ; Sequence 5, Application US/10670454
 ; Publication No. US20040229357A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Stephen G
 ; APPLICANT: Hedden, Peter
 ; TITLE OF INVENTION: Gibberellin 2-Oxidase
 ; FILE REFERENCE: 0623.0970000
 ; CURRENT APPLICATION NUMBER: US/10/670,454
 ; CURRENT FILING DATE: 2003-09-26

; PRIOR APPLICATION NUMBER: US/09/719,108
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: PCT/GB99/01857
 ; PRIOR FILING DATE: 1999-06-11
 ; PRIOR APPLICATION NUMBER: GB 9812821.8
 ; PRIOR FILING DATE: 1998-06-12
 ; PRIOR APPLICATION NUMBER: GB 9815404.0
 ; PRIOR FILING DATE: 1998-07-15
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 1318
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1243, 1265)
 ; OTHER INFORMATION: unidentified residue
 ; US-10-670-454-5

Query Match 27.1%; Score 356.6; DB 8; Length 1318;
 Best Local Similarity 63.2%; Pred. No. 4.7e-93;
 Matches 586; Conservative 0; Mismatches 329; Indels 12; Gaps 2;
 Qy 132 CTTGTTTCAAGGATTCCTGTGTGACCTCAGCCACCCCGATGCCAAGATCTCATAG 191
 Db CCGGTTCTCTTAATCCCGTTATAGATATGTCTGACCCCAAGATCCAAACATGCCCTCG 137
 Qy 192 TGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGCTGTTCCATTGGAGT 251
 Db TGAAGCATGGAGACTTCGGCTTCTTCAAGGTGATCAACATGCGTTTCCGAGAGC 197
 Qy 252 TAATGGCCAAATTGAAGAAACGAGGCCCTCAGGTTCTTTAAAAAAATCTCAGTCCGAGAAAG 311
 Db TAGTCTCTGTTTGAAGAACACGAGACCGTCTGTTCTCTCGTTGCCAAGTCAGAGAAAA 257
 Qy 312 ACAGAGCTGTGTCCTCCCGACCTTTCGGCTATGTGTAGCAAGAGGATTTGCCCAACCGGTG 371
 Db CCCAAGTCG---CAGGTTATCCCTTCGGATACGGGAACAGTAAGATTTGGTCGGAATGGTG 314
 Qy 372 ATGTCGGTTGGTGAATACCTCTCTCAACACCAACCCCTGATGTTATCTCACCCAAAT 431
 Db ACGTGGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 374
 Qy 432 CACTTTGCAATTTCCGAGAAATCCTCATCAATTTCCAGGCGGTGGTGGAGAACTACATTA 491
 Db TATTTCCAAGTCTTCTCAAGCCCGGGAACCTTTCAGAAACGCAATTTGGAAGAGTACACAA 434
 Qy 492 CAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTTGATGCGGAGGGGTGGGGATAA 551
 Db CATCAGTCAGAAAAATGACATTCGATGTTTGGAGAGATCACAGATGGGCTAGGGATCA 494
 Qy 552 GGCAGAGAAATACGTTAAGCAGGTTGCTGAAGAGTGAAGAGTGAATGATGCTCTTCAGGT 611
 Db AACCGAGGAACACACTTAGCAAGCTTGTCTGACCAAAACACCGACTCGATTTAGAGAC 554
 Qy 612 TGAACCACTTACCGCTTTCCTCAGGTCGAGCAAGCACTGAAC-----CGGAATTTGG 662
 Db TTAATCACTATCCACCATGTCTCTTACCAATAAGAAACCAATGGTGTGAAGATGTGA 614
 Qy 663 TTGGGTTTGGGAGCACACAGACCCACAGATTAATTTCTGTCTTAAGATCTAACAGACAT 722
 Db TTGGTTTGGTGAACACACAGATCTCAATCATCTGTCTTTAAGATCTAACACACTT 674
 Qy 723 CTGGCTTCAATCTGTCTCAGATGGCCTTGGGTTTCACTCCACCTGATCAGACTT 782
 Db CTGGTCTCAATTAATCTAAATGATGGCTCAATGATCTCTGTCTCCCTCCGATCACACTT 734
 Qy 783 CTTTTTTCATCAATCTTGTGACGCTCTACAGGTAATCACTAATGGAGGTTTAAAGTG 842
 Db CTTCTTCTTCAACGTTGGTGAATCTCTCCAGGTGATGACAAATGGAGGTTCAAGAGCG 794
 Qy 843 TAAAGCATAGGTTTGGCTGACACAAAGTCAAGGTTATCAATGATCTACTTTGGAG 902

Db 795 TGAGGCATAGGGTTTATAGCTAACTGTAATAAATACTAGGGTTTCTATGATTTACTTCGCTG 854
 Qy 903 GACCAGGTTGAGTGAATAATATAGCACCTTTACCTTCAGTGATGTTTAAAGAGGAGGAGT 962
 Db 855 GACCTTCATGACTCAGAGAATCGCTCCGTTGACATGTTTGAATAGCAATATGAGGACGAGA 914
 Qy 963 GTTTGTACAAAGATGTCACATGCTGTGAATACAAAGAGGCTGGTACACTTCAAGGCTAG 1022
 Db 915 GGTGTACGAGGATTTACTTGTGCTGAATACAAAACCTCTACCTAACACTCTAGATTGT 974
 Qy 1023 CTGATAATAGGCTTGCCCTTTCCAGA 1049
 Db 975 CTGATAATAGGCTTCAACCAATTCGAAA 1001

RESULT 13
 US-10-392-325-3
 ; Sequence 3, Application US/10392325
 ; Publication No. US2004006080A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tanaka, Hiroshi
 ; APPLICANT: Kayano, Toshiaki
 ; APPLICANT: Matsuoka, Makoto
 ; APPLICANT: Kobayashi, Masatomo
 ; APPLICANT: Saito, Tamio
 ; APPLICANT: Sakamoto, Tomoaki
 ; APPLICANT: Sakai, Miho
 ; TITLE OF INVENTION: GIBBERELLIN 2-OXIDASE GENE, FUNCTIONS AND USES THEREOF
 ; FILE REFERENCE: SHZ-014
 ; CURRENT APPLICATION NUMBER: US/10/392,325
 ; CURRENT FILING DATE: 2003-03-18
 ; NUMBER OF SEQ ID NOS: 7
 ; PRIOR APPLICATION NUMBER: JP 2002-276051
 ; PRIOR FILING DATE: 2002-09-20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 984
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(984)
 ; OTHER INFORMATION:
 US-10-392-325-3

Query Match 26.9%; Score 354; DB 7; Length 984;
 Best Local Similarity 60.9%; Pred. No. 2.3e-92;
 Matches 598; Conservative 0; Mismatches 375; Indels 9; Gaps 1;
 Qy 69 TGGTTGTTCTGCTCAGCCAGCATTTGAACAGTTTTCCTCTGAAACCATTCAGTGCA 128
 Db 5 TGGTTCTGCTGCGCCGCGCGTGCATCATCCCGTGTGAGGTCCGCGGACCCCG 64
 Qy 129 CGCCCTTGTTCAGGGGATTCCTGTGCTGCACCTCAGCACCCCGATGCCAAGAATCTCA 188
 Db 65 GCGACGTCTTCTCGCGGTGCGGTGCTGACCTCGCGACCCCGCGGGGAGGCGG 124
 Qy 189 TAGTAAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCAATGTTTCCATTGG 248
 Db 125 TGGTGACGCTCGGAGCGGTACGGGTTCTTCAAGGTCGTCAACACCGCGGTGCCACGG 184
 Qy 249 AGTTAATGCCAATTTAGAAAACGAGCCCTCAGGTTCTTTAAATAATCTCAGTCCGAGA 308
 Db 185 ACAGATGGAACAGGCGGAGTCGAGGCGGTCTAGGTTCTTCTCCAGACGCGACCCGACA 244
 Qy 309 AAGACAGAGTGTGTCGCCCGCCAGCCCTTTCGGCTATGTTAGCAAGAGGATTTGCCCAAACG 368
 Db 245 AGGACCGCTCCGCGCCGCGCTACCGTTGCGGTACGCGCAGCAGCGATCGGTTCAATG 304
 Qy 369 GTGATGTGGGTCGGAATACCTCTCTCAACACCAACCCCTGATGTTATCTCAACCA 428
 Db 305 GCGACATGGGGTGGCTCGAGTACCTCTCTCTCGCCCTCGACGACGCGGTGCTCGCGGACG 364

Qy 429 AATCACTTTGCAATTTCCGAGAAATTCCTCATCTTTAGGCGGTGGTGAGAACTACA 488
 Db 365 CTGACACCGTCCGCTCTCG-----CGGTCTTCGGGCGCGTCTGAACGAGTACA 415
 Qy 489 TTACAGCAGTGAAGAACATGTGCTATGCGGTGTGGAATTTGATGCGGAGGGGTTCGGGA 548
 Db 416 TCTCGGGGTGCGGAAGGTGGCGGTGATGAGGCGGATGTCGAGGGGCTGGGCA 475
 Qy 549 TAAGGAGAGGAATAGCTTTAAGCAGGTTGCTGAAGATGAGAAAGTGAATTCGTGCTTCA 608
 Db 476 TTGCGCAGGCGGACCGCGCTGAGCGCTGTCACGCGGAAGGAGCGACCAAGGTGTTCC 535
 Qy 609 GGTGAACCACTACCCGCTTGCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGGT 668
 Db 536 GCGTGAACCACTACCGCGCTGCGCGGCTGCGAGGGGTCTCGCTGCACGCGTACCGGCT 595
 Qy 669 TTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACACACATCTGGCT 728
 Db 596 TCGGCGAGCACACCGACCGCAGCTGCTCGGTGCTCCGCTCAACCGCACGTCGCGCC 655
 Qy 729 TCGAATCTGCTCACAGATGCGACTTGGGTTTCAGTCCCACTGATCAGACTTCCCTTTT 788
 Db 656 TGCAGATCGCGTCCGCGACCGCCAGTGGGTGTCGCTGCGCTCCGACCGCGACTCCTTCT 715
 Qy 789 TCATCAATGTTGCTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAAGC 848
 Db 716 TGTCAACGTCGCGACTGTTGCGAGTTCTGACCAATGGGAGGTTCAAGAGCGTGAAGC 775
 Qy 849 ATAGGTTTGTGTCACACAAAGTCAAGGTTATCAATGATCTACTTTGAGGAGGACAG 908
 Db 776 ACAGGTTGTGGCCACAGCCTAAAGTCTAGGTTTCTCTCATCTACTTTGAGGGCCAC 835
 Qy 909 CGTTGAGTGAATAATATAGCACCTTTACCTTCAGTGTATGTTTAAAGAGGAGGAGTGT 968
 Db 836 CGTTAGACAGAGGATTCACCATTTGCCACAGCTGCTGGGGGAGGAGGAGAGGCTGT 895
 Qy 969 ACAAGAGTTACATGCTGTGAATAACAAGAGGCTGCGTACACTTCAAGGCTAGCTGATA 1028
 Db 896 ACAAGAGTTCACTGGGATGAGTACAGAGGCTGCTCAAAATCAAGGCTTGGAGACA 955
 Qy 1029 ATAGGCTTGCCTTTTCCAGAA 1050
 Db 956 ACAGGCTGGCCCGGTTTGAGAA 977

RESULT 14
 US-10-437-963-78659
 ; Sequence 78659, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 78659
 ; LENGTH: 1260
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_78444C.1
 US-10-437-963-78659

Query Match		26.9%;	Score 354;	DB 7;	Length 1260;
Best Local Similarity		60.9%;	Pred. No. 2.6e-32;		
Matches 598;		Conservative 0;	Mismatches 375;	Indels 9;	Gaps 1;
QY	69	TGGTTGTTCTGTCAGCCAGCATTAACCAAGTTTCTTCTGAAACCATTCAGTCCA	128		
DB	144	TGGTTCTCGTGGCCGCCCGCGTCGATCATCCCGTCTGAGGTGCGCGGACCCCG	203		
QY	129	CGCCCTTGTTCACGGGGATTCCTGTGTGTCGACTCACGCACCCCGATGCCAAGATCTCA	188		
DB	204	CGACGCTCTCTCCGGCGTCCGGTCTGCGACTCGGCAGCCCGCGGGGCGGCG	263		
QY	189	TAGTGAACCCCTGTAGGAGCTTCGGCTTCTCAAGCTGTGAAACCATGTGTTCATTGG	248		
DB	264	TGGTGGACCCCTGCGAGCGGTACCGGTCTTCAAGGTGCTCAACACCGCGGTGGCACGG	323		
QY	249	AGTTAATGSCCAATTTAGAAACAGAGGCCCTCAGGTCTTTTAAATAATCTCAGTCCGAGA	308		
DB	324	ACACGATGACAAAGCCGAGTCGGAGGCCGTGAGGTCTTCTCCAGAGCGCAGCCGACA	383		
QY	309	AAGACAGAGCTGGTCCCGCCCGACCTTTCCGCTATGTGTAGCAAGAGGATTTGGCCCAACG	368		
DB	384	AGGACCGCTCCGGCCCGGCTTACCGTTCGGGTACGGCAGCAAGCGGATCGGGTTCAATG	443		
QY	369	GTGATGTGGTGTGGTGTGAATACCTCTCTCAACACCAACCCCTGATGTATCTCAACCA	428		
DB	444	GGACATGGGGTGGCTCGAGTACCTCTCTCGCCCTCGACACGCGTCTCGCCGACG	503		
QY	429	AATCACTTTGCAATTTCCGAGAAATCTCATCATTTTCAGGGCGGTGTGGAGACTACA	488		
DB	504	CTGCAACCGTCCCGTCTCTGCG-----CGGTCTTCGGGCGGCTCTGAAACGAGTACA	554		
QY	489	TTACAGCAGTGAAGAACATGTCTATGCGGTGTGGAATTTGATGCGGAGGGGTGGGGA	548		
DB	555	TCTCGGGGTGCGGAAGGTGGCGGTGCGGCTGATGAGGCGATGTGGAAGGGCTGGGCA	614		
QY	549	TAAAGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAGTGAATTCGTCTCA	608		
DB	615	TTGCGCAGCGGACGCGCTGAGCGGCTGTGTGACGCGGAGGAGGACCAAGGTGTCTCC	674		
QY	609	GTTGAACCACTACCGGCTTCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGGT	668		
DB	675	CGGTGAACCACTACCGCGCGTCCCGCGCTGACGGGCTCGGCTGACGCGTCAACCGGT	734		
QY	669	TTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACTCTGGCT	728		
DB	735	TCGGCGAGCACACACCCGCGAGCTCGTCTCGTGTCTCGCTCAACCGCAGCTCCGGCC	794		
QY	729	TGCAATCTGTCTCAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTCTTTT	788		
DB	795	TGCAGATCGCGCTCCCGACGGCCAGTGGGTGTCCGTGCGCTCCGACCGCACTCTTCT	854		
QY	789	TCATCAATGTTGTGACGCTCTACAGGTATGACTAATGGGAGGTTTAAAGTGTAAAGC	848		
DB	855	TCGTCAACGTCGCGACTCGTTGCGAGGTTCTGACCAATGGGAGGTTCAAGACGCTGAAGC	914		
QY	849	ATAGGTTTGGCTGCACACAAGAGTCAAGGTATCAATGATCTACTTTTGAGGACCCAG	908		
DB	915	ACAGGTTGTGCCCAACAGCCTTAAAGTCTAGGGTTTCTTCACTACTTTTGAGGGCCAC	974		
QY	909	CGTTGAGTGAATAATATAGCACCTTTACCTTTCAGTGTATGTTTAAAGGAGGAGGTGTTGT	968		
DB	975	CGTTAGCAGAGGATTCACCATTTGCCACAGCTGCTGGGGAGGAGAGCAGACCTGT	1034		
QY	969	ACAAAGATTCTATGTTGTGAATACAGAGGCTGCGTACACTTCAAGGCTAGCTGATA	1028		
DB	1035	ACAAGAGTTCTATGGAATGAGTACAGAGGCTGCCTTACAAATCAAGGCTTGGAGACA	1094		
QY	1029	ATAGGCTTGGCCCTTTCCAGAA	1050		
DB	1095	ACAGGCTGGCCCGATTGAGAA	1116		

RESULT 15					
US-10-425-115-69575					
; Sequence 69575, Application US/10425115					
; Publication No. US20040214272A1					
; GENERAL INFORMATION:					
; APPLICANT: La Rosa, Thomas J.					
; APPLICANT: Kovalic, David K.					
; APPLICANT: Zhou, Yihua					
; APPLICANT: Cao, Yongwei					
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with					
; FILE REFERENCE: 38-21(53222)B					
; CURRENT APPLICATION NUMBER: US/10/425,115					
; CURRENT FILING DATE: 2003-04-28					
; NUMBER OF SEQ ID NOS: 369326					
; SEQ ID NO 69575					
; LENGTH: 1611					
; TYPE: DNA					
; ORGANISM: Zea mays					
; FEATURE:					
; OTHER INFORMATION: Clone ID: MRT4577_163444C.1					
US-10-425-115-69575					
Query Match		24.0%;	Score 315.8;	DB 8;	Length 1611;
Best Local Similarity		58.9%;	Pred. No. 4.8e-81;		
Matches 586;		Conservative 0;	Mismatches 397;	Indels 12;	Gaps 2;
QY	59	ACAACAACCATGTGTTCTGCTCTCAGCCAGCATTTGAACCAAGTTTCTTCTTCTGAAACCA	118		
DB	169	ACAGCATGTGTGTCGCGCAACCGCTCTGTCGACCAAGATCCCGCTCTCTCGGGTCC	228		
QY	119	TTCAGTCTCACGCCCTTTGTTTTCACGGGGATTCCTGTGTGTCGACCTCAACCAACCCGATGCC	178		
DB	229	CCGGCCCCCAGGACAGCTTCTCGGAGTGCCTGCGTCTGACCTCTCCAGCCACGCGCG	288		
QY	179	AAGAACTCTATAGTGAACGCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGACCATGGT	238		
DB	289	CGCGGGCGCATCGTGCAGCGCTTCGAGCGCTTCGGGTTCTTCAAGGTCTCAACCAACCGC	348		
QY	239	GTTCATTTGAGGTTAATGGCCAAATTTAGAAAAAGAGGCCCTCAGGTCTCTTAAAAAATCT	298		
DB	349	GTGGCGCGGCCACCATGGAACAGGGCCGAGTCCGAGGCCGTCAGGTCTTTCGCGCAGGGC	408		
QY	299	CAGTCCGAGAAGAAGACAGAGCTGGTCCCGCCGACCTTTTCGGCTATGTTAGCAAGAGATT	358		
DB	409	CAGCGGACAAAGGACCGCGCGGGCGCGCTACCGTTTCGGGTACGCGCAGCAAGCGGATC	468		
QY	359	GGCCCAACCGGTGATGTGCGTTGGGTGGAATACCTCTCTCTCAACCAACCCCTGATGTT	418		
DB	469	GGGCTCAATGGCGACATGGGGTGGCTCGAGTACCTCTCTCTCGCGCTCGACCGCGCTCG	528		
QY	419	ATCTCACCCAAATCACTTTTGCAATTTTCGAGAAAAATCCTCATCTTCAGGGCGGTGGTG	478		
DB	529	CTCTCCGAGCGCTGCCCGCTCCAGCG-----CGCGTTCCGAGCGCGCTG	579		
QY	479	GAGAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAAATGATGCGCGAG	538		
DB	580	AACGAGTACGTCGCGGCGTTCGGAAGGTGGCGCGCGTGTGCTGAGGCGGATGCGGAG	639		
QY	539	GGGTTGGGGATTAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAGTGT	598		
DB	640	GGCCTGGGCATTTGGGACCGCGACCGCTGAGTCCATGTTGAGCGCGCGCGGAGCGGAC	699		
QY	599	TCGTGCTTCAGTTGAACCACTACCGCTTTCCTGAGGTGCAAGCACTGAACCGGAAT	658		
DB	700	CAGGTGTTCCGCGTGAACCACTACCGCTTTCCTCCCGCGCTGACGGGCTGGGCTGCGAC	759		
QY	659	TTGGTTGGGTTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGC	718		
DB	760	GCCACGGGCTTCGCGGAGCACACCGACCGCAGATCATCTCGTCTCCGCTCCCAACGCG	819		
QY	719	ACATCTGGCTTGCAAAATCTGTCTCAGATGGCAC---TTGGGTTTCAGTCCCACTGAT	775		

Db	820	ACCTCCGGCCTGCAGATCGCGCTCCGCGACGGCGCGCAGTGGGTCTCCGTGCCCTCCGAC	879
Qy	776	CAGACTTCCTTTTTCATCAATGTGGTGACGCTCTACAGTAAATGAGGTTT	835
Db	880	CGCGACGCCCTTCTTCGTTAACGTGCGGCACTCGTTGCAGGTGCTGACCAACGGGAGTTC	939
Qy	836	AAAAGTGTAAGCATAGGGTTTTGGCTGACACAAACGAAGTCAAGGTTATCAATGATCTAC	895
Db	940	AGGAGCGTGAAGCACCGGGTGGTGACCAACAGCCTCAAGTCCAGAGTTTTCTTCATCTAC	999
Qy	896	TTTGGAGGACCAAGCGTTGAGTGAATAATATAGCACCTTTACCTTCAGTGATGTTAAAGGA	955
Db	1000	TTCCGGGGGCCGCCGCTGGGGCAGCGGATCGCGCCGCTGCCGAGGTGCTGGCGGAGGA	1059
Qy	956	GAGGAGTGTGTTGTACAAAGAGTTCACATGTTGTGAATACAAGAAAGGCTGCGTACACTTCA	1015
Db	1060	GAGGAGAGCTGTACAAAGAGTTCACGTGGGGCGAGTACAAAGAGCCCGGTACAAAGACG	1119
Qy	1016	AGGCTAGCTGAATAATAGGCTTGCCCTTTTCCAGAA	1050
Db	1120	AGGCTCGGCGACAAACAGGCTGGGCCAGTTTGAGAA	1154

Search completed: December 28, 2005, 01:23:05
Job time : 1242.83 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM nucleic - nucleic search, using SW model

Run on: December 27, 2005, 18:17:41 ; Search time 237.513 Seconds
(without alignments)
2879.764 Million cell updates/sec

Title: US-10-670-454-1
Perfect score: 1318
Sequence: 1 gttctctctctaccctgct.....caaaaaaaaaaaaaaaaa 1318

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 8336576

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA New:
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2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
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10: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:

*red. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	56.4	4.3	1017	US-11-152-892-5	Sequence 5, Appl1
2	40.8	3.1	3159	US-10-750-185-48573	Sequence 48573, A
3	40.6	3.1	164527	US-11-121-086-71	Sequence 71, Appl1
4	40	3.0	1011	US-11-152-892-3	Sequence 3, Appl1
5	39.2	3.0	3861	US-11-152-892-2	Sequence 2, Appl1
6	39.2	3.0	1125000	US-10-995-561-13286	Sequence 13286, A
7	38.8	2.9	150437	US-11-112-908-44	Sequence 44, Appl1
8	38.8	2.9	182314	US-11-112-908-45	Sequence 45, Appl1
9	38.6	2.9	130472	US-10-995-561-13312	Sequence 13312, A
10	38.4	2.9	1258	US-10-997-437A-1	Sequence 1, Appl1
11	37.4	2.8	4873	US-10-750-185-64795	Sequence 64795, A
12	37.2	2.8	201	US-10-995-561-52521	Sequence 52521, A
13	37.2	2.8	2555	US-10-750-185-53362	Sequence 53362, A
14	37	2.8	158410	US-11-121-086-46	Sequence 46, Appl1
15	36.8	2.8	1276	US-10-750-185-59293	Sequence 59293, A
16	36.8	2.8	3926	US-10-909-125-796	Sequence 796, App
17	36.4	2.8	1688	US-10-750-185-31828	Sequence 31828, A
18	36.4	2.8	645179	US-10-995-561-13293	Sequence 13293, A
19	36.2	2.7	159497	US-11-112-908-61	Sequence 61, Appl1
20	36.2	2.7	166639	US-11-121-086-52	Sequence 52, Appl1
21	36	2.7	842	US-10-750-185-42851	Sequence 42851, A
22	36	2.7	2171	US-11-152-892-1	Sequence 1, Appl1
23	36	2.7	18059	US-10-995-561-13195	Sequence 13195, A

C	24	36	2.7	142605	7	US-11-121-086-64	Sequence 64, Appl1
C	25	35.6	2.7	1778	6	US-10-750-185-37195	Sequence 37195, A
C	26	35.6	2.7	137935	6	US-10-995-561-13278	Sequence 13278, A
C	27	35.6	2.7	163317	7	US-11-117-187-212	Sequence 212, App
C	28	35.4	2.7	1229	6	US-10-750-185-57430	Sequence 57430, A
C	29	35.4	2.7	3720	6	US-10-927-641-127	Sequence 127, App
C	30	35.4	2.7	237326	7	US-11-157-389-2	Sequence 2, Appl1
C	31	35.2	2.7	1464	6	US-10-750-185-48102	Sequence 48102, A
C	32	35.2	2.7	1828	6	US-10-750-185-47560	Sequence 47560, A
C	33	35.2	2.7	1887	6	US-10-750-185-42377	Sequence 42377, A
C	34	35.2	2.7	40887	6	US-10-995-561-13303	Sequence 13303, A
C	35	35	2.7	1080	6	US-10-750-185-54120	Sequence 54120, A
C	36	35	2.7	3770	7	US-11-174-166-19	Sequence 19, Appl1
C	37	34.8	2.6	1126	6	US-10-750-185-34028	Sequence 34028, A
C	38	34.8	2.6	1082144	7	US-11-117-187-211	Sequence 211, App
C	39	34.6	2.6	162173	7	US-11-121-086-72	Sequence 72, Appl1
C	40	34.6	2.6	175673	7	US-11-121-086-55	Sequence 55, Appl1
C	41	34.4	2.6	1419	6	US-10-821-234-73	Sequence 73, Appl1
C	42	34.4	2.6	3575	6	US-10-750-185-28226	Sequence 28226, A
C	43	34.4	2.6	169047	7	US-11-121-086-15	Sequence 15, Appl1
C	44	34.2	2.6	1633	6	US-10-955-054A-103	Sequence 103, App
C	45	34.2	2.6	3454	6	US-10-793-626-4305	Sequence 4305, Ap

ALIGNMENTS

RESULT 1
US-11-152-892-5
; Sequence 5, Application US/11152892
; Publication No. US20050251883A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M.
; APPLICANT: Schomburg, Fritz M.
; APPLICANT: Michaels, Scott D.
; APPLICANT: Bizzell, Colleen M.
; TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
; FILE REFERENCE: 960296, 97605
; CURRENT APPLICATION NUMBER: US/11/152,892
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US/10/155,435
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Arabidopsis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1014)
US-11-152-892-5

Query Match 4.3%; Score 56.4; DB 7; Length 1017;
Best Local Similarity 55.7%; Pred. No. 3.2e-06;
Matches 108; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY	741	TCACAGATGCACTTGCGTTTACGTCACCTGATCAGACTTCCTTTTCATCATGTTG	800
DB	704	TCAAGACATATGATGATGATCGCTGTTAACTTAATCTTAAGCTCTCATATCAATATG	763
QY	801	GTGAGCTCTTACAGTAAGTAAGTAAGGAGTTTAAAGTGAAGCATAGGTTTGG	860
DB	764	GTGACTTATTTACGAGTACGATGAGCAATGAGATGACAAAGTGTGAACCGGTATATA	823
QY	861	CTGACACAAGAGTCAAGTTATCATGATCTACTTTGAGAGACCAAGCGTTGAGTGAA	920
DB	824	CGAACCAAGAGTGAAGATTTCTAAGCGCTTATTTATGTGTCCATATCAAGACCGG	883
QY	921	ATTATGACCTTTA 934	
DB	884	TTATAGAGTTTCA 897	


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RESULT 2
US-10-750-185-48573/c
; Sequence 48573, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: KMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48573
; LENGTH: 3159
; TYPE: DNA
; ORGANISM: Bovine 1986680619350
US-10-750-185-48573

Query Match
Best Local Similarity 3.1%; Score 40.8; DB 6; Length 3159;
Matches 90; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 1046 CAGAAATCTGCTGCTGATTAACCAACACCCCTCAATTCATCTTAAACGACGT 1105
DB 1298 CAGAACTTATGCTTATGTAATAATATCCGAACTCCAAACG 1239

QY 1106 GTTATTAACCCCATTTCTTCTTTCTTCTTCTGTCGTCTGATGTTCAACAGT 1165
DB 1238 TTTCTTCCTCTAATTTATTCATCTGTTTCACAGCTGTTATTTGTTAGATTAGACACT 1179

QY 1166 TGACTCTACTTGACATATATAGAAATGATTAAGTTTATCATTT 1217
DB 1178 TGACGAATCTGTTACTTCTTCAATTAATGACATCATATGTTCAAGATTT 1127

RESULT 3
US-11-121-086-71
; Sequence 71, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; PRIOR FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 71
; LENGTH: 164527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-71

Query Match
Best Local Similarity 3.1%; Score 40.6; DB 7; Length 164527;
Matches 91; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1060 TGATTACCAACACACCCCTTCAATTCACACTATTTCAGCAGGTATTAACCCCAAT 1119
DB 149090 TGCTTAATAAAGTAACAGTAACCTTTCCTATCTTTAAGAAAGTGGATTATAGTGATT 149149
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QY 1120 TTTCTTCCCTTTTCTTTCTTCTGTCGTCTGATGTTCAAAACATGACTCTACTGAC 1179
DB 149150 TTTATTTCTTTAAATTTATGTTGTTTCCAAATTTCTTTAAGAACATATACTTCAT 149209

QY 1180 ATATATGAATAATGAATAGATTAGATGTTTATCATTTTCTTTCTTGTTCAT 1234
DB 149210 AATATATATAAATCATTTCTTGGGTTTTTGTGTTTTTTTTTTTTTTTGGAGAT 149264

RESULT 4
US-11-152-892-3
; Sequence 3, Application US/11152892
; Publication No. US20050251883A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M.
; APPLICANT: Schomburg, Fritz M.
; APPLICANT: Michaelis, Scott D.
; APPLICANT: Bizzell, Colleen M.
; TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
; FILE REFERENCE: 960296.97605
; CURRENT APPLICATION NUMBER: US/11/152,892
; PRIOR FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US/10/155,435
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1011
; TYPE: DNA
; ORGANISM: Arabidopsis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1008)
US-11-152-892-3

Query Match
Best Local Similarity 3.0%; Score 40; DB 7; Length 1011;
Matches 85; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 747 ATGCACTTGGGTTTCAGTCCACATGATCAGACTTCTTTTTCATCAATGTTGGTACG 806
DB 713 ATGCAATGATGATGACCGTAAACCTTGCTGGAACCCCTTACAGTCACATTTGGGGATA 772

QY 807 CTCTACAGGTAATGACTAATGAGAGGTTTAAAGTAAAGCATAGGGTTTGGCTGACA 866
DB 773 TGTTTACGACACTGAGTAATGAGTGTACCAAGCGTGAACATAGAGTATTTCTCCAG 832

QY 867 CAACGAATCAGGTTATCATGATCTACTTTGGAGACG 906
DB 833 CAAATATGAGAGATGCAATATGCTTCTTCTGTATGTC 872

RESULT 5
US-11-152-892-2
; Sequence 2, Application US/11152892
; Publication No. US20050251883A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M.
; APPLICANT: Schomburg, Fritz M.
; APPLICANT: Michaelis, Scott D.
; APPLICANT: Bizzell, Colleen M.
; TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
; FILE REFERENCE: 960296.97605
; CURRENT APPLICATION NUMBER: US/11/152,892
; PRIOR FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US/10/155,435
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3861
; TYPE: DNA
; ORGANISM: Arabidopsis
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US-11-152-892-2

Query Match 3.0%; Score 39.2; DB 7; Length 3861;
Best Local Similarity 56.1%; Pred. No. 0.65; Indels 0; Gaps 0;
Matches 74; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 179 AAGAACTCTAATGACGCGCTGTAGGACCTTGGCTTCTTCAAGCTTGAACCATGT 238
DB 194 AAGAAAGCAATTCGAGAGCTTCGAGGAGTGGGGAATTTTCAAGTAAACCATGGA 253
QY 239 GTTCCATTGAGTTAATGCGCAATTTAGAAAAGCGCCCTCAGCTTTTAAAAATCT 238
DB 254 ATATCAATGATGTGTGGAGAAAGATGACAAGACCAATTTAGGTCTTTAGAGGCTT 313
QY 299 CAGTCCGAGAA 310
DB 314 TTGACAGAA 325

RESULT 6

US-10-995-561-13286
; Sequence 13286; Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13286

; LENGTH: 1125000

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(1125000)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-995-561-13286

Query Match 3.0%; Score 39.2; DB 6; Length 1125000;
Best Local Similarity 50.5%; Pred. No. 19; Indels 0; Gaps 0;
Matches 95; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 1124 TTTCCTTTCTTTCTGCTGTCTAGGTTCAACAGTGAAGTCTTACATAT 1183
DB 278403 TTTTATTTTATTTTCCCTAAATTTTATTTATTTATTTGCTATTTACTAGTAT 278462
QY 1184 ATGAAATGAATAGGTTAAGATTTATCATTTCTTTTCTTTCTTTCACTAAGTGA 1243
DB 278463 TCTGCTTCAAAAGTCTCGAGTCTTTCTTTATCTTTATTCATTTATCTTTA 278522
QY 1244 ACAGTGTGTCAACTCCCTTCCCTCAATGTCAGAAAGCAAGCACTAGTACAAA 1303
DB 278523 ACATTTTATTTATTTCTCTTTTATATCATGTGTAGTAGGCAAGATAGCTGCTAGG 278582
QY 1304 AAAAAAA 1311
DB 278583 ACAAATA 278590

RESULT 7

US-11-112-908-44/C

; Sequence 44; Application US/11112908

; Publication No. US20050260659A1

; GENERAL INFORMATION:

; APPLICANT: Harris, Cole

; APPLICANT: Harris, Lisa M.

; TITLE OF INVENTION: Breast Cancer Biomarkers

; FILE REFERENCE: 04-164-US

; CURRENT APPLICATION NUMBER: US/11/112,908

; CURRENT FILING DATE: 2005-04-22

; PRIOR APPLICATION NUMBER: US 60/564,758

; PRIOR FILING DATE: 2004-04-23

; PRIOR APPLICATION NUMBER: US 60/575,978

; PRIOR FILING DATE: 2004-06-01

; PRIOR APPLICATION NUMBER: US 60/631,702

; PRIOR FILING DATE: 2004-11-30

; PRIOR APPLICATION NUMBER: US 60/633,826

; PRIOR FILING DATE: 2004-12-07

; NUMBER OF SEQ ID NOS: 511

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 44

; LENGTH: 150437

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-112-908-44

Query Match 2.9%; Score 38.8; DB 7; Length 150437;
Best Local Similarity 58.8%; Pred. No. 7.6; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 836 AAAAGTGAAGCATAGGCTTTGGCTGACACACAGAGTCAAGCTTATCATATGATGAT 895
DB 2392 ACAAATAAAGCAAGAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 2333
QY 896 TTGGAGGACCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 949
DB 2332 GATTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2279

RESULT 8

US-11-112-908-45/C

; Sequence 45; Application US/11112908

; Publication No. US20050260659A1

; GENERAL INFORMATION:

; APPLICANT: Harris, Cole

; APPLICANT: Harris, Lisa M.

; TITLE OF INVENTION: Breast Cancer Biomarkers

; FILE REFERENCE: 04-164-US

; CURRENT APPLICATION NUMBER: US/11/112,908

; CURRENT FILING DATE: 2005-04-22

; PRIOR APPLICATION NUMBER: US 60/564,758

; PRIOR FILING DATE: 2004-04-23

; PRIOR APPLICATION NUMBER: US 60/575,978

; PRIOR FILING DATE: 2004-06-01

; PRIOR APPLICATION NUMBER: US 60/631,702

; PRIOR FILING DATE: 2004-11-30

; PRIOR APPLICATION NUMBER: US 60/633,826

; PRIOR FILING DATE: 2004-12-07

; NUMBER OF SEQ ID NOS: 511

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 45

; LENGTH: 182314

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-112-908-45

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Best Local Similarity 58.8%; Pred. No. 8.5; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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DB 64972 GATTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 64919

RESULT 9

US-10-995-561-13312

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Result No.	Score	Query		Length	DB	ID	Description
		Match	†				
1	996	100.0	999	6	Q8999251		Sequence
2	996	100.0	1318	6	BD243009		Enzyme. 7
3	996	100.0	1318	6	AX444991		Sequence
4	996	100.0	1318	6	AX008671		Sequence
5	996	100.0	1318	15	PC0132438		Phaseolus
6	920.8	92.4	1360	15	AB181372		Vigna an
7	827.4	83.1	1359	6	AR528429		Sequence
8	483.8	48.6	1406	15	AY588978		Nerium o
9	463.8	46.6	1245	15	AY594292		Nerium o
10	461.2	46.3	1383	15	CWA315663		Cucurbita
11	458	46.0	1308	15	CWA302041		Cucurbita
12	443	44.5	1292	15	AB125232		Nicotiana
13	436	43.8	1479	15	MM709113		M. macrocar
14	424.4	42.6	1026	6	AX506655		Sequence
15	424.4	42.6	1036	6	AX651428		Sequence
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17	424.4	42.6	1223	15	ATH132436		Arabidopsi
18	424.4	42.6	1237	6	BD243013		Enzyme. 7

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QY 721 TTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTTAATGGGAGGTTTAAAAGTGTAAAG 780
Db 788 TTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTTAATGGGAGGTTTAAAAGTGTAAAG 847
QY 781 CATAGGGTTTGGCTGACACAACGAAGTCAAGGTTATCAATGATCTACTTTTGGAGGACCA 840
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Db 908 GCGTTGAGTGAATAATAGCATTTCCTTCAGTGTATGTTAAAAGAGAGAGGTTTGG 967
QY 901 TACAAGAGTTCACATGGTGTGAATACAGAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 960
Db 968 TACAAGAGTTCACATGGTGTGAATACAGAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 1027
QY 961 AATAGGCTTGGCCCTTTCAGAGAAATCTGCTGCTGAT 996
Db 1028 AATAGGCTTGGCCCTTTCAGAGAAATCTGCTGCTGAT 1063

RESULT 3
AR444991
LOCUS AR444991 1318 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1 from patent US 6670527.
ACCESSION AR444991
VERSION AR444991.1 GI:42672879
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1318)
AUTHORS Thomas,S.G., Hedden,P. and Phillips,A.L.
TITLE Gibberellin 2-oxidase
JOURNAL Patent: US 6670527-A 1 30-DEC-2003;
The University of Bristol; Bristol;
GBX;
FEATURES
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.2e-291;
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QY 61 ACGCCCTTGTTCACGGGGATTCCTGTGTGCGACTCAGCAGCCCCGATGCCAAGAATCTC 120
Db 128 ACGCCCTTGTTCACGGGGATTCCTGTGTGCGACTCAGCAGCCCCGATGCCAAGAATCTC 187
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Db 188 ATAGTGAAACGCTGTAGGAGCTTCGGCTTCTTCAAGCTTGTGAACATGGTGTTCATTG 247
QY 181 GAGTTAATGGCCAAATTAGAAACAGGCGCTTCAGGTTCTTTAAAATACTCAGTCCGAG 240
Db 248 GAGTTAATGGCCAAATTAGAAACAGGCGCTTCAGGTTCTTTAAAATACTCAGTCCGAG 307
QY 241 AAAGACAGAGCTGGTCCCCCGACCTTTCGGCTATGTAGCAAGAGGATTGGCCCCAATC 300
Db 308 AAAGACAGAGCTGGTCCCCCGACCTTTCGGCTATGTAGCAAGAGGATTGGCCCCAATC 367
QY 301 GGTGATGTCTGGTTCGAATACCTCTCTCAACACCAACCTGATTTATCTCACCC 360

Db 368 GGTGATGTCTGGTTCGAATACCTCTCTCAACCAACCCCTGATTTATCTCACCC 427
QY 361 AAATCACTTTGTCATTTCCGAGAAATCCTCATCATTTTCAGGGCGGTGGTGGAGAACTAC 420
Db 428 AAATCACTTTGTCATTTCCGAGAAATCCTCATCATTTTCAGGGCGGTGGTGGAGAACTAC 487
QY 421 ATTACAGCAGTGAAGAACATGTCTATCGGTGTGGAAATTTGATGGCGGAGGGTTGGGG 480
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QY 481 ATAAGGAGAGGAAATACGTTTAAGCAGGTTTCTGTAAGGATGAGAAAAGTCAATTCGTCTTC 540
Db 548 ATAGGAGAGGAAATACGTTTAAGCAGGTTTCTGTAAGGATGAGAAAAGTCAATTCGTCTTC 607
QY 541 AGGTTGAACCACTACCCCGCTTGCCTCAGGTGCAAGCACTGAACCGGAATTTGGTTGGG 600
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QY 661 TTGCAAACTGTCTCAGATGGCACTTGGGTTTTCAGTCCCACTGATCAGACTTCCTTT 720
Db 728 TTGCAAACTGTCTCAGATGGCACTTGGGTTTTCAGTCCCACTGATCAGACTTCCTTT 787
QY 721 TTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTTAATGGGAGGTTTAAAAGTGTAAAG 780
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QY 781 CATAGGGTTTGGCTGACACAACGAAGTCAAGGTTATCAATGATCTACTTTTGGAGGACCA 840
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QY 841 GCGTTGAGTGAATAATAGCATTTCCTTCAGTGTATGTTAAAAGAGAGAGGTTTGG 900
Db 908 GCGTTGAGTGAATAATAGCATTTCCTTCAGTGTATGTTAAAAGAGAGAGGTTTGG 967
QY 901 TACAAGAGTTCACATGGTGTGAATACAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 960
Db 968 TACAAGAGTTCACATGGTGTGAATACAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 1027
QY 961 AATAGGCTTGGCCCTTTCAGAGAAATCTGCTGCTGAT 996
Db 1028 AATAGGCTTGGCCCTTTCAGAGAAATCTGCTGCTGAT 1063

RESULT 4
AX008671
LOCUS AX008671 1318 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 1 from Patent WO9966029.
ACCESSION AX008671
VERSION AX008671.1 GI:9996195
KEYWORDS
SOURCE Phaseolus coccineus
ORGANISM Phaseolus coccineus
REFERENCE 1
AUTHORS Phillips,A.L., Hedden,P. and Thomas,S.G.
TITLE Enzyme
JOURNAL Patent: WO 9966029-A 1 23-DEC-1999;
PHILLIPS ANDREW LEONARD (GB); HEDDEN PETER (GB); UNIV BRISTOL (GB);
THOMAS STEPHEN GREGORY (GB)
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Query Match		100.0%; Score 996; DB 6; Length 1318;
Best Local Similarity		100.0%; Pred. No. 2.2e-291;
Matches 996; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	ATGGTTGTTCTGTCTCAGGCAGCATTTGAACAGATTTTCTCTCTGAAACCATTTCAAGTCC 60
DB	68	ATGGTTGTTCTGTCTCAGGCAGCATTTGAACAGATTTTCTCTCTGAAACCATTTCAAGTCC 127
QY	61	ACGCCCTTGTTCACGGGGATTCCTGTGTGCTCAGCCTCAGCACCACCCGATGCCAAGATCTC 120
DB	128	ACGCCCTTGTTCACGGGGATTCCTGTGTGCTCAGCCTCAGCACCACCCGATGCCAAGATCTC 187
QY	121	ATAGTGAACGCTGTAGGACATTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTG 180
DB	188	ATAGTGAACGCTGTAGGACATTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTG 247
QY	181	GAGTTAATGCCCAATTTAGAAAACGAGGCTCAGGTTCTTTAAAAAATCTCAAGTCCGAG 240
DB	248	GAGTTAATGCCCAATTTAGAAAACGAGGCTCAGGTTCTTTAAAAAATCTCAAGTCCGAG 307
QY	241	AAAGACAGAGCTGCTCCCCCGACCTTTCCGCTATGTAGCAAGAGGATGGCCCCAAAC 300
DB	308	AAAGACAGAGCTGCTCCCCCGACCTTTCCGCTATGTAGCAAGAGGATGGCCCCAAAC 367
QY	301	GGTGATGTGGGTTGGGTGCAATACCTCTCTCAACACCAACCCCTGATGTATCTCACCC 360
DB	368	GGTGATGTGGGTTGGGTGCAATACCTCTCTCAACACCAACCCCTGATGTATCTCACCC 427
QY	361	AAATCACTTTGATTTTCCGAGAAATCTCATCATTTTCCGCGCGTGGTGAGAACTAC 420
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QY	421	ATTACAGCAGTGAAGACATGTCTATGGGTGTTGGAATTTGATGCGGAGGGGTTGGG 480
DB	488	ATTACAGCAGTGAAGACATGTCTATGGGTGTTGGAATTTGATGCGGAGGGGTTGGG 547
QY	481	ATAAGCAGAGGAATACGTTAAGCAGGTGCTGAAGGATGAGAAAAGTGATCGTCTTC 540
DB	548	ATAAGCAGAGGAATACGTTAAGCAGGTGCTGAAGGATGAGAAAAGTGATCGTCTTC 607
QY	541	AGTTGAAACACTACCGGCTTCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGG 600
DB	608	AGTTGAAACACTACCGGCTTCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGG 667
QY	601	TTTGGGGAGCACACAGCCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGC 660
DB	668	TTTGGGGAGCACACAGCCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGC 727
QY	661	TTGCAAAATCTGTCTCAGATGGCACTTGGGTTTTCAGTCCCACTGATCAGACTTCCTTT 720
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DB	788	TTTCAATGTTGGTGAGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGAAG 847
QY	781	CATAGGTTTTTGGCTGACACAAACGAACTCAAGGTATCAATGATCTACTTTGGAGACCA 840
DB	848	CATAGGTTTTTGGCTGACACAAACGAACTCAAGGTATCAATGATCTACTTTGGAGACCA 907
QY	841	GCCTTGAGTGAATAATAGCACCTTTACCTTTCAGTGTATTTAAAGGAGGAGTGTG 900
DB	908	GCCTTGAGTGAATAATAGCACCTTTACCTTTCAGTGTATTTAAAGGAGGAGTGTG 967
QY	901	TACAAAGAGTTTCAATGGTGTGAATACAGAAGGCTCGGTAACCTTCAAGGCTAGCTGAT 960
DB	968	TACAAAGAGTTTCAATGGTGTGAATACAGAAGGCTCGGTAACCTTCAAGGCTAGCTGAT 1027
QY	961	AATAGGCTTGGCCCTTTCCAGGAATCTGCTGCTGAT 996
DB	1028	AATAGGCTTGGCCCTTTCCAGGAATCTGCTGCTGAT 1063

RESULT 5	PC0132438	1318 bp	mRNA	linear	PLN 20-APR-1999
LOCUS	Phaseolus coccineus mRNA for GA 2-oxidase, gene gazoxl.				
DEFINITION	AJ132438				
ACCESSION	AJ132438.1	GI:4678585			
VERSION	GA 2-oxidase; ga2oxl gene.				
KEYWORDS	Phaseolus coccineus				
SOURCE	Phaseolus coccineus				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.				
REFERENCE	1	Thomas, S.G., Phillips, A.L. and Hedden, P.			
AUTHORS	Molecular cloning and functional expression of gibberellin 2-oxidases, multifunctional enzymes involved in gibberellin deactivation				
TITLE	Proc. Natl. Acad. Sci. U.S.A. 96 (8), 4698-4703 (1999)				
JOURNAL	10200325				
PUBMED	2 (bases 1 to 1318)				
REFERENCE	Phillips, A.L.				
AUTHORS	Direct Submission				
TITLE	Submitted (18-JAN-1999) Phillips A.L., Plant Sciences, IACR Long Ashton Research Station, Long Ashton Research Station, Bristol, BS41 9AP, UK				
JOURNAL	Location/Qualifiers				
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ORIGIN					
Query Match	100.0%; Score 996; DB 15; Length 1318;				
Best Local Similarity	100.0%; Pred. No. 2.2e-291;				
Matches 996; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	ATGGTTGTTCTGTCTCAGGCAGCATTTGAACCATTTTCTCTCTGAAACCATTTCAAGTCC 60			
DB	68	ATGGTTGTTCTGTCTCAGGCAGCATTTGAACCATTTTCTCTCTGAAACCATTTCAAGTCC 127			
QY	61	ACGCCCTTGTTCACGGGGATTCCTGTGTGCTCAGCCTCAGCACCACCCGATGCCAAGATCTC 120			
DB	128	ACGCCCTTGTTCACGGGGATTCCTGTGTGCTCAGCCTCAGCACCACCCGATGCCAAGATCTC 187			
QY	121	ATAGTGAACGCTGTAGGACATTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTG 180			
DB	188	ATAGTGAACGCTGTAGGACATTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTG 247			
QY	181	GAGTTAATGCCCAATTTAGAAAACGAGGCTCAGGTTCTTTAAAAAATCTCAAGTCCGAG 240			
DB	248	GAGTTAATGCCCAATTTAGAAAACGAGGCTCAGGTTCTTTAAAAAATCTCAAGTCCGAG 307			
QY	241	AAAGACAGAGCTGCTCCCCCGACCTTTCCGCTATGTAGCAAGAGGATGGCCCCAAAC 300			

308	AAAGACAGAGCTGGTCCCCCGACCCCTTTTCGGGTATGTAGCAAGAGGATTGGCCCAAC	367
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368	GGTGATGTGGTGGGTGGAATACCTCTCTCAACACCAACCCCTGATGTATCTCACCC	427
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428	AAATCACTTTGCATTTTCGAGAAATCTCATCATTTTCAGGCGGTGGTGAGAACTAC	487
421	ATTACAGCAGTGAAGAACATGCTATGCGGTGTTGGAATTCATGCGGAGGTTGGGG	480
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481	ATAAGSCAGAGGAATACGTTAAAGCAGGTTGCTGAAGGATGAGAAAGTGAATTCGTGCTTC	540
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541	AGTTTGAACCACTACCCGCTTGCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGG	600
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601	TTTGGGAGCACACAGACCCACAGATAATTTCTGCTTAAGATCTAACAGCACATCTGCC	660
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721	TTTCATCAATTTGGTGACGCTCTACAGGTAATGACTAATGGAGGTTTAAAAAGTGTAAAG	780
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781	CATAGGTTTTCGCTGACACAGCAAGTCAAGTTATCAATGATCTACTTTGGAGACCA	840
848	CATAGGTTTTCGCTGACACAGCAAGTCAAGTTATCAATGATCTACTTTGGAGACCA	907
841	GGCTTGAGTGAATAATAGCACCTTTACCTTCAGTGTATGTTAAAAAGGAGGAGTGTTG	900
908	GGCTTGAGTGAATAATAGCACCTTTACCTTCAGTGTATGTTAAAAAGGAGGAGTGTTG	967
901	TACAAAGAGTTACATGGTGTGAATACAAAGAGGCTGCGTACACTTCAAGGCTAGCTGAT	960
968	TACAAAGAGTTACATGGTGTGAATACAAAGAGGCTGCGTACACTTCAAGGCTAGCTGAT	1027
961	AATAGGCTTGGCCCTTTCAGAAATCTGCTGCTGAT	996
1028	AATAGGCTTGGCCCTTTCAGAAATCTGCTGCTGAT	1063
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LOCUS	AB181372	
DEFINITION	Vigna angularis VaGA2oxA1 mRNA for gibberellin 2-oxidase, complete cds.	
ACCESSION	AB181372	
VERSION	AB181372.1	GI:67077811
KEYWORDS	Vigna angularis (adzuki bean)	
SOURCE	Vigna angularis	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.	
REFERENCE	1	
AUTHORS	Park,S., Nakajima,M., Xu,Z., Tomioka,K., Sakane,M. and Yamaguchi,I.	
TITLE	Gibberellin 2-oxidases from adzuki bean hypocotyl	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 1360)	
AUTHORS	Nakajima,M., Xu,Z., Park,S., Tomioka,K., Sakane,M. and Yamaguchi,I.	
TITLE	Direct Submission	
JOURNAL	Submitted (08-JUN-2004) Masaotoshi Nakajima, The University of	

Tokyo, Dept. Appl. Biol. Chem., Fac. of Agriculture; 1-1-1 Yayoi, Bunkyo, Tokyo, 113-8657, Japan (E-mail:nkimg@grl.ch.a.u-tokyo.ac.jp, Tel:81-3-5841-5192, Fax:81-3-5841-8025)

FEATURES

source

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ORIGIN

Query Match 92.4%; Score 920.8; DB 15; Length 1360;

Best Local Similarity 95.3%; Pred. No. 1.8e-268;

Matches 949; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Db 83 ATGGTTGTTCTGCTCAGCCAGCATTTGAACCAAGTTTTCCTTCTGAAACCATTCAGTCC 142

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Db 143 ACGCCCTTGTTCACGGGATTCCTGTGTGACACCTCAGCACCCGATGCCAAGATCTC 202

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Qy 361 AAATCACTTTGCATTTTCGAGAAAATCCTCATCATTTTCAGGCGGTGGTGAGAACTAC 420

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Qy 421 ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTCATGCGGAGGTTGGGG 480

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QY 721 TTCATCAATGTGGTTCAGCGCTTACAGGTAATGACTAAATGGGAGGTTTAAAGTGTAAAG 780
Db 803 TTCATCAATGTGGTTCAGCGCTTACAGGTAATGACTAAATGGGAGGTTTAAAGTGTAAAG 862
QY 781 CATAGGGTTTGGCTGACACCAACGAAGTCAAGGTTATCAATGATCTACTTTTGGAGGACCA 840
Db 863 CATAGGGTTTGGCTGACACCAACGAAGTCAAGGTTATCAATGATCTACTTTTGGAGGACCA 922
QY 841 GCCTTGAGTGAATAATATAGACCTTTACCTTTCAGTATGATGTTAAAGAGAGAGAGTCTTTG 900
Db 923 GCCTTGAGTGAATAATATAGACCTTTACCTTTCAGTATGATGTTAAAGAGAGAGAGTCTTTG 982
QY 901 TACAAGAGTTACATGGTGTGAATACAGAGGCTCGGTACACTTCAAGGCTAGCTGAT 960
Db 983 TACAAGAGTTACATGGTGTGAATACAGAGGCTCGGTACACTTCAAGGCTAGCTGAT 1042
QY 961 AATAGGCTTGGCCCTTTTCCAGAAATCTGCTGCTGAT 996
Db 1043 AATAGGCTTGGCCCTTTTCCAGAAATCTGCTGCTGAT 1078

RESULT 7
AR528429 1359 bp DNA linear PAT 08-OCT-2004
LOCUS AR528429
DEFINITION Sequence 62 from patent US 6723897.
ACCESSION AR528429
VERSION AR528429.1 GI:53916494
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1359)
AUTHORS Brown,S.M., Elich,T.D., Heck,G.R., Kishore,G.M., Logusch,B.W.,
Logusch,S.J., Pillier,K.J., Rao,S., Ream,J.E. and Baerson,S.R.
TITLE Methods for controlling gibberellin levels
JOURNAL Patent: US 6723897-A 62 20-APR-2004;
Monsanto Technology, LLC; St. Louis, MO
FEATURES
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    1..1359
    /organism="unknown"
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ORIGIN

Query Match 83.1%; Score 827.4; DB 6; Length 1359;
Best Local Similarity 89.9%; Pred. No. 4.9e-240;
Matches 898; Conservative 1; Mismatches 97; Indels 3; Gaps 1;
QY 1 ATGGTTGTTCTGTCTCAGCCAGCAATGAACCACTTTTCTCTCTGAACCACTTCAAGTCC 60
Db 102 ATGGTTGTTCTGTCTCAGCCAGCAATGAACCACTTTTCTCTCTGAACCACTTCAAGTCC 161
QY 61 ACGCCCTTGTTCACGGGGATTCCTGTGGTGCAGCTCAGCACCCCGATGCCAAGAATCTC 120
Db 162 ACGCCCTTGTTCGGGGATTCCTGTGGTGCAGCTCAGCACCCCGATGCCAAGACCCAC 221
QY 121 ATAGTGAACGCCCTGTAGGAGCTTTCGGCTTCTTCAAGCTTGTGAACCACTGTTCCATTG 180
Db 222 ATAGTGAACGCCCTGTAGGAGCTTTCGGCTTCTTCAAGCTTGTGAACCACTGTTCCGTTA 281
QY 181 GAGTTAATGCCCAATTTAGAAACGAGGCGCTCAGGTTCTTTTAAATAATCTCAGTCCGAG 240
Db 282 CAGTTTATGGCCAAATTTGGAAACGAAACCCCTGGGTTCTTCAAAAACCTCAATCCGAG 341
QY 241 AAAGACAGAGCTGGTCCCCCGACCCCTTTCCGGCTATGGTAGCAAGAGGATTTGGCCCCAAC 300
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Db 342 AAAGACAGAGCTGGTCCCCCTGACCTTTTGGCTACGGCAGCAAGAGGATTTGGCCCTAAC 401
QY 301 GGTGATGTCCGTTGGGTGGAATACCTCTCTCAACACCAACCCCTGTATCTCACC 360
Db 402 GCGATGTCCGTTGGGTGGAATACCTCTCTCAACACCAACCCCTGTATCTCACC 461
QY 361 AAATCACTTTTGCATTTTCCGAGAAATCTCATCTTTTCCAGGGCGGTGGTGGAGAACTAC 420
Db 462 AAGTCACTTTTGCATTTTCCGAGAAATCTCATCTTTTCCAGGGCGGTGGTGGAGAACTAC 521
QY 421 ATTACAGCAGTGAAGAAATGTGCTATGCGGTGTTGGAATTTGATGCGGAGGGGTTGGG 480
Db 522 ATTACAGCAGTGAAGAAATGTGCTATGAGGTGTTGGAATTTGATGCGGAGGGGTTGGG 581
QY 481 ATAAGCAGAGAAATACGTTTAAGCAGGTTGCTGAAGGATGAGAAATGATCTCGTCTTC 540
Db 582 ATAAGCAGAGAAATGTTGTTGAGTGGTGGTGAAGGATGAGAAATGATCTCGTCTTC 641
QY 541 AGGTTGAACCACTTACCCGCTTTGCCCTGAGGTGCAAGCACTGAAC---CGGAATTTGGTT 597
Db 642 AGACTTAACTTACCTACCCGCTTTGCCCTGAGGTGCAAGCACTTGAACGGAAGGAAATTTGGTT 701
QY 598 GGGTTTGGGAGACACACAGACCAAGATAATTTCTGTCTTAAGATCTTAACAGCACATCT 657
Db 702 GGAATTTGGAGAGACACACAGACCAAGATAATTTCTGTCTTGAGATCTTAACAGCACATCT 761
QY 658 GGCCTTGAATCTGTCTCAGATGGCACTTGGGTTTTCAGTCCCACTGATCAGACTTCC 717
Db 762 GGCCTTGAATCTGTCTCAGATGGCACTTGGGTTTTCAGTCCCACTGATCAGACTTCC 821
QY 718 TTTTTCATCAATGTTGGTGCAGCTCTTACAGGTAATGACTAAATGGGAGGTTTAAAGTGTA 777
Db 822 TTTTTCATCAATGTTGGTGCAGCTCTTACAGGTAATGACTAAATGGGAGGTTTAAAGTGTA 881
QY 778 AAGCATAGGTTTGGCTGACCAACGAAGTCAAGGTTATCAATGATCTACTTTTGAGGA 837
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QY 838 CCAGCGTTCAGTGAAATATAGCACTTTACCTTCAGTATGTTTAAAGGAGGAGTGT 897
Db 942 CCAGCGTTCAGTGAAATATAGCACTTTACCTTCAGTATGTTTAAAGGAGGAGTGT 1001
QY 898 TTGTACAAAGAGTTTCAATGTTGTAATACAAAGAGGCTCGGTACACTTCAAGGCTAGCT 957
Db 1002 TTCTACAAAGAGTTTCAATGTTGTAATACAAAGAGGCTCGGTACACTTCAAGGCTAGCT 1061
QY 958 GATAATAGGCTTGGCCCTTTTCCAGAAATCTGCTGCTGAT 996
Db 1062 GATAATAGGCTTGGCCCTTTTCCAGAAATCTGCTGCTGAT 1100

RESULT 8
AY588978 1406 bp mRNA linear PLN 01-MAY-2005
LOCUS AY588978
DEFINITION Nerium oleander gibberellin 2 oxidase (GA2ox3) mRNA, complete cds.
ACCESSION AY588978
VERSION AY588978.1 GI:50293060
KEYWORDS
SOURCE Nerium oleander (common oleander)
ORGANISM Nerium oleander
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Gentianales; Apocynaceae; Apocynoidae;
Wrighteae; Nerium.
REFERENCE 1 (bases 1 to 1406)
AUTHORS Ubeda-Tomas,S., Garcia-Martinez,J.L. and Lopez-Diaz,I.
TITLE Isolation, characterization and multi-site polyadenylation of genes
GA 20-oxidases and GA 2-oxidases in Nerium oleander
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1406)
AUTHORS Ubeda-Tomas,S., Garcia-Martinez,J.L. and Lopez-Diaz,I.
TITLE Direct Submission
```

JOURNAL Submitted (02-APR-2004) Instituto de Biologia Molecular de Plantas, CSIC/Universidad Politecnica de Valencia, Avda de los Naranjos sn, Valencia 46022, Spain

FEATURES
source Location/Qualifiers
1..1406
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/mol_type="mRNA"
/db_xref="taxon:63479"
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/gene="GA2ox3"
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ORIGIN
Query Match 48.6%; Score 483.8; DB 15; Length 1406;
Best Local Similarity 71.1%; Pred. No. 2.1e-135;
Matches 669; Conservative 0; Mismatches 266; Indels 6; Gaps 2;
QY 51 ATTCAAGTCCAGCCCTTGTTCACGGGAGTATCTGTGTGTCGACCTCACCCACCCGATGC 110
DB 57 ATTCCCTCCACCAACTTCTACGAAGAAATCTCTGTGATTGACCTTCTCAAACTCGAGGC 116
QY 111 CAAGATCTCATAGTGAAGCCCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATCG 170
DB 117 AAACACTGAATAGTTAAGCCCTGTCAAGAGTTTGAATCTTTAAGGTGATCAATCATG 176
QY 171 TGTTCATTGGAGTTAATGCCAAATTTAGAAACAGAGGCCCTCAGGTTCTTTAAAAAATC 230
DB 177 TGTCTCTTGGAGTTCTAATACGAGCTAGAAGTGAAGCTGTCAAGTCTTCTCAATTACC 236
QY 231 TCAGTCCGAGAAAGACAGAGCTGTCCTCCCGACCTTTCCGGGTATGGTAGCAAGAGAT 290
DB 237 CCAACACAGAGAAAGAAAGTTCCGCTCTCTAAACCTTTTGGCTATGGTAAACAAGAGAT 296
QY 291 TGGCCCAACCGGTGATGTCGGTGGTTCGAATACCTCTCTCAACACCAACCCGTATG 350
DB 297 TGGCCAGAACGGGTGATGTCGGTGGATGAGTATCTTCTCTTAACACCAATCTCTGAAC 356
QY 351 TATCTCACCAATCACTTTGCAATTTCCGAGAAATCTCATCAATTTCCAGGCGGTGT 410
DB 357 AGTTTACGAGAAAGCGT---CACCATCCCGCGGATTCAGAACCTTTCTGCTTGTGT 413
QY 411 GGAGAACTCATTTACAGCAGTAGGAAGAACATGTGCTATGCGGTGTGGAAATGATGCCGA 470
DB 414 GAATGACTATGTTCAGCGGTGAGAAGTATGGCTGTGTGATGTTCTGGACATGATTGCAG 473
QY 471 GGGTTGGGGATAAGCAGAGAAATACGTTAGCAGGTTGCTGAAGGATGAGAAAGTGA 530
DB 474 TGGACTGAAGATTTGGGCCAAGGAATGTGCTGAGCAGGCTTTTAAAGAGATGAGAAAGCG 533
QY 531 TTCTGTCCTTCAGGTGAACCACTTACCCGCTTGGCCCTGAGGTGCAAGCACTGAAC--CG 587
DB 534 CGTGTCTTCAGGCTAAACCATATCCACCATGTCCAGAGCTTCAAGCATTTAGTGGTGC 593
QY 588 GAATTTGGTTGGTTGGGGAGACACAGACCCACAGATAAATTTCTGTCTTTAAGATCTAA 647
DB 594 AAATTTGATGGTTCGGAGAACACACAGATCTCTCAATAATATCTGTTGTGAGATCTAA 653
QY 648 CAGCACATCTGGTTCGAATCTGTCTCACAGATGGCACTTGGGTTTCACTCCACCTGA 707
DB 654 CAACACATCAGGCCTGCAAAATCTCTCTGAAGATGGGACATGGGTTTCACTCCCTCTGA 713

QY 708 TCAGACTTCCCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGAGGTT 767
DB 714 TCAGTACTCCTTTTTCATTAATGTTGGTGATTCCTTGCAGGTAATGACTAATGGAGATT 773
QY 768 TAAAGTCTAAGCATAGGTTTTCGCTGACACACGAGTCAAGGTTATCAATGATCTA 827
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QY 828 CTTTCGAGGACACAGCTTTCAGTGAATAATATAGCACTTTACCTTCAGTGATGTTAAAAAG 887
DB 834 CTTAGGAGGACCACTTTGGATGAAGAAGTAGCCCTTTATCTCTCACTAATGGAGGAGG 893
QY 888 AGAGGAGTGTGTACAAAGAGTTCACATGTTGTAATACAGAAAGGTCGCTACACTTC 947
DB 894 TGAAGAAAGTTGTATAAGGAATTCACATGGTGTGAATACAGAAAGTCACTTACAAGAC 953
QY 948 AAGGCTAGCTGATATAGCTTGCCTTCCCTTCCAGAAATCTG 988
DB 954 GAGGCTTGGTGACACAGGCTCAAAATCTTTTGAGAAATCTG 994

RESULT 9
AY594292 1245 bp mRNA linear PLN 30-APR-2005
LOCUS Nerium oleander GA 2-oxidase 2 mRNA, complete cds.
DEFINITION AY594292
ACCESSION AY594292
VERSION AY594292.1 GI:51011365
KEYWORDS
SOURCE Nerium oleander (common oleander)
ORGANISM Nerium oleander
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Gentianales; Apocynaceae; Apocynoidae; Wrightieae; Nerium.
REFERENCE 1 (bases 1 to 1245)
Ubeda-Tomas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I.
Isolation, characterization and multi-site polyadenylation of GA 20-oxidases and GA 2-oxidases in Nerium oleander
Unpublished
2 (bases 1 to 1245)
Ubeda-Tomas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I.
Submitted (08-APR-2004) Instituto de Biologia Molecular y Celular de Plantas, Consejo Superior de Investigaciones Cientificas (CSIC), Universidad Politecnica de Valencia, Avda. de los Naranjos s/n, Valencia 46022, Spain
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source Location/Qualifiers
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ORIGIN
Query Match 46.6%; Score 463.8; DB 15; Length 1245;
Best Local Similarity 68.0%; Pred. No. 2.5e-129;
Matches 677; Conservative 0; Mismatches 312; Indels 6; Gaps 2;
QY 1 ATGGTTGTTCTGCTCAGCCAGCATTTGACCAAGTTTTTCTTCTGNAACCATTCAGTCC 60
DB 1 ATGGTGGTCTTGTGTCANACCAGCAATGGAACGATCTCTGCTTAGTCAAGAACTGTAAAGCT 60

QY 61 ACGCCCTTGTTCACGGGATTCCTGTGGTGCAGCTCAGGCACCCCGATGCCAAGATCTC 120
Db 61 CCACATATTCGGGGTTCATTTGATAGACTCTCGAAGCTGACTCGAAGACCTTC 120
QY 121 ATAGTGAACGCTGTAGGGACTTCGGCTTCTCAAGCTTGTGAACCATGCTGTTCATTTG 180
Db 121 CTGTGTAAGGCTGTCAAGAGTTGGATTTTCAAAGTCATTAATCAAGCTGTTCACACC 180
QY 181 GAGTTAATGGCCATTTAGAAACGAGGCCCTCAGGTTCTTTAAATAATCTCAGTCGAG 240
Db 181 GAATTCATCAACCAACTTGAGTCTGAAGCTGTCAAAATTTCTTCTTTGGCCCTTTCCGAT 240
QY 241 AAAGACAGAGCTGTCCCCCGACCTTTCCGGCTATGTAGCAAGAGGATGGCCCAAC 300
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Db 301 GCGATATCGATGGGTTGAATACATCTATCCACCAATTCGGAATTCATTTACCAA 360
QY 361 AATCACTTTGCAATTTCCGAGAAATCCTCATCTTTCAGGCGGTGTGGAGACTAC 420
Db 361 AGATTTGAATCAATTTTGGCATGACCCCAAAAAAATTTCTGATGCTGTATGACTAC 420
QY 421 ATTACAGCAGTGAAGAACATGCTATGCGGTGTGGAAATTTGATGGCGAGGGTTGGGG 480
Db 421 GTATCATCAGTAAGAAATATGGCTTGTGAATATCTTGAATTAATGAGCAGAGTTGAAT 480
QY 481 ATAAGGCAGAGGAATACGTTAAGCAGTTGCTGAAGGATGAGAAAAAGTGAATTCGCTTC 540
Db 481 ATTACGCAAGAAGCTGTTTCAGCAAGCTCTTGAATGATGAACAGAGTGAATTTAAAT 540
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QY 658 GGCTTGCAATCTGTCTCAGAGATGGCATTGGGTTTTCAGTCCCACTGATCAGACTTC 717
Db 661 GGCCTTCAATACAAATTTGAAGATGGAAGCTGATATCCATTCACCTGATCAGAGTTCA 720
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Db 781 AAGCATAGGGTTTTGGCAACAGATATGAAATCCAGGCTTTCGATGATTTATTTGGAGGA 840
QY 838 CCAGCGTTGAGTGAATAATAGCACCTTTTACCTTCAGTGAATGTTAAAGGAGAGGATGT 897
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QY 898 TTGTACAAAGAGTTTACATGGTGTGAATACAAAGAGCTCGGTACACTTCAAGGCTAGCT 957
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QY 958 GATAATAGGCTTGCCCTTTCCAGAAATCTGCTGC 992
Db 958 GATAACAGACTGCTCTGTTTGAGAAATTTGCTGC 992

RESULT 10
CMA315663 1383 bp mRNA linear PLN 19-JUN-2003
LOCUS Cucurbita maxima partial mRNA for Gibberellin 2-oxidase (ga2ox
DEFINITION gene).
ACCESSION AJ315663
VERSION AJ315663.1 GI:32127336

KEYWORDS
SOURCE
ORGANISM

ga2ox gene; gibberellin 2-oxidase.
Cucurbita maxima (winter squash)
Cucurbita maxima

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.

REFERENCE

1 Frisae A. and Lange T.
Gibberellin biosynthesis in young seedlings of Cucurbita maxima L
Unpublished
2 (bases 1 to 1383)
Lange, T.
Direct Submission
Submitted (19-JUN-2001) Lange T., Botanical Institute, TU
Braunschweig, Mendelssohnstr. 4, D-38106 Braunschweig, GERMANY
related entry AJ315662.
Location/Qualifiers

FEATURES
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WLSVPDHSFFINVGDLSIQVNTNGRFKSVKRVLTNSKSRVSMIYFGPPLSEKIA
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ORIGIN

Query Match 46.3%; Score 461.2; DB 15; Length 1383;

Best Local Similarity 69.0%; Pred. No. 1.6e-128;

Matches 647; Conservative 0; Mismatches 288; Indels 3; Gaps 1;

QY 58 TCACGCCCTTGTTCACGGGATTCCTGTGGTGCAGCTCAGGCACCCCGATGCCAAGAT 117
Db 64 TCTGCAGCATTTCTACTCTGGGATTCATTTGATAGACCTCTCTGCACAGATGCTAAACA 123
QY 118 CTCATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTCCA 177
Db 124 CTATTTGTCAAGCTTGTGAAGACTCGGATCTTTAAGTTGTCAACATGGTGTCCCC 183
QY 178 TTGGAGTTAATGGCCAAATTTAGAAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCC 237
Db 184 ATGGAATTAATCTCTCTCTTGAATCAGAATCCACCAAAATCTCTCCCTTCCCTCTCT 243
QY 238 GAGAAAGACAGAGCTGGTCCCCCGACCTTTTCGGCTATGGTAGCAGAGGATTTGCCCA 297
Db 244 GAAAAACAGAGAGCTGGCCCTCTCTCCCTTTTGGCTATGGAAACAAACAAATTTGCCGC 303
QY 298 AACGGTGTATGCTGGTGGGTGCAATACCTCTCTCAACACCAACCCCTGATGTTATCTCA 357
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QY 358 CCCAAATCACTTTTGCAATTTCCGAGAAAAATCTCATCATTTTCAGGGCGGTGGGAAC 417
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QY 418 TACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTGTGGAATTTGATGGCGGAGGGTTG 477
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QY 478 GGGATGAAGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTCGTGC 537
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Db 484 AAGATTCAACACGAAACGTTTACAGTACGTTGATGATGAAACAGAGGACCTCTGTT 543
QY 538 TTCAAGTTGAACCACTACCGCTTCCCTGAGGTGCAAGCACTGACCG---GAATTTG 594
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Db 544 TTCAGAGTGAACCAATTATCCGCAATGTCAGACCTTCAAGCTTTAAAGGAACAACATG 603
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Db 604 ATTGGATTGGAGAACACAGACCCCTCAATCATTTTCAGTTTGGATCAACACACT 663
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Db 664 TCTGGATTCAAAATCTCTCGCAGATGGAATTTGGATATCTGTTCTCCCGATCACAGC 723
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Db 724 TCTTCTCTCATCAATGTTGGTGAAGCTCTTACAGGTGATGACTAATGGAAGATTTCAAAAGT 783
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Db 844 GGGCCACCTTGAAGTGAATAATAGCACCTTTACCTTCAAGTGAATGTTAAAGGAGAGGAG 903
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Db 904 AGTTTGTACAAAGATTTACATGTTGTTGATGACAAAGATGAGCTTTACAACTCCAGGTTG 963
QY 955 GCTGATAATAGCTTCCCTTTCACAGAAATCTGTCG 992
Db 964 GCTGACACAGCTTGTGCTTTGAAAGATTGACG 1001

RESULT 11

CMA302041 1308 bp mRNA linear PLN 16-DEC-2002
Cucurbita maxima mRNA for gibberellin 2-oxidase (ga2ox gene).
AJ302041
AJ302041.1 GI:27123664
ga2ox gene; gibberellin 2-oxidase.
Cucurbita maxima (winter squash)
Cucurbita maxima

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.

REFERENCE

Frisee,A. and Lange,T.
Expression studies on the major Gibberellin dioxygenases in
developing seeds of Cucurbita maxima L
Unpublished
2 (bases 1 to 1308)
Lange,T.

JOURNAL

Submitted (14-DEC-2000) Lange T., Botanical Institute, Dept. Plant
Physiology and Biochemistry, TU Braunschweig, Mendelssohnstr. 4,
Braunschweig, D-38106, GERMANY

FEATURES

Location/Qualifiers
1..1308
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87..1052
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CDS

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DEQSDSVFRVNHYPCCDLQALKNTNMGFCHEITDQIISVLRNNTSGFOJSLADGN
WISVPDHSFFINVDLSQVNTNGRFSVGRVLTNLSKRSVMIIYFGGPIFSEKIA
PLASLMQGEERSLYKEFTWFYKRSAYNSRLADNRLVPPFRTAAS"

ORIGIN

Query Match 46.0%; Score 458; DB 15; Length 1308;
Best Local Similarity 68.8%; Pred. No. 1.5e-127; Indels 3; Gaps 1;
Matches 645; Conservative 0; Mismatches 290;
QY 58 TCCAGCCCTTGTTCACGGGGATTCCTGTGTGTCGACCTCAGCACCCCGATGCCAAGAT 117
|||
Db 108 TCTGCAGCATTTCTACTCTGGGATTCCTATTGATAGACCTCTCTGCACCATGCTTAAACAA 167
QY 118 CTCATAGTGAACGCTGTAGGACTTTCGCTTCTTCAAGCTTGTGAACCATGCTGTTC 177
|||
Db 168 CTCATTGTCAAAAGCTTGTGAAGAACTCGGATTTCTTTAAGTTTGTCAAAACATGTC 227
QY 178 TTGGAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCC 237
|||
Db 238 ATGGAATTAATCTCTCTCTTGAATCAGAATCCACAAATCTCTCCCTTCCCTCTCT 287
QY 238 GAGAAAGACAGAGCTGTGTCCTCCCGACCTTTTCGGCTATGTGAGCAAGAGGATTTGGCCCA 297
|||
Db 288 GAAAACAGAGAGCTGCGCCCTCTTCCCTTTTGGCTATGGAACAAACAAATTTGGCCGC 347
QY 298 AACGTTGATGTCGGTGGGTGGAATACCTCTCTCTCAACCAACCACTGATGTTATCTCA 357
|||
Db 348 AATGGCATGTGCGTGGGTGGAATATCTCTCTTGAACACATCTCATCTCGAATCCAACTCG 407
QY 358 CCCAAATCACITTTGATTTCCGAGAAATCTCTCATCTTTTCAGGGCGGTGGAGAAC 417
|||
Db 408 GATGGTTTCTCTCCATGTTTGGCCAGACCCACAAAACCTCCGCTCTCTGTGAACGAT 467
QY 418 TACATTACAGCAGTCAAGAACATGTGCTATGCGGTGTTGGAAATGATGCGGAGGGTTG 477
|||
Db 468 TACATCTCGCTGTGAGGAACATGCGGGTGAATCTCTCGACTAATGCGCGAGGGTTG 527
QY 478 GGGATAAGGAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATCGTGC 537
|||
Db 528 AAGATTCAACCAACGAAACGTTTCAAGTCTGTCGATGATGAACAGACGACTCTGTT 587
QY 538 TTCAGTTGMAACCACTACCGCTTCCCTGAGGTGCAAGCACTGAACG---GAATTTG 594
|||
Db 588 TTCAGAGTGAACCAATTATCCGCAATGTCAGACCTTCAAGCTTTAAAGGAACAACATG 647
QY 595 GTTGGTTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAAGATCTTAACAGCACA 654
|||
Db 648 ATTGATTTGGAGAACACACAGACCCCTCAATCATTTTCAGTTTGGATCAACACACT 707
QY 655 TCTGCTTGCAAAATCTGCTCAGATGGCACTTGGGTTTTCAGTCCCACTGATCAGACT 714
|||
Db 708 TCTGGATTTCAAAATCTCTCTCGAGATGGGAATTTGGATATCTGTTCTCCCGATCACAGC 767
QY 715 TCTTTTTCATCAATGTTGGTGAAGCTCTACAGGTAAATGACTAATGGGAGGTTTAAAGT 774
|||
Db 768 TCTTCTTTCATCAATGTTGGTGAAGCTCTTTACAGGTGATGACTAATGGAGAGATTTCAAAAGT 827
QY 775 GTAAAGCATAGGTTTTCGCTGACCAACGAAGTCAAGGTATCAATGATCTACTTTCGA 834
|||
Db 828 GTGAAGCATAGGTTTTCGACAAACAGCTCGAAGTCAAGGTTTCAATGATCTACTTCGCT 887
QY 835 GGACCAGCGTTGAGTGAATAATATAGCACTTTTACCTTTCAGTGAATGTTTAAAGGAGAGGAG 894

Search completed: December 27, 2005, 21:42:44
Job time : 5303.67 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 16:12:28 ; Search time 671.461 Seconds
(without alignments)
9885.961 Million cell updates/sec

Title: US-10-670-454-1_COPY_68_1063

Perfect score: 996

Sequence: 1 atggtgtctgtctcagcc.....tccagaaatctgtgtgat 996

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	996	100.0	999	13	ADT62692
2	996	100.0	1318	3	AAZ55912 DNA encod
3	827.4	83.1	1359	3	AAZ55912 Runner be
4	827.4	83.1	1359	3	AAZ99471 Soybean g
5	424.4	42.6	1026	6	AD40261 Soybean G
6	424.4	42.6	1026	6	ABZ13545 Arabidops
7	424.4	42.6	1026	8	AD467975 Arabidops
8	421.4	42.3	1352	12	AAZ55916 Arabidops
9	419.8	42.1	1365	12	AAZ55916 Arabidops
10	418.2	42.0	1403	3	AAZ99472 Soybean D
11	418.2	42.0	1403	3	AAZ99472 Soybean g
12	381.6	38.3	1008	3	AD40262 Soybean G
13	362.6	36.4	1473	12	AD40262 Soybean G
14	356.6	35.8	1224	3	AAZ55917 Arabidops
15	356.6	35.8	1316	3	AAZ55917 Arabidops
16	355.6	35.7	1651	14	AAZ55915 Arabidops
17	354	35.5	984	8	AB67733 Rice geno
18	354	35.5	984	12	AD470120 Rice geno
19	354	35.5	1271	14	ADK00081 Rice cDNA
					AB67784 Rice geno

20	354	35.5	1650	12	ADM94203	Adm94203 Rice Diox
21	314.2	31.5	1555	12	ADM94201	Adm94201 Corn Diox
22	307.8	30.9	783	3	AAZ99474	Aaz99474 Cotton g1
23	307.8	30.9	783	6	AAZ99474	Aaz99474 Cotton g1
24	301.6	30.3	831	13	ADX11608	Adx11608 Plant ful
25	285	28.6	927	12	AD145210	Adi45210 Rice isop
26	272.6	27.4	860	13	ADX13286	Adx13286 Plant ful
27	188.6	18.9	1322	13	ADX09682	Adx09682 Plant ful
28	187	18.8	1065	8	ADA69812	Ada69812 Rice gene
29	172.2	17.3	919	13	ADX63586	Adx63586 Plant ful
30	166	16.7	811	3	AAZ99478	Aaz99478 Maize gib
31	166	16.7	811	6	AD40268	Ad40268 Maize gib
32	161.8	16.2	95769	8	AD468659	Ad468659 Arabidops
33	156.2	15.7	504	12	AD145683	Ad145683 Corn isop
34	155.6	15.6	403	3	AAZ99473	Aaz99473 Soybean g
35	155.6	15.6	403	6	AD40263	Ad40263 Soybean G
36	154.8	15.5	406	3	AAZ99475	Aaz99475 Cotton g1
37	154.8	15.5	406	6	AD40265	Ad40265 Cotton GA
38	152.4	15.3	966	6	AAZ99469	Aaz99469 Arabidops
39	152.4	15.3	966	6	AD40259	Ad40259 A. thalia
40	150.4	15.1	537	12	AD145522	Ad145522 Banana is
41	141	14.2	480	3	AAZ50271	Aaz50271 Arabidops
42	132	13.3	683	3	AAZ54605	Aaz54605 Arabidops
43	130.4	13.1	687	3	AAZ53074	Aaz53074 Arabidops
44	120	12.0	426	3	AAZ99477	Aaz99477 Maize gib
45	120	12.0	426	6	AD40267	Ad40267 Maize GA

ALIGNMENTS

RESULT 1

ADT62692	ID	ADT62692 standard; DNA; 999 BP.
XX	AC	ADT62692;
XX	DT	13-JAN-2005 (first entry)
XX	DE	DNA encoding Phaseolus coccineus gibberellin 2-oxidase.
XX	KW	DNA plasmid; transfer DNA; T-DNA; Agrobacterium Ti plasmid; transgene;
XX	KW	expression cassette; transgenic plant; transgenic; plant;
XX	KW	gibberellin 2-oxidase; ds.
XX	OS	Phaseolus coccineus.
XX	XX	WO2004092390-A2.
XX	PD	28-OCT-2004.
XX	PF	09-APR-2004; 2004WO-US011000.
XX	PR	09-APR-2003; 2003US-0461459P.
XX	XX	(MONS) MONSANTO TECHNOLOGY LLC.
XX	PI	Gilbertson L, Krieger E, Zhang W, Ye X;
XX	DR	WPI; 2004-758349/74.
XX	PT	New DNA plasmid comprising a T-DNA comprising an Agrobacterium Ti plasmid
XX	PT	first border region linked to a transgene linked to an Agrobacterium Ti
XX	PT	plasmid second border region, useful for enhancing production of
XX	PT	transgenic plants.
XX	XX	Example 1; SEQ ID NO 3; 77pp; English.
XX	PS	The present invention relates to a DNA plasmid comprising a transfer DNA
XX	CC	(T-DNA) comprising an Agrobacterium Ti plasmid first border region linked
XX	CC	to at least one transgene linked to an Agrobacterium Ti plasmid second
XX	CC	border region, and located in the DNA plasmid outside of the T-DNA is a
XX	CC	plant expression cassette comprising a plant cell non-lethal negative

selectable marker gene linked to a vector backbone DNA. Also disclosed are a method for enhancing the selection of transgenic plants that do not contain vector backbone DNA, a method for reducing the copy number of a transgene in a plant cell, and a transgenic plant produced by the method. The DNA plasmid comprises the expression cassette comprising a promoter that functions in plant cells operably linked to a plant cell non-lethal negative selection marker gene. The promoter is a constitutive promoter. The promoter expresses the linked non-lethal negative selection marker gene product in tissue culture during plant regeneration. The plant cell non-lethal negative selectable marker gene comprises a plant hormone biosynthetic pathway gene, degradative gene, biosynthetic pathway substrate-diverting gene or signalling gene, or metabolic interference gene. The transgene is a plant positive selectable marker gene selected from antibiotic resistance and herbicide resistance. The transgene comprises a transgene of agronomic interest. The plant hormone biosynthetic pathway gene is selected from gibberellin acid pathway genes, cytokinin pathway genes, auxin pathway genes, ethylene pathway genes, and abscisic acid pathway genes. The plasmid is useful for enhancing the production of commercially viable transgenic plants. The present sequence represents DNA encoding phaseolus coccineus gibberellin 2-oxidase. The sequence is used as a non-lethal negative selectable marker gene.

XX
SQ Sequence 999 BP; 263 A; 221 C; 249 G; 266 T; 0 U; 0 Other;

Query Match 100.0%; Score 996; DB 13; Length 999;
Best Local Similarity 100.0%; Pred. No. 5.8e-310; Indels 0; Gaps 0;
Matches 996; Conservative 0; Mismatches 0;

QY 1 ATGTTGTTCTCTCTCAGCAGCATTGAACCACTTTTCTCTGAAACCAATTCAGTCC 60
DB |||||
QY 61 AGCCCTTGTTCACGGGGATTCCTGTGTGTCGACCTCAGGCACCCCGATGCCAAGATCTC 120
DB |||||
QY 61 AGCCCTTGTTCACGGGGATTCCTGTGTGTCGACCTCAGGCACCCCGATGCCAAGATCTC 120
DB |||||
QY 121 ATAGTGAACGCTGTAGGACCTTCGGCTTCTTCAAGCTTGTGAACCATGTGTTCATTG 180
DB |||||
QY 181 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTCTCTTTAAAAATCTCAGTCCGAG 240
DB |||||
QY 241 AAAGACAGAGCTGGTCCCCCGACCCCTTCGGCTATGTGTAGCAGAGGATTCGCCCAAC 300
DB |||||
QY 301 GGTGATGTCGGTGGTTCGAATACCTCCTCCTCAACACCAACCCCTGATGTTATCTCACCC 360
DB |||||
QY 361 AAATCACTTTGCAATTTCCGAGAAAATCCTCATCTTCAGGCGCGTGTGGAGAACTAC 420
DB |||||
QY 421 ATTACAGCAGTGAAGAACATGTCTATGCGGTGTTGGAATTGATGCGGAGGGGTTGGGG 480
DB |||||
QY 481 ATAAGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTCGTCTTC 540
DB |||||
QY 541 AGGTTGAACCACTACCCGCTTGCCTGTAGGTGCAAGCACTGAACCGGAATTTGGTGGG 600
DB |||||
QY 601 TTTGGGAGCAGACAGACCCAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGC 660
DB |||||

QY 661 TTGCAAAATCTGTCTCACAGATGCGACTTGGGTTTCAGTCCACCTGATCAGACTTCCTTT 720
DB |||||
QY 721 TTGCAAAATCTGTCTCACAGATGCGACTTGGGTTTCAGTCCACCTGATCAGACTTCCTTT 720
DB |||||
QY 721 TTGCAAAATCTGTCTCACAGATGCGACTTGGGTTTCAGTCCACCTGATCAGACTTCCTTT 720
DB |||||
QY 721 TTGCAAAATCTGTCTCACAGATGCGACTTGGGTTTCAGTCCACCTGATCAGACTTCCTTT 720
DB |||||
QY 781 CATAGGGTTTGGCTGACACACAGGAGTCAAGGTTTATCAATGATCTACTTTCGAGGACCA 840
DB |||||
QY 781 CATAGGGTTTGGCTGACACACAGGAGTCAAGGTTTATCAATGATCTACTTTCGAGGACCA 840
DB |||||
QY 841 GCGTTGAGTGAATAATATAGCACCTTTACCTTCAGTGTATTTAAAAGGAGAGGAGTGTTCG 900
DB |||||
QY 841 GCGTTGAGTGAATAATATAGCACCTTTACCTTCAGTGTATTTAAAAGGAGAGGAGTGTTCG 900
DB |||||
QY 901 TACAAAGAGTTTCAATGTTGTTGAGTCAAGGTTTATCAATGATCTACTTTCGAGGAGTGTTCG 960
DB |||||
QY 901 TACAAAGAGTTTCAATGTTGTTGAGTCAAGGTTTATCAATGATCTACTTTCGAGGAGTGTTCG 960
DB |||||
QY 961 AATAGGCTTGGCCCTTCCAGAAATCTGCTGCTGAT 996
DB |||||
QY 961 AATAGGCTTGGCCCTTCCAGAAATCTGCTGCTGAT 996
DB |||||

RESULT 2
AA255912
ID AA255912 standard; cDNA; 1318 BP.
XX
AC AA255912;
XX AC
DT 10-APR-2000 (first entry)
XX
DE Runner bean gibberellin 2-oxidase PCGA2ox1 cDNA.
XX
KW Gibberellin 2-oxidase; PCGA2ox1; runner bean; 2-beta-hydroxylation;
inactivation; growth inhibition; ss.
XX
OS Phaseolus coccineus.
XX
FH Key Location/Qualifiers
FT CDS 68..1066
FT /*tag= a
FT /product= "Gibberellin 2-oxidase PCGA2ox1"
FT /transl_except= {pos:1058..1063, aa:Ala}
XX
FN WO9966029-A2.
XX
PD 23-DEC-1999.
XX
PF 11-JUN-1999; 99WO-GB001857.
XX
PR 12-JUN-1998; 98GB-00012821.
PR 15-JUL-1998; 98GB-00015404.
XX
PA (UYBR-) UNIV BRISTOL.
XX
PI Thomas SG, Hedden P, Phillips AL;
XX
DR WPI; 2000-097742/08.
DR P-PSDB; AAY58597.
XX
PT New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used
to produce transgenic plants with improved or altered growth
characteristics.
XX
PS Claim 1; Fig 1; 42pp; English.
XX
CC This sequence represents cDNA encoding a runner bean gibberellin (GA) 2-
oxidase, PCGA2ox1. This enzyme is a GA 2-beta-hydroxylase that acts on
C19-GAs and for which 2-beta-hydroxylation is its only activity.
CC Hydroxylation at the 2-beta position of a GA results in a biologically
inactive product, and is the most important route for GA metabolism in
CC

CC plants, ensuring that the active hormones do not accumulate in plant
 CC tissues. The nucleic acids can be used to transform plants so that
 CC gibberellin 2-oxidase can be constitutively over-expressed or otherwise
 CC enhanced to reduce the concentration of bioactive GAs in the plants and
 CC therefore to inhibit plant growth. Growth inhibition is useful in many
 CC agricultural and horticultural applications such as enhancing lodging-
 CC resistance and grain yield in cereals, improving seedling quality,
 CC reducing the growth of amenity grasses, reducing shoot growth in orchard
 CC and ornamental trees, improving tolerance to cold, drought and infection,
 CC and increasing yields (by the diversion of assimilates from vegetative to
 CC reproductive organs). The nucleic acids may also be used to induce male
 CC and/or female sterility (by expression in floral organs), prevent pre-
 CC harvest sprouting, reduce shoot growth in hedging plants, inhibit
 CC reversibility in the development or germination of seeds and reduce shoot
 CC growth in commercial wood species. Antisense constructs of the nucleic
 CC acids can also be used to transform plants to reduce the expression of GA
 CC 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set
 CC and growth in seedless grapes, citrus fruits and pears), improve skin
 CC texture and fruit shape in apples, increase stem length and therefore
 CC yield in sugar cane, increase yield and earliness in celery and rhubarb,
 CC improve malting yields and quality in cereals (particularly barley), and
 CC increase growth in woody species

XX
 SQ Sequence 1318 BP; 358 A; 296 C; 282 G; 382 T; 0 U; 0 Other;

Query Match 100.0%; Score 996; DB 3; Length 1318;

Best Local Similarity 100.0%; Pred. No. 6.7e-310;

Matches 996; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTCTCTCAGCCAGCATGAACAGATTTTCCTCTGAACACCATTCAGTCC 60
 DB |||||
 QY 68 ATGGTGTCTCTCAGCCAGCATGAACAGATTTTCCTCTGAACACCATTCAGTCC 127
 DB |||||
 QY 61 AGCCCTTGTTCACGGGATTCCTGTGTCGACCTCAGCACCCGATGCCAAGATCTC 120
 DB |||||
 QY 128 AGCCCTTGTTCACGGGATTCCTGTGTCGACCTCAGCACCCGATGCCAAGATCTC 187
 DB |||||
 QY 121 ATAGTGAACGCTGTAGGACTTCGGCTCTTCAAGCTTGTGAACCATGTGTTCCATTTG 180
 DB |||||
 QY 188 ATAGTGAACGCTGTAGGACTTCGGCTCTTCAAGCTTGTGAACCATGTGTTCCATTTG 247
 DB |||||
 QY 181 GAGTTAATGGCCAAATTAGAACAAGAGCCCTCAGTCTTTAAAAATCTCAGTCCGAG 240
 DB |||||
 QY 248 GAGTTAATGGCCAAATTAGAACAAGAGCCCTCAGTCTTTAAAAATCTCAGTCCGAG 307
 DB |||||
 QY 241 AAAGACAGAGCTGTGTCCTCCGACCTTTCGGCTATGTTAGCAAGAGATTGCGCCAAAC 300
 DB |||||
 QY 308 AAAGACAGAGCTGTGTCCTCCGACCTTTCGGCTATGTTAGCAAGAGATTGCGCCAAAC 367
 DB |||||
 QY 301 GGTGATGTGGTGTGGAATACCTCTCTCAACACCAACCTGTATCTCAACC 360
 DB |||||
 QY 368 GGTGATGTGGTGTGGAATACCTCTCTCAACACCAACCTGTATCTCAACC 427
 DB |||||
 QY 361 AAATCACTTGCATTTCCGAGAAATCTCATCATTTTCAGGCGGTGTGAGAACTAC 420
 DB |||||
 QY 428 AAATCACTTGCATTTCCGAGAAATCTCATCATTTTCAGGCGGTGTGAGAACTAC 487
 DB |||||
 QY 421 ATTACAGCAGTCAAGAACATGCTATGCGGTGTGGAATTCATGCGGAGGGTTGGG 480
 DB |||||
 QY 488 ATTACAGCAGTCAAGAACATGCTATGCGGTGTGGAATTCATGCGGAGGGTTGGG 547
 DB |||||
 QY 481 ATAAGCCAGAGGAATACGTTAAGCAGGTTGCTGAAAGGATGAGAAAAGTATTTCGTGCTTC 540
 DB |||||
 QY 548 ATAAGCCAGAGGAATACGTTAAGCAGGTTGCTGAAAGGATGAGAAAAGTATTTCGTGCTTC 607
 DB |||||
 QY 541 AGGTTGAACCACTACCCGCTTGCCTGAGGTGCAAGCACTGAACCGGAATTTGGTGGG 600
 DB |||||
 QY 608 AGGTTGAACCACTACCCGCTTGCCTGAGGTGCAAGCACTGAACCGGAATTTGGTGGG 667
 DB |||||
 QY 601 TTTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGACATCTGCG 660
 DB |||||
 QY 668 TTTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGACATCTGCG 727
 DB |||||

QY 661 TTGCAAAATCTGTCTCACAGATGGGCATTTGGGTTTCAGTCCACCTGATCAGACTTCCTTT 720
 DB |||||
 QY 728 TTGCAAAATCTGTCTCACAGATGGGCATTTGGGTTTCAGTCCACCTGATCAGACTTCCTTT 787
 DB |||||
 QY 721 TTCAATCAATGTTGGTGCAGCTCTACAGGTAATGACTAATGGAGGTTTAAAAAGTGTAAAG 780
 DB |||||
 QY 788 TTCAATCAATGTTGGTGCAGCTCTACAGGTAATGACTAATGGAGGTTTAAAAAGTGTAAAG 847
 DB |||||
 QY 781 CATAGGGTTTTGGCTGACACAAACGAAGTCAAGGTTTATCAATGATCTACTTTGGAGGACCA 840
 DB |||||
 QY 848 CATAGGGTTTTGGCTGACACAAACGAAGTCAAGGTTTATCAATGATCTACTTTGGAGGACCA 907
 DB |||||
 QY 841 GCGTTGAGTGAATAATATAGCACCTTTACCTTCAGTGAATGTTAAAGAGAGAGAGTGTG 900
 DB |||||
 QY 908 GCGTTGAGTGAATAATATAGCACCTTTACCTTCAGTGAATGTTAAAGAGAGAGAGTGTG 967
 DB |||||
 QY 901 TACAAAGAGTTTCACATGTTGTGAATACAAAGAGGCTGCTACACTTCAAGGCTAGCTGAT 960
 DB |||||
 QY 968 TACAAAGAGTTTCACATGTTGTGAATACAAAGAGGCTGCTACACTTCAAGGCTAGCTGAT 1027
 DB |||||
 QY 961 AATAGGCTTGGCCCTTTTCCAGAAATCTGCTGCTGAT 996
 DB |||||
 QY 1028 AATAGGCTTGGCCCTTTTCCAGAAATCTGCTGCTGAT 1063
 DB |||||
 RESULT 3
 ID AAZ99471 standard; cDNA; 1359 BP.
 XX AAZ99471;
 AC AAZ99471;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE Soybean gibberellic acid 2-oxidase 1 cDNA sequence.
 XX
 KW Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
 KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
 KW seed germination; seedling growth; gibberellin biosynthetic pathway;
 KW transgenic plant; hypocotyl; epicotyl; ss.
 XX
 OS Glycine max.
 XX
 FH Key Location/Qualifiers
 FT CDS 102..1103
 FT /*tag= a
 FT /product= "gibberellic acid 2-oxidase 1"
 FT /trans except= (pos: 633..635, aa: Xaa)
 FT /note= "Xaa is an unspecified amino acid"
 XX
 PN WO200009722-A2.
 XX
 XX
 PD 24-FEB-2000.
 XX
 PF 10-AUG-1999; 99WO-US018066.
 XX
 PR 10-AUG-1998; 98US-0096111P.
 PR 07-JUN-1999; 99US-0137977P.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Brown SM, Ellich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
 PI Piller KJ, Rao S, Ream JE;
 XX
 XX WPI; 2000-224351/19.
 DR P-FSDB; AAY84099.
 XX
 PT Obtaining transgenic plant useful for controlling seed germination and
 PT seedling growth comprises transgene comprising a sequence expressing
 PT altered levels of an essential hormone.
 XX
 PS Claim 45; Page 248; 267pp; English.
 XX
 CC The present sequence encodes a gibberellic acid 2-oxidase 1 protein

CC sequence, which is used in the method of the invention. The specification
 CC describes methods for the inhibition and control of gibberellic acid
 CC levels. Gibberellic acid levels may be inhibited or controlled by use of
 CC a chimeric expression construct expressing a RNA or protein which
 CC suppresses the gibberellin biosynthetic pathway sequence, diverts
 CC substrate from the pathway, or degrades pathway substrates or products.
 CC The methods uses copalyl diphosphate synthase, 3beta-hydroxylase, 2-
 CC oxidase, phytoene synthase, C-20 oxidase, and a 2beta,3beta-hydroxylase
 CC polynucleotides to achieve this. The method is used to control seed
 CC germination and seedling growth especially to regulate gene products of
 CC gibberellin biosynthetic pathway and restoration of normal seed
 CC germination, in transgenic plants. The plants produced are gibberellin
 CC deficient, and have shortened hypocotyl and/or epicotyl phenotypes
 CC compared to normal plants
 XX
 SQ Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;

Query Match 83.1%; Score 827.4; DB 3; Length 1359;
 Best Local Similarity 89.9%; Pred. No. 1.7e-255;
 Matches 898; Conservative 1; Mismatches 97; Indels 3; Gaps 1;

QY 1 ATGGTGTCTGCTCAGCCAGCAATTGAACCAAGTTTCTCTTCTGAAACCAATTCAGTCC 60
 DB |||||
 QY 102 ATGGTGTCTGCTCAGCCAGCAATTGAACCAAGTTTCTCTTCTGAAACCAATTCAGTCC 161
 DB |||||
 QY 61 ACGCCCTTGTTCACGGGATTCCTGTGGTGCAGCTCAGCCACCCGATGCCAAGATCTC 120
 DB |||||
 QY 162 ACGCCCTTGTTCGGGGATTCCTGTGGTGCAGCTCAGCCACCCGATGCCAAGATCTC 221
 DB |||||
 QY 121 ATAGTGAACGCTGTAGGAGCTTCGGCTTCTTCAAGCTTGTGAACCATGTGTTCATTG 180
 DB |||||
 QY 222 ATAGTCAATGCTGCAGGAGTTCGGCTTCTTCAAGCTGTGAACCATGTGTTCATTG 281
 DB |||||
 QY 181 GAGTTAATGGCCAAATTAGAAACGAGGCGCTCAGGTTCTTTAAATACTCAGTCCGAG 240
 DB |||||
 QY 282 CAGTTTCATGGCCAAATTGGAAACGAAACCTCGGGTCTTCAAAATACTCAGTCCGAG 341
 DB |||||
 QY 241 AAAGACAGAGCTGGTCCCGCCAGCCCTTTCGGCTATGGTAGCAAGAGGATTCGCCCAAC 300
 DB |||||
 QY 342 AAAGACAGAGCTGGTCCCGCCAGCCCTTTCGGCTATGGTAGCAAGAGGATTCGCCCAAC 401
 DB |||||
 QY 301 GGTGATGTCGGTGGTGGTGAATACCTCTCCTCAACACCAACCTGATGTATCTCAACC 360
 DB |||||
 QY 402 GCGGATGTCGGTGGTGGTGAATACCTCTCCTCAACACCAACCTGATGTATCTCCCC 461
 DB |||||
 QY 361 AATCACTTTGCAATTTCCGAGAAATCCTCATCTTCAAGCGGCTGGTGGAGACTAC 420
 DB |||||
 QY 462 AAGTCACAGTTCAATTTTCAGAGAAGGTCTCTCAGAAATTTTCAGGCGGTGGTGGAGGAATAC 521
 DB |||||
 QY 421 ATTACAGCAGTGAAGAACATGTCTATGCGGTGTGGAAATGATGCGGAGGGGTGGGG 480
 DB |||||
 QY 522 ATTAGAGCGGTGAAGAACATGTCTATGAGTGTGGAAATGATGCTGAGGATTTGGGG 581
 DB |||||
 QY 481 ATAAGCAGAGGAATACGTTTAAGCAGGTTGCTCAAGAGATGAGAAAGTGAATTCGTCCTC 540
 DB |||||
 QY 582 ATAACGAGAGGAATGTTGAGTAGTGTCTCAAGGATGAGAAGAGTGAATTCGTCCTC 641
 DB |||||
 QY 541 AGTTGAACCACTACCGGCTTCCCTGAGTGTCAAGCACTGAAC---CGGAATTTGGTT 597
 DB |||||
 QY 642 AGACTTTAACCACTACCGGCTTCCCTGAGTGTCAAGCACTGAAGAGGAATTTGGTT 701
 DB |||||
 QY 598 GGGTTTTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTTAACAGCACATCT 657
 DB |||||
 QY 702 GGAATTTGGAGAGCACACAGACCCACAGATAATTTCTGTCTTGAGATCTTAACAGCACCTCA 761
 DB |||||
 QY 658 GGCTTGAATCTGTCTCAGATGGCACTTGGGTTTTCAGTCCCACTGATCAAGATTC 717
 DB |||||
 QY 762 GGCCTGCAATCTGTCTCAGATGGCACTTGGGTTTCTGTCCCACTGATCAAACTTC 821
 DB |||||
 QY 718 TTTTTCATCAATTTGGTGGCTCTCAGGTTAATGACTAATGGGAGGTTTAAAGTGA 777
 DB |||||
 QY 822 TTTTTCATCAATTTGGTGGCACTCTTTCAGGTAATGACTAATGGGAGGTTTAAAGTGA 881
 DB |||||

QY 778 AAGCATAGGTTTGGCTGACACCAAGAGTCAAGGTTATCAATGATCTACTTTGGAGGA 837
 DB |||||
 QY 882 AAGCATAGGTTTGGCTGACCCCAAGTCAAGGTTGTAATGATCTACTTTGGAGGA 941
 DB |||||
 QY 838 CAGCGTTTCAAGTCAAAATATAGCACCCTTTACCTTCAGTGTATGTTAAAGGAGGAGTCT 897
 DB |||||
 QY 942 CCACCCCTTGTGTGAAAAGATAGCACCCTTTACCTTCATCTCATGTTAAAGGAGGAGAGT 1001
 DB |||||
 QY 898 TTGTACAAAGAGTTTCAATGTTGTGAATACAAAGAGGCTGCGTACACTTTCAAGGCTAGCT 957
 DB |||||
 QY 1002 TTCTACAAAGAGTTTCAATGTTGGGATACAAAGGCTGCGTACGCTCAGGCTAGCG 1061
 DB |||||
 QY 958 GATAATAGGCTTGCCTTTCCAGAAATCTGCTGTGAT 996
 DB |||||
 QY 1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGTGAT 1100
 DB |||||

RESULT 4
 AAD40261
 ID AAD40261 standard; cDNA; 1359 BP.
 XX
 AC AAD40261;
 XX
 DT 22-OCT-2002 (first entry)
 XX
 DE Soybean GA 2-oxidase 1 cDNA.
 XX
 KW Gibberellin; transgenic plant; seed germination; seedling growth;
 KW transgenic; 2-oxidase 1; enzyme; GA; soybean; gene; ss.
 XX
 OS Glycine max.
 XX
 FH Key Location/Qualifiers
 CDS 102..1103
 FT /tag= a
 FT /product= "GA 2-oxidase 1 protein"
 FT /transl_except= (pos:633..635, aa:Xaa)
 FT /note= "Xaa = any amino acid"
 XX
 PN US2002053095-A1.
 XX
 PD 02-MAY-2002.
 XX
 PF 10-AUG-1999; 99US-00371307.
 XX
 PR 10-AUG-1999; 99US-00371307.
 XX
 PA (BROW/) BROWN S M.
 XX
 PI Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
 PI Pillar KJ, Rao S, Ream JE;
 XX
 DR WPI; 2002-489107/52.
 DR P-PSDB; AAE24921.
 XX
 PT Control of gibberellin levels in plants useful to avoid unfavorable
 PT conditions in crops to increase yields, using transgenic plants having
 PT reduced seed germination and early seedling growth then treatment to
 PT restore these properties.
 XX
 PS Claim 45; Page 92-93; 155pp; English.
 CC
 CC The invention relates to control of gibberellin (GA) levels in plants.
 CC The method involves producing transgenic plants having a phenotype of
 CC reduced seed germination and reduced early seedling growth, then
 CC restoring seed germination and early seedling growth by treating plants
 CC with an appropriate compound when conditions are favourable. The method
 CC is useful to control seed germination and/or early seedling growth in
 CC agricultural production so that unfavorable environmental conditions
 CC normally reducing agronomic output can be avoided and yields increased.
 CC Plants also demonstrate increased uniformity of germination, emergence
 CC and seedling vigor, so increasing yields at harvest. The method is
 CC especially useful in crop plants such as e.g. canola, soybean, cotton,

Qy	679	GATGGCACTTGGGTTTCAGTCCCACTGATCAGACTCTCCCTTTTCATCAATGTTGGTGAC	738
Db	688	GATGGAAGTTGGGTGGCTGCTCCCTCCTCATCACTCTCTTCTTCTCAATAATGTTGGAGAT	747
Qy	739	GCTCTACAGGTAACTGACTAATGGGAGGTTTAAAAGTGTAAAGCATAGGGTTTGGCTGAC	798
Db	748	GCTCTTCAGGTTATGACTAAACGGGAGGTTCAAGAGTGTAAACACACAGGGTCTTAGGCCGAT	807
Qy	799	ACACCAAGCTCAAGGTTTATCAATGATCTACTTTTGGAGGACCAGCGTTGTAGTGAATAATATA	858
Db	808	ACAAAGAGATCGAGGATTTCAATGATATATTTCCGGCGGACCGCCATTGACCGAAGAGATC	867
Qy	859	GCACCTTTTACCTTTCAGTGATGTTTAAAAGGAGAGGAGTGTTTGTACAAAGAGTTTCACATGG	918
Db	868	GCACCATTCGCCATGCCTTGTCCCTGAGCAAGATGATTGGCTTTACAAAGAATTCACATTGG	927
Qy	919	TGTGAATACAAAGAGGCTGCGTACACTTTCAAGGCTAGCTGATAATAGGCTTGGCCCTTTC	978
Db	928	TCTCAATACAAACTTCTGCTTCTACAACTTAAGCTTGGTGATTATAGACTTTGGTCTCTTT	987
Qy	979	CAGAAA	984
Db	988	GAGAAA	993

RESULT 7
AAZ55916
ID AAZ55916 standard; cDNA; 1237 BP.
XX
XX AAZ55916;
XX AC
XX AC
XX
DT 10-APR-2000 (first entry)
XX
XX Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox2 cDNA.
DE
XX
XX Gibberellin 2-oxidase; AtGA2ox2; 2-beta-hydroxylation; inactivation;
KW Gibberellin 2-oxidase; AtGA2ox2; 2-beta-hydroxylation; inactivation;
KW growth inhibition; ss.
KW

OS	Arabidopsis thaliana.
XX	
FF	Key
HH	Location/Qualifiers
FT	109. .1134
CDS	/tag= a
FT	/product= "Gibberellin 2-oxidase AtGA2ox2"
FT	
FT	
XX	
PN	WO9966029-A2.
XX	
PD	23-DEC-1999.
XX	
PX	11-JUN-1999; 99WO-CB001857.
PF	
XX	
PR	12-JUN-1998; 98GB-00012821.
PR	15-JUL-1998; 98GB-00015404.
XX	
PA	(UYBR-) UNIV BRISTOL.

Thomas SG, Hedden P, Phillips AL;
WPI; 2000-097742/08.
P-PSDB; AAY58599.
New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used to produce transgenic plants with improved or altered growth characteristics.

PS Example 3; Fig 7; 42pp; English.

This sequence represents cDNA encoding an Arabidopsis thaliana gibberellin (GA) 2-oxidase, PGGAox2. This enzyme is a GA 2-beta-hydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is its only activity. Hydroxylation at the 2-beta position of a GA results in a biologically inactive product, and is the most important route for GA metabolism in plants, ensuring that the active hormones do not

accumulate in plant tissues. The nucleic acids can be used to transform plants so that gibberellin 2-oxidase can be constitutively over-expressed or otherwise enhanced to reduce the concentration of bioactive GAs in the plants and therefore to inhibit plant growth. Growth inhibition is useful in many agricultural and horticultural applications such as enhancing lodging-resistance and grain yield in cereals, improving seedling quality, reducing the growth of amenity grasses, reducing shoot growth in orchard and ornamental trees, improving tolerance to cold, drought and infection, and increasing yields (by the diversion of assimilates from vegetative to reproductive organs). The nucleic acids may also be used to induce male and/or female sterility (by expression in floral organs), prevent pre-harvest sprouting, reduce shoot growth in hedging plants, inhibit reversibility in the development or germination of seeds and reduce shoot growth in commercial wood species. Antisense constructs of the nucleic acids can also be used to transform plants to reduce the expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set and growth in seedless grapes, citrus fruits and pears), improve skin texture and fruit shape in apples, increase stem length and therefore yield in sugar cane, increase yield and earliness in celery and rhubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species

Sequence 1237 BP; 356 A; 277 C; 280 G; 324 T; 0 U; 0 Other;

Query Match	42.6%	Score 424.4	DB 3	Length 1237
Best Local Similarity	67.5%	Pred. No. 1.6e-125		
Matches 612	Conservative 0	Mismatches 291	Indels 3	Gaps 1
QY	79	ATTCCTGTGGTCGACCTCAGCACCCCGATGCCAAGAAATCTCATAGTCGAACGCCCTGTAGG	138	
Db	199	ATCCCGTGTCAACCTAGCCGATCCGGACGGAAACCCGNAATCGTAAGACCTCGCAG	258	
QY	139	GACTTCGGCTTCTTCAAGCTTGTGAACCATCGGTTCATTTGGAGTTAATGGCCAAATTTTA	198	
Db	259	GAGTTCCGGTCTTCAAGTTCGTAACACCGAGTCCGACCGCAACTCATGACTCGGTTA	318	
QY	199	GAATAACGAGGCCCTCAGGTTCTTTTAAAAAATCTCAGTCGGAGNAAGACAGAGCTGGTCCC	258	
Db	319	GAGCAGGAGGCTATTTGGCTTCTTCGGCTTGCTCAGTCTCTTAAAAACCGGCCCGTCCA	378	
QY	259	CCCGACCTTTCGGCTATGTGTAGCAAGAGGATTTGCCCAACGGTGATGTCCGTTGGGTC	318	
Db	379	CCTGACCGTAGGTTATGTGTAAATACGGATTTGGACCAACGGTGAAGTTGGTTGGATT	438	
QY	319	GAATACCTCTCTCTCAACACCAACCCCTGATGTTATCTCACCCAAATCACTTTTGCATTTTC	378	
Db	439	GAGTATCTCCTCTCAATGCTAACTCCTCAGCTCTCCTCTCTCTCTCTCTCTCTCTCTCTCT	498	
QY	379	CGAGAAAATCTCATCATCTTTCAGGGCGGTGTGGAGAACTACATTTACAGCAGTAGAGAC	438	
Db	499	CGTCAAAACCCCTCAAAATTTTCCGTTGAGTCGGTGGAGGAGTACATGAAGGAGATTAAAGAA	558	
QY	439	ATGTGCTATGCGGTGTGGAAATTCATGCGCGAGGGTTGGGATGAAGGCAGAGGAATACG	498	
Db	559	GTGTGCTACAAGGTGTGGAGATGTTGCCGAGAACTAGGGATAGAGCAAGGACACT	618	
QY	499	TTAAGCAGGTTTCTGAAGGATGAGAAAAGTATGTTCTGTCCTTCAGGTTGAACCACTACCCG	558	
Db	619	CTGAGTAAATGCTCTGAGAGATGAGAGAGTGAAGTCTGCTGCTGAGACTAAACCATATCCG	678	
QY	559	CCTTGCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGGTTTGGGGAGCACACAGAC	618	
Db	679	GC---GGCGAGGAAGAGCGCGGAGAAAGATGTTGAAGTGGGGTTTTGGGGAAACACACAGAC	735	
QY	619	CCACAGATAATTTCTGTCTTAAGATCTAAACGCAATCTGGCTTCGCAATCTGTCTCA	678	
Db	736	CCACAGATAATTTCTGAGTCTAAGATCTAAATACACGGCGGGTCTTCAATCTGTGTGAAA	795	
QY	679	GATGGCATTGGGTTTCAAGTCCCACTCATCAGACTTCTCTTTTTCATCAATCTTGGTGAC	738	
Db	796	GATGGAAGTTGGTGGCTGCTCCCTCCTGATCACTCTTCTTCTTCTTCTTCTTCTTCTTCTT	855	
QY	739	GCTCTACAGGTAATGACTAAATGGGAGGTTTTAAAGTGAAGCATAGGGTTTGGCTGAC	798	

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Db      856  GCTCTTCAGGTTATGACTAAACGGAGGTTCAAGAGTGTTAAACACACAGGCTTTAGCCGAT 915
QY      799  ACACCAAGCTCAGGTTATCAATGATCTACTTTGGAGGACCGAGCTTGATGTAATATA 858
Db      916  ACAAGGAGATCGAGGATTTCAATGATATATTTGCGCGGACCGCCATTGAGCAGAGATC 975
QY      859  GCACCTTTACCTTCAGTGATGTTAAAGGAGAGAGAGTGTTGTACAAAGAGTTTCACATGG 918
Db      976  GCACCAATGCCATGCCCTTGCTCCTGAGCAGAGATGATGGCTTTACAAAGATTCACCTTGG 1035
QY      919  TGTGAATACAAGAGGCTCGTACACTTCAAGCTAGCTGTAATAGGCTTGCCCTTTTC 978
Db      1036  TCTCAATACAAATCTTCTGCTTACAAGTCTAAGCTTGGTGATATAGACTTGGTCTCTTT 1095
QY      979  CAGAAA 984
Db      1096  GAGAAA 1101

RESULT 8
ADM94213
ID      ADM94213 standard; cDNA; 1352 BP.
XX
AC      ADM94213;
XX
DT      17-JUN-2004 (first entry)
XX
DE      Soybean Dioxynase cDNA #2.
XX
KW      Soybean; ss; plant; plant metabolism;
KW      GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase;
KW      Dioxynase; Ent-kaurane Synthase A; GA-20 oxidase;
KW      Gibberellin 3-beta hydroxylase; Riboflavin specific deaminase;
KW      Ethylene response factor; Acyl-CoA thioesterase II;
KW      ABC transporter GGN20-like; P-glycoprotein I; P-glycoprotein 3;
KW      P-glycoprotein ATPGP; P-glycoprotein HVMR2; ABC transporter;
KW      PMP70 ABC transporter; MRP4 ABC transporter; transgenic.
XX
OS      Glycine max.
XX
XX      US6677502-B1.
XX
XX      13-JAN-2004.
XX
PF      12-JUL-2000; 2000US-00614912.
XX
PR      12-JUL-1999; 99US-0143401P.
PR      12-JUL-1999; 99US-0143412P.
PR      30-JUL-1999; 99US-0146650P.
PR      15-DEC-1999; 99US-0170906P.
PR      21-DEC-1999; 99US-0172946P.
PR      21-DEC-1999; 99US-0172959P.
XX
PA      (DUPO ) DU PONT DE NEMOURS & CO E I.
PA      (PION-) PIONEER HI-BRED INT INC.
XX
PI      Allen SM, Kinney AJ, Rafalski JA, Orozco EM, Miao G, Famodu OO;
PI      Lee J, Lohman KN, Rendina AR, Sakai H, Weng Z, Caiami PG, Fang Y;
PI      Shen JB, Zoughi IL, Anderson SL, Shi J, Lu G, Helentjaris TG;
PI      Li CP;
XX
XX      WPI; 2004-088430/09.
DR      P-PSDB; ADM94214.
XX
XX      New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate
PT      synthase nucleic acid and proteins, useful for creating transgenic plants
PT      where polypeptides are present at higher or lower levels.
XX
PS      Example 3; SEQ ID NO 13; 186pp; English.
XX
XX      The invention relates to an isolated polynucleotide comprising a
CC      nucleotide sequence encoding a polypeptide having GTP cyclohydrolase
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CC      II/3,4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing as
CC      ADM94266. Also included are a vector comprising the polynucleotide, a
CC      recombinant DNA construct comprising the polynucleotide operably linked
CC      to at least one regulatory sequence, transforming a cell with the
CC      polynucleotide, a cell comprising the recombinant DNA construct,
CC      producing a plant (comprising transforming a plant cell with the
CC      polynucleotide and regenerating a plant from the transformed plant cell),
CC      a plant comprising the recombinant DNA construct and a seed comprising
CC      the recombinant DNA construct. Also disclosed as new are nucleic acid
CC      (cDNA) fragments and assembled contigs encoding plant metabolism proteins
CC      chosen from GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate
CC      synthase, Dioxynase, Ent-kaurane Synthase A, GA-20 oxidase, Gibberellin
CC      3-beta hydroxylase, Riboflavin specific deaminase, Ethylene response
CC      factor, Acyl-CoA thioesterase II, ABC transporter GGN20-like, P-
CC      glycoprotein I, P-glycoprotein 3, P-glycoprotein ATPGP, P-glycoprotein
CC      HVMR2, ABC transporter, PMP70 ABC transporter and MRP4 ABC transporter.
CC      The nucleic acid fragments may be used to create transgenic plants where
CC      the polypeptides are present at higher or lower levels than normal or in
CC      cell types or in developmental stages in which they are not normally
CC      found. The polynucleotides can be used as probes for genetically and
CC      physically mapping genes and as markers for traits linked to those genes.
CC      The nucleic acid fragments may be used as restriction fragment length
CC      polymorphism (RFLP). It can also be used to probe Southern blots
CC      containing restriction endonuclease-treated genomic DNAs of a set of
CC      individuals representing parent and progeny of a defined genetic cross.
CC      The nucleic acid fragments may also be used as hybridisation probes
CC      against PCR amplification products generated from the mutation population
CC      using the mutation tag sequence primer in conjunction with an arbitrary
CC      genomic site primer. The peptides can also be used to immunise animals to
CC      produce polyclonal or monoclonal antibodies with specificity for peptides
CC      or proteins comprising the amino acid sequences. Antibodies are useful
CC      for detecting the polypeptides in situ in cells or in vitro in cell
CC      extracts. The present sequence encodes a plant metabolism protein (or
CC      fragment).
```

XX SQ Sequence 1352 BP; 439 A; 255 C; 243 G; 415 T; 0 U; 0 Other;

Query Match 42.3%; Score 421.4; DB 12; Length 1352;
Best Local Similarity 65.7%; Pred. No. 1.6e-124;
Matches 652; Conservative 0; Mismatches 326; Indels 15; Gaps 2;

```
QY      1  ATGGTTGTTCTGTCTCAGCAGCATTTGACACCAATTTTCTCTTCTGAAACCATTCAGTCC 60
Db      159  ATGGTGTGTTGTTCTCCAAAGCAACACAGAAACAATACTCTCTACATTAAAGAACTGCATGCCA 218
QY      61  AGCCCTTGTTCACGGGGATTCCTGTGTGCGACCTCAGCCACCCCGATGCCAGAAATCTC 120
Db      219  ACCAAATTTTCTCAACAAATTCCTCATAGTGGACCTCTCCAAACCTGATGCAAGACCCCTT 278
QY      121  ATAGTGAACGCTGTAGGACCTTCGCTTCTTCAAGCTTGTGAACCATGCTGTTCATTG 180
Db      279  ATAGTGAAGCTTGTGAGGAGTTGGATTCTTCAAGTCAATCAATCAUGTGTCTCCATG 338
QY      181  GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTTAAAAAAATCTCAGTCCGAG 240
Db      339  GAAGCTATATCCGAATTTGGAATATGAGCTTCAAAATCTTCTCTATGTCACCTCAATGAA 398
QY      241  AAAGCAGAGCTGGTTCCTCCCGACCCCTTTCGGCTATGCTGATGAGAGAGATTGGCCCAAC 300
Db      399  AAGGAAAAAGTAGGACCTCCCAATCCATTGGGTATGGTAGCAAGAAAAATTGGACACAAT 458
QY      301  GGTGATGTCGGTTGGTTCGAATTTTCTCTCTCCCAACCAACCCCTGATGTTTCTCACC 360
Db      459  GGGGAGCTTGGTTGGATTGATGACCTTCTTCTCAACACCAATCAAGAACACAACT----- 513
QY      361  AAATCACTTTGCAATTTTCCGAGAAAAATCTCATATTTTCAGGGCGGTGGTGAGAACTAC 420
Db      514  -----TCTCTGTTTATGGGAAAAACCTGAGAAATTCAGGTGTCTGTGTGAACAGTTAC 566
QY      421  ATTACAGCAGTGAAGAACATGTCTATGCGGTGTGTGGAATTTGATGCGGAGGGGTGGGG 480
Db      567  ATGTCTCTCTGAGGAAGATGGCATGTGAGATTCTTGAGTTGTGTCAGTAGCAGAGGGTTGAAG 626
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Db 504 -----TCTCTGTTTATGCGCAAAACGCTGAGAAATTTAGTGTGTTGTTGAACAGTTAC 556
Qy 421 ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAAATTTGATGCGGAGGGTTGGGG 480
Db 557 ATGTCTTCTGTGAGGAAATGCGATGTGAGATTTCTTGAGCTGATGCGAAGAGTTGAAG 616
Qy 481 ATAAGCAGAGAAATAGCTTAAGCAGGTGCTGAGGATGAGAAAGTGAATTCGTGCTTC 540
Db 617 ATACAAACAAAATGTTGTTAGCAAGCTTCTATGATAAAGAGAGTGAATCTGTGTTTT 676
Qy 541 AGTTGAACCACTTACCCGCTTGGCTGAGGTGCAAGCACTGAACCGGAATTTGTTGGG 600
Db 677 AGGTGAATCACTACCTCTGCTGCTGAACTT---GTGAATGGTCAAAACATGATAGG 733
Qy 601 TTTGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGC 660
Db 734 TTTGGAGAACACAGGAGCCACAAATCAITTTCTTACTTATGCTCCAAACAATACTTCAGGC 793
Qy 661 TTGCAATCTGTCTACAGATGCGACTTGGGTTTCAGTCCACCTGATCAGACTTCCTTT 720
Db 794 CTTCAATTTTCTTAGAGATGAAACTGGATTTCAAGTCCCACTGATCACAATCTTTTC 853
Qy 721 TTCATCAATGTTGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAAG 780
Db 854 TTCATAAATGTTGGTGAATCTCTTCAGGTTATGACCAATGGAAGGTTTCGAAGTGTGAA 913
Qy 781 CATAGGTTTTGGCTGACACAACGAAGTCAAGGTTATCAATGATCTACTTTTCGAGGACCA 840
Db 914 CACAGATTTTGACAAATGATTAAGTCTAGACTCAATGATTTACTTTGGAGTCCA 973
Qy 841 GCGTTGAGTGAATAATAGCACTTTTACCTTCAGTGAATTTAAAGGAGAGGAGTTTG 900
Db 974 CCAATTGAGTGAATAATAGTACCAITATCTTCACITATG---AAAGGAAAGAAAGCTTA 1030
Qy 901 TACAAGAGTTTACATGTTGATGATACAGAGGCTGCTACACTTCAGGCTAGCTGAT 960
Db 1031 TACAAGAGTTTACGTTGGTTCGAGTATAAAAATTTAAACCTATGCTTCAAGATTTGGCTGAT 1090
Qy 961 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGT 993
Db 1091 AATAGGCTTGGACATTTTCAGAGAAATTTGTTGCT 1123

RESULT 11
ID AAD40262
XX AAD40262 standard; cDNA; 1403 BP.
AC AAD40262;
XX
DT 22-OCT-2002 (first entry)
DE Soybean GA 2-oxidase 2 cDNA.
XX
KW Gibberellin; transgenic plant; seed germination; seedling growth;
transgenic; 2-oxidase 2; enzyme; GA; soybean; gene; ss.
XX
OS Glycine max.
XX
Key Location/Qualifiers
FH 149..1129
CDS /*tag= a
FT /product= "GA 2-oxidase 2 protein"
XX
US2002053095-A1.
XX
PD 02-MAY-2002.
XX
PF 10-AUG-1999; 99US-00371307.
XX
PR 10-AUG-1999; 99US-00371307.
XX
PA (BROW/) BROWN S M.
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XX Brown SM, Blich TD, Heck GR, Kishore GM, Logusch BW, Logusch SJ;
PI Pillier KJ, Rao S, Ream JE;
XX
DR WPI; 2002-489107/52.
DR P-PSDB; AAE24922.
XX
PT Control of gibberellin levels in plants useful to avoid unfavorable
PT conditions in crops to increase yields, using transgenic plants having
PT reduced seed germination and early seedling growth then treatment to
PT restore these properties.
XX
PS Claim 45; Page 94-95; 155pp; English.
XX
CC The invention relates to control of gibberellin (GA) levels in plants.
CC The method involves producing transgenic plants having a phenotype of
CC reduced seed germination and reduced early seedling growth, then
CC restoring seed germination and early seedling growth by treating plants
CC with an appropriate compound when conditions are favourable. The method
CC is useful to control seed germination and/or early seedling growth in
CC agricultural production so that unfavorable environmental conditions
CC normally reducing agronomic output can be avoided and yields increased.
CC Plants also demonstrate increased uniformity of germination, emergence
CC and seedling vigor, so increasing yields at harvest. The method is
CC especially useful in crop plants such as e.g. canola, soybean, cotton,
CC etc., and is also useful in storage and transport of seeds to reduce
CC premature germination which may affect agronomic or food quality of the
CC seeds. The present sequence is soybean GA 2-oxidase 2 cDNA
XX
SQ Sequence 1403 BP; 440 A; 269 C; 261 G; 433 T; 0 U; 0 Other;

Query Match 42.0%; Score 418.2; DB 6; Length 1403;
Best Local Similarity 66.2%; Pred. No. 1.7e-123;
Matches 657; Conservative 0; Mismatches 318; Indels 18; Gaps 3;

Qy 1 ATGGTTGTTCTGTCTCAGCCAGCATTTGAACCAAGTTTTCCTTCTGAACCATTCAGTCC 60
Db 149 ATGGTTGTTGCTGTCCAGGCCAACACAGAACAACTACTCTACATCAAGAACTACATGCCA 208
Qy 61 ACGCCCTTTGTTCAAGGGGATTCCTGTGTGCACTTCAGCCACCCCGATGCCAAGAACTCTC 120
Db 209 ACGGCAATTCCTCAACAATTTCCCGTAGTGGACCTCTCCAAACAGATGCAAGACCTTC 268
Qy 121 ATAGTGAACGCTGTGAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTTTCCATTTG 180
Db 269 ATAGTGAAGGCTGTGAGGAAATTTGGAATTTTCAAAAGTCATCAACCATGTTTCCCATG 328
Qy 181 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAATCTCAGTCCGAG 240
Db 329 GAAACTATATCCCAATTCGAATCTGAAGCCTTCAAGTTCTTCTATGCCACTCAATGAG 388
Qy 241 AAAGCAGAGCTGGTCCCGGACCCCTTTTCGCTATGTAGCAAGAGATTCGCCCAAC 300
Db 389 AAGGAAAAGTAGGCCCTCCCAACCATATGGTATGTAGCAAGAAATTTGACACAAAT 448
Qy 301 GGTGATGTGGTTGGTTCGAATACCTCTCTCAACACCAACCCCTGATTTATCTCACCC 360
Db 449 GGGATGTTGGTTGGTTGAGTACCTTCTCTCAACACCAATCAAGAACACAACT----- 503
Qy 361 AAATCACTTTGATTTTCCGAGAAAATCCTCATCATTTTCAGGCGGTGGTGAGAACTAC 420
Db 504 -----TCTCTGTTTATGGCAAAAACGCTGAGAAATTTAGGTGTTTGTGAACAGTTAC 556
Qy 421 ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAAATTTGATGCGGAGGGTTGGGG 480
Db 557 ATGTCTTCTGTGAGGAAATGCGATGTGAGATTTCTTGAGCTGATGCGAAGAGATGAAG 616
Qy 481 ATAAGCAGAGAAATACCTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTCGTGCTTC 540
Db 617 ATACAAACAAAATGTTGTTAGCAAGCTTCTTATGGAATTAAGAGAGTGAATCTGTGTTTT 676
Qy 541 AGTTGAACCACTACCCGCTTGGCTGAGGTGCAAGCACTGAACCGGAATTTGTTGGG 600
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Db 677 AGGTGAATCACTACCTGCTGCCCTGAACTT---GTGAATGGTCAAAACATGATAGGG 733
QY 601 TTTGGGAGACACAGACACACAGATAATTTCTGTCTTAAGATCTTAACAGCACATCTGGC 660
Db 734 TTTGGAGAACACAGCGACCCACAAATCTTCTACTTAGTCCACATATCTCAGGC 793
QY 661 TTGCAAAATCTGTCTCAGATGACACTTGGGTTTCAGTCCCACTGATCAGACTTCCTTT 720
Db 794 CTTTCAGATTTTCTTAGAGATGAAACTGGATTTTCAGTCCCACTGATCACAATCTTTC 853
QY 721 TTCAATCAATTTGGTACGCTCTACAGGTAATCACTAATGGGAGGTTTAAAGTGTAAAG 780
Db 854 TTCAATAATTTGGTGATCTTCTTCAGGTTATGCAATGGAAGGTTTTCGAAGTGTGAA 913
QY 781 CATAGGTTTGGCTGACACAAACAGTCAAGGTTCATGATCTACTTTTGGAGGACCA 840
Db 914 CACAGAGTTTGGCAAAATGGAATTAAGTCTAGACTCTCAATGATTTACTTTGGAGTCCA 973
QY 841 GCCTTGAGTGAATAATATAGCACCTTTTACCTTTCAGTGTATGTTAAAGGAGGAGTGTG 900
Db 974 CCATTGAGTGAGAAATAGTACCATTATCTTCACTTATG---AAAGGAAAGAAAGCTTA 1030
QY 901 TACAAGAGTTTCACTGCTGTGAATACAGAAGCTGCGTACACTTCAAGGCTAGCTGAT 960
Db 1031 TACAAGAGTTTACGTTGTTGCGAGTATAAAATTTAACTTATGCTTCAAGATTGGCTGAT 1090
QY 961 AATAGGCTTGCCTCTTCCAGAAATCTGCTGCT 993
Db 1091 AATAGGCTTGGACATTTTGAGAGATTTGTTGCT 1123

RESULT 12
ID AAZ55917 standard; DNA; 1008 BP.
XX AAZ55917;
XX 10-APR-2000 (first entry)
XX Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox3 DNA.
XX Gibberellin 2-oxidase; AtGA2ox3; 2-beta-hydroxylation; inactivation;
XX growth inhibition; ds.
XX Arabidopsis thaliana.
FH Key Location/Qualifiers
FT CDS 1..1008
FT /tag= a
FT /product= "Gibberellin 2-oxidase AtGA2ox3"
XX WO966029-A2.
XX 23-DEC-1999.
XX 11-JUN-1999; 99WO-GB001857.
XX 12-JUN-1998; 98GB-00012821.
XX 15-JUL-1998; 98GB-00015404.
XX (UYBR-) UNIV BRISTOL.
XX Thomas SG, Hedden P, Phillips AL;
XX WPI; 2000-097742/08.
XX P-PSDB; AAY58600.
XX New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used
XX to produce transgenic plants with improved or altered growth
XX characteristics.
XX Example 3; Fig 9; 42pp; English.
XX

CC This sequence represents cDNA encoding an Arabidopsis thaliana
CC gibberellin (GA) 2-oxidase, PG2ox3. This enzyme is a GA 2-beta-
CC hydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is
CC its only activity. Hydroxylation at the 2-beta position of a GA results
CC in a biologically inactive product, and is the most important route for
CC GA metabolism in plants, ensuring that the active hormones do not
CC accumulate in plant tissues. The nucleic acids can be used to transform
CC plants so that gibberellin 2-oxidase can be constitutively over-expressed
CC or otherwise enhanced to reduce the concentration of bioactive GA in the
CC plants and therefore to inhibit plant growth. Growth inhibition is useful
CC in many agricultural and horticultural applications such as enhancing
CC lodging-resistance and grain yield in cereals, improving seedling
CC quality, reducing the growth of amenity grasses, reducing shoot growth in
CC orchard and ornamental trees, improving tolerance to cold, drought and
CC infection, and increasing yields (by the diversion of assimilates from
CC vegetative to reproductive organs). The nucleic acids may also be used to
CC induce male and/or female sterility (by expression in floral organs),
CC prevent pre-harvest sprouting, reduce shoot growth in hedging plants,
CC inhibit reversibility in the development or germination of seeds and
CC reduce shoot growth in commercial wood species. Antisense constructs of
CC the nucleic acids can also be used to transform plants to reduce the
CC expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to
CC improve fruit set and growth in seedless grapes, citrus fruits and
CC pears), improve skin texture and fruit shape in apples, increase stem
CC length and therefore yield in sugar cane, increase yield and earliness in
CC celery and rhubarb, improve malting yields and quality in cereals
CC (particularly barley), and increase growth in woody species
XX
XX Sequence 1008 BP; 296 A; 212 C; 232 G; 268 T; 0 U; 0 Other;
QY Query Match 38.3%; Score 381.6; DB 3; Length 1008;
Db Best Local Similarity 64.7%; Pred. No. 9.2e-112;
Matches 586; Conservative 0; Mismatches 314; Indels 6; Gaps 1;
QY 79 ATTCTGTGGTGCAGCTCAGCACCCCGATGCCAAGAATCTCATAGTGAACCGCTGTAGG 138
Db 79 ATCCCTGTTATAGACTTAACCGACTCAGATGCCAAACCCAAATCGTCAAGCGCATGTGAA 138
QY 139 GACTTGGGCTCTTCAAGCTTGTGAACCATGTTTCCATTGGAGTTAATGGCAATTTA 198
Db 139 GAGTTTGGGTTCTTCAAGTCTATCAACCATGGGTCGCGACCCGATCTTTGACTCAGTTG 198
QY 199 GAAACGAGGCGCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAAGACAGAGTGGTCCC 258
Db 199 GAGCAGAGGCGCATCAACTTCTTTGCTTTCATCTCTCTCAAGACAAAGCGGTCCA 258
QY 259 CCGACCTTTTCGGCTATGCTAGCAAGAGGATTTGCCCAAACGGTGATGTCGGTTGGTC 318
Db 259 CCTGACCCGTTTGGTTACGGTACTAAAGAGATTGGACCCCAATGGTGACCTTGGCTGGCT 318
QY 319 GAATACCTCTCTCAACACCAACCTGATGTTTATCTCAACCCCAATCACTTTTGCAATTTTC 378
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QY 439 ATGTGCTATGCGGTGTGGAAATTTGATGGCGAGGGGTTGGGGATTAAGGAGAGGAATACG 498
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Db 499 CTGAGCCGTTTGGTGAAGTGAAGAAAGTATTCGTGCTGAGAAATGAACCACTACCCG 558
QY 559 CCTTGGCTTGAAGTGAACCACTGAACCCGAAATTTTGGTTGGGTTTGGGGAGGACACAGAC 618
Db 559 -----GAGAGGAGAGAGACTCGGTCAAGGAAGAGATTGGGTTCCGTGAGCACACTGAT 612
QY 619 CCACAGATAATTTCTGTCTTAAGATCTAAACAGACATCTGGCTTGCATAATCTGTCTCACA 678
Db 613 CCACAGTTGATATCACTGCTCAGTCAAAACGACACAGAGGGTTTGCATAATCTGTGTCAAA 672


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Db 488 CTGCGCCGCTCCGCTCCTCGC-----CGCTCTTCCGGGCGGCGCTGAACGAGTACA 538
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Db 539 TCGCGCGGTGCGAAGGTGGCGGTGCGGTGATGGAAGGATGCGGAGGGGCTGGGCA 598
QY 482 TAAGGCAGAGGAATACGTTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTGCTGTTC 541
Db 599 TTGCGGCCGTGGACGCGCTGAGCGGATGCTGACGCGGAGGGGAGCCGACGAGTGTTC 658
QY 542 GGTGAACACATCACCGCGCTTCCCTGAGTGCAAGCATTGAACCGGAATTTGGTTGGGT 601
Db 659 GGGTGAACCATACACCGCGCTGCGACGCGTGCAGGGGCTGGGCTGCAGCGCCACCGGCT 718
QY 602 TTGGGAGGACACAGACCCACAGATATTTCTGCTTTAAGATCTACACGACATCTGGCT 661
Db 719 TCGCGAGGACACGGACCGCGACGCTCATCTCGTCTGCGCTCCAACGGCAGCTCGGGC 778
QY 662 TGCAAATCTGCTCACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCCTTT 721
Db 779 TGCAGATCGGCTCCAGACGGGCACTGGGTGTCCTGCGCTCGGACCGGACGCTTCT 838
QY 722 TCATCAATGTTGCTGACGCTCTACAGTAACTAATGAGGTTTAAAGTGTAAGC 781
Db 839 TCGTCAACGTCGGCGACTCGTTGACGCTGCTGACCAACGGGAGGTTCAAGAGCGTGAAGC 898
QY 782 ATAGGCTTTGGCTGACACACGAAGCTCAAGTTATCAATGATCTACTTTGGAGGACCA 841
Db 899 ACAGGCTGGTGGCCACAGCCTTAAGTCTAGGGTTTCCATGATCTACTTTGGAGGCGC 958
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DT 17-OCT-2000 (first entry)
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
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PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000BP-00301439.
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Qy	485	GGCAGAGGAATACTTTAAGCAGGTTGCTGAAAGGATGAGAAAAGTGATTCGTGCTTCAGGT 544
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 Qy 956 CTGATATAGGCTTGGCCCTTTCCAGA 982
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RESULT 15
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 ID AAZ55915 standard; cDNA; 1316 BP.
 XX AAZ55915;
 AC
 DT 10-APR-2000 (first entry)
 XX Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox1 cDNA.
 DE
 XX Gibberellin 2-oxidase; AtGA2ox1; 2-beta-hydroxylation; inactivation;
 KW growth inhibition; ss.
 XX Arabidopsis thaliana.
 OS

Key Location/Qualifiers
 CDS 41..1030
 FT /*tag= a
 FT /product= "Gibberellin 2-oxidase AtGA2ox1"
 XX WO9966029-A2.
 XX 23-DEC-1999.
 XX 11-JUN-1999; 99WO-GB001857.
 XX 12-JUN-1998; 98GB-00012821.
 XX 15-JUL-1998; 98GB-00015404.
 XX (UYBR-) UNIV BRISTOL.
 XX Thomas SG, Hedden P, Phillips AL;
 XX WPI: 2000-097742/08.
 XX P-PSDB; AAY58598.
 XX New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used
 XX to produce transgenic plants with improved or altered growth
 XX characteristics.
 XX Example 3; Fig 5; 42pp; English.

This sequence represents cDNA encoding an Arabidopsis thaliana
 gibberellin (GA) 2-oxidase, PcgA2ox1. This enzyme is a GA 2-beta-
 hydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is
 its only activity. Hydroxylation at the 2-beta position of a GA results
 in a biologically inactive product, and is the most important route for
 GA metabolism in plants, ensuring that the active hormones do not
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 plants so that gibberellin 2-oxidase can be constitutively over-expressed

CC or otherwise enhanced to reduce the concentration of bioactive GAs in the
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 CC lodging-resistance and grain yield in cereals, improving seedling
 CC quality, reducing the growth of amenity grasses, reducing shoot growth in
 CC orchard and ornamental trees, improving tolerance to cold, drought and
 CC infection, and increasing yields (by the diversion of assimilates from
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 CC induce male and/or female sterility (by expression in floral organs),
 CC prevent pre-harvest sprouting, reduce shoot growth in hedging plants,
 CC inhibit reversibility in the development or germination of seeds and
 CC reduce shoot growth in commercial wood species. Antisense constructs of
 CC the nucleic acids can also be used to transform plants to reduce the
 CC expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to
 CC improve fruit set and growth in seedless grapes, citrus fruits and
 CC pears), improve skin texture and fruit shape in apples, increase stem
 CC length and therefore yield in sugar cane, increase yield and earliness in
 CC celery and rhubarb, improve malting yields and quality in cereals
 CC (particularly barley), and increase growth in woody species
 XX
 SQ Sequence 1316 BP; 440 A; 249 C; 252 G; 375 T; 0 U; 0 Other;

Query Match 35.8%; Score 356.6; DB 3; Length 1316;
 Best Local Similarity 63.2%; Pred. No. 1.2e-103;
 Matches 586; Conservative 0; Mismatches 329; Indels 12; Gaps 2;

Qy 65 CCTGTGTTACGGGATTCTCTGTCGACCTCAGCAGCCGCCGATGCCAAGAACTCATAG 124
 Db 78 CCGGGTTCTCTAATCCCGGTTATAGATATGTCGACCAGAAATCAACATGCCCTCG 137
 Qy 125 TGAACCGCTGTAGGGACTTCTCGGCTTCTCAAGCTTGTGAACCACTGGTTCCATTTGAGT 184
 Db 138 TGAAGCATGCGAAGACTTCTCGGCTTCTCAAGGTGATCAACCATGGCTTTCGCGAGAGC 197
 Qy 185 TAATGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAG 244
 Db 198 TAGTCTCTGTTTGAACACGAGACCGTCGATTTCTTCTCTGTTGCCAAGTTCAGAGAAA 257
 Qy 245 ACAGAGCTGTCCCGGACCTTTCGGCTATGTTAGTAGCAGAGGATTTGCCCAACCGGTG 304
 Db 258 CCCAAGTCG---CAGGTTATCTCCGATACGGGAACAGTAAGATTTGGTTCGGAATGGTG 314
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 Db 315 ACGTGGTTGGGTGAGTACTTGTGATGAACGCTAATCATGATTCGGTTCGGGTCCAC 374
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 Qy 425 CAGCAGTGAAGAACATGCTATGCGGTGTTGGAAATTGATGGCGGAGGGTTGGGGATAA 484
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 Qy 545 TGAACCACTACCGCGCTTGGCTGAGGTGGAAGCACTGAAC-----CGGAATTTGG 595
 Db 555 TTAATCACTATCCACCATGTCCTTTAGCAATAAGAAAACCAATGGTGGTGAAGATGTGA 614
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
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Scoring table: IDENTITY_NUC
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: gb_est3:*
- 4: gb_est4:*
- 5: gb_est5:*
- 6: gb_est6:*
- 7: gb_est7:*
- 8: gb_est8:*
- 9: gb_est9:*
- 10: gb_est10:*
- 11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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12	335.4	33.6	567	BM893076	Arabidops
13	334.8	33.4	478	AL382874	Arabidops
14	332.8	33.1	893	DN589159	Arabidops
15	329.2	32.5	792	C1935635	Arabidops
16	323.4	31.5	1554	AY104425	Zea mays
17	314.2	30.8	625	CV292693	EST81070
18	307.2	30.8	642	CV292668	EST81045
19	307.2	30.8	438	BP940509	BP940509
20	305.6	30.7	755	BM690134	BM690134
21	305.6	30.7	776	BM692820	BM692820
22	305.6	30.7	776	BM692820	BM692820

C 23	305.6	30.7	779	3	BJ571134	BJ571134
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C 26	303.6	30.5	663	7	CV292717	EST881094
C 27	300.6	30.2	753	3	BI968577	GM830005B
C 28	300.6	30.1	743	2	BG646259	EST507878
C 29	298.2	29.9	789	5	BM685035	BM685035
C 30	293.8	29.5	517	3	BP074757	BP074757
C 31	293.8	29.5	520	3	BP074168	BP074168
C 32	292.6	29.4	579	6	CA844444	EA27D12a
C 33	292.6	29.4	724	6	CA844443	EA23G12a
C 34	288.6	28.8	847	8	DN982067	SV6_43H10
C 35	287	28.8	619	1	AW584268	N210259e
C 36	286.6	28.8	789	7	CV470333	43176.1 C
C 37	279.8	28.1	611	1	AW309039	sf94B04.y
C 38	279.4	28.1	501	3	BP060951	BP060951
C 39	278.4	28.0	604	7	CV630114	MDst6013a
C 40	277.6	27.9	853	7	CV469374	41999.1 C
C 41	273.6	27.5	800	3	BI970132	GM830009B
C 42	273	27.4	685	2	BG523146	BG523146
C 43	273	27.4	698	8	DR399076	TKN037C04
C 44	272.2	27.3	711	1	AW222239	EST299050
C 45	270.6	27.2	655	5	BQ404995	GA_Ed007

ALIGNMENTS

RESULT 1
AW184969
LOCUS
DEFINITION
AW184969
se84f09.y1 Gm-cl023 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl023-1410 5' similar to TR:O04162 O04162 DIOXYGENASE. i, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
AUTHORS
1 (bases 1 to 653)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Other ESTs: BU544870 corresponding to Gm-cl088-979 (3')
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: eschewatson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert length: 1472 Std Error: 0.00
High quality sequence stop: 436.

FEATURES

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Location/Qualifiers
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="T157"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl023-1410"

/tissue_type="seed coats of greenhouse grown plants"
/lab_host="DH10B"
/clone_lib="Gm-cl023"
/notes="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
cDNA library was constructed from mRNA isolated from seed
coats (100-200mgs) of greenhouse grown plants. The
library was prepared using the Life Technologies
pSuperScript cDNA library construction kit. Complementary
DNA was synthesized from mRNA using a poly (dT) sequence
with a Not I restriction site. Sal I linkers adapters
were ligated to the blunt-ended cDNA fragments followed by
Not I digestion. The cDNA fragments were directionally
cloned into the Not I-Sal I restriction site of the
pSPORT1 vector. The ligated cDNA fragments were
transformed into E.coli Electromax DH10B host cells. This
library was constructed by Dr. Lila Vodkin and Dr. Anu
Khanna."

ORIGIN

Query Match 45.6%; Score 454; DB 1; Length 653;
Best Local Similarity 87.2%; Pred. No. 1.8e-127;
Matches 496; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1 ATGGTTGTTCTGCTCAGCCAGCATTTGAACACAGATTTTCTCTGAAACCATTTCAAGTCC 60
DB 84 ATGGTTGTTCTGCTCAGCCAGCATTTGAACACAGATTTTCTCTGAAACCATTTCAAGTCC 143
QY 61 ACCGCTTGTTCACGGGGATTCCTGTGTCGACCTCAGCCACCCGATGCCAGATCTC 120
DB 144 ACGCCCTTGTTCGCGGGATTCCTGTGTCGACCTCAGCCACCCGATGCCAGATCTC 203
QY 121 ATAGTGAAGCCCTGTAGGAGCTTCGGCTTCTTCAAGCTGTGAACCATGTTTCCATTG 180
DB 204 ATAGTCAATGCCCTGAGGAGCTTCGGCTTCTTCAAGCTGTGAACCATGTTTCCATTG 263
QY 181 GAGTTAATGGCCAAATTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240
DB 264 CAGTTTCATGGCCAAATTGGAAAACGAAACCTCGGGTCTTCAAAAAAATCTCAGTCCGAG 323
QY 241 AAAGACAGAGCTGGTCCCCCGACCTTTCGGCTATGTTAGCAGAGGATTTGCCCAAC 300
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QY 301 GGTGATGTCGGTGGGTGCGAATACCTCTCCTCAACACCAACCTGATGTTATCTCACCC 360
DB 384 GGGATGTCGGTGGGTGCGAATACCTCTCCTCAACACCAACCTGATGTTATCTCACCC 443
QY 361 AATCATCTTTGCAATTTCCGAGAAAATCCTCATCATTTTCAGGCGGTGGGAGAACTAC 420
DB 444 AAGTCACAGTTTCATTTTCAGAGAAGGTCCTCAGAAATTCANGGCGGTGGGAGGAATAC 503
QY 421 ATTACACAGTGAAGAACATGCTATGCGGTGTTGGAATGATGCGGAGGGTGGG 480
DB 504 ATTAGAGCGGTGAAGAACATGCTATGAGGTGTTGGAATGATGCTGANGGATTTGGG 563
QY 481 ATAAGCAGAGGAATACGTTTAAGCAGGTGCTGAAGGATGAGAAAAGTGAATCGTCTTC 540
DB 564 ATAAACCATAGGATGTTGATGATGTTGCTGAACGATGAGAGGATGATCTTCTGCTTC 623
QY 541 AGGTTGAACACTACCCGCTTGCCTGA 569
DB 624 AGACNTTACCACTACCCGCTTGCCTGA 652

RESULT 2
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LOCUS
DEFINITION
saj34h07.y1 Gm-cl066 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl066-4957 5' similar to TR:Q9XG83 Q9XG83 GA 2-OXIDASE. ; mRNA
sequence.
ACCESSION
BM085298
VERSION
BM085298.1 GI:16995926
KEYWORDS
EST.

SOURCE
ORGANISM

Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE
AUTHORS

1 (bases 1 to 566)
Shoemaker R., Kelm P., Vodkin L., Erpelding J., Corvett V.,
Khanna A., Bolla B., Marra M., Hillier L., Kucaba T., Martin J.,
Beck C., Wylie T., Underwood K., Steptoe M., Theising B., Allen M.,
Bowers Y., Person B., Swaller T., Gibbons M., Pape D., Harvey N.,
Schurk R., Ritter E., Kohn S., Shin T., Jackson Y., Cardenas M.,
McCann R., Waterston R. and Wilson R.
Public Soybean EST Project
Unpublished (1999)

TITLE
JOURNAL
COMMENT

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 426.

FEATURES
source

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/cultivar="Williams"
/db_xref="taxon:3847"
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/tissue_type="Leaf and shoot tip, salt stressed, 2 week
old seedling"
/lab_host="DH10B"
/clone_lib="Gm-cl066"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from unexpanded leaves and the shoot tips of 2 week old
seedling from the cultivar Williams. The 2 week old
seedlings were salt stressed in a solution of 500mM NaCl
for 3 days prior to harvesting. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
Shoemaker."

ORIGIN

Query Match 44.5%; Score 443.4; DB 3; Length 566;
Best Local Similarity 88.0%; Pred. No. 3.1e-124;
Matches 493; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1 ATGGTTGTTCTGCTCAGCCAGCATTTGAACACAGATTTTCTCTGAAACCATTTCAAGTCC 60
DB 18 ATGGTTGTTCTGCTCAGCCAGCATTTGAACACAGATTTTCTCTGAAACCATTTCAAGTCC 77
QY 61 ACGCCCTTGTTCACGGGGATTCCTGTGTCGACCTCAGCCACCCGATGCCAGATCTC 120
DB 78 ACGCCCTTGTTCACGGGGATTCCTGTGTCGACCTCAGCCACCCGATGCCAGATCTC 137
QY 121 ATAGTGAAGCCCTGTAGGAGCTTCGGCTTCTTCAAGCTGTGAACCATGTTTCCATTG 180
DB 138 ATAGTGAAGCCCTGTAGGAGCTTCGGCTTCTTCAAGCTGTGAACCATGTTTCCATTG 197
QY 181 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240

Db 198 GAGTTTCAGCCCAATTTGGAAACGAAACCCCTCAGGTTCTTCAAAAAACCTCAGTCCGAC 257
Qy 241 AAAGCAGAGCTGGTCCCCCGACCTTTCGGCTATGGTAGCAGAGGATTGGCCCAAC 300
Db 258 AAAGCAGAGGCTGGTCCCCCTGATCTTTGGCTACGCGCAGCAGAGGATTGGCCCTAAC 317
Qy 301 GGTGATGTCGGTGGGTGGAATACCTCTCTCCCAACACCAACCTGATGTTATCTCACCC 360
Db 318 GCGGATGTCGGTGGGTGGAATACCTCTCTCCCAACACCAACCTGATGTTATCTCACCC 377
Qy 361 AAATCATTGATGTTTCGCGAAGAAATCTCATCTTTTCAGGCGGTGGTGAGACTAC 420
Db 378 AAGTCAGGTCATTTTTCGCGAAGAAATCTCATCTTTTCAGGCGGTGGTGAGACTAC 437
Qy 421 ATTACAGCAGTCAAGAACATGTGCTATGCGGTGTTGGAAATTCATGCGCGAGGGGTTGGGG 480
Db 438 ATTAGGCGCTGAGNACATGTGCTATGAGGTGTTGGAAATTAATGGCGAGGGCTTGGGA 497
Qy 481 ATAAGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAGTATTCGTGCTTC 540
Db 498 ATAATCAGAGGAATGCGTTGAGTAGTTGCTGGAAGGATGAGAAAGTATTCGTGCTTC 557
Qy 541 AGGTTGAAC 549
Db 558 AGACTTAAC 566

RESULT 3

CNSOAC6N 1365 bp mRNA linear HTC 06-FEB-2004
LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
DEFINITION GSLT7B2E01 of Flowers and buds of strain col-0 of Arabidopsis
thaliana (thale cress).

ACCESSION

VERSION BX814544.1 GI:42472102

SOURCE HTC; GSLT cDNA.

ORGANISM Arabidopsis thaliana (thale cress)

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1 (bases 1 to 1365)

Castelli, V., Aury, J.M., Jallou, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Queller, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation

Unpublished

2 (bases 1 to 1365)

Genoscope.

Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Life Technologies (a division of Invitrogen)

The sequences are based on single pass reads.

Full-length libraries construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli

V., Aury J.M., Jallou O., Wincker P., Menard M., Cruaud C.,

Schachter V., Weissenbach J., Salanoubat M.

URV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis

genome released by MIPS (Munich Information center for Protein

Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full

length

http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

Location/Qualifiers

1. .1365

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/db_xref="taxon:3702"

FEATURES

source

gene
ORIGIN
Query Match 42.7%; Score 424.8; DB 4; Length 1365;
Best Local Similarity 67.2%; Pred. No. 2.1e-118;
Matches 616; Conservative 0; Mismatches 297; Indels 3; Gaps 1;
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Db 195 ATCCCGTGTGCGACTCAGCACCCCGATGCGAAGAAATCTCATAGTGAACCCCTGTAGG 254
Qy 139 GACTTCGGCTTCTTCAAGCTTGTGAACCATGCTGTTCCATTGGAGTTAATGCGCAATTTA 198
Db 255 GAGTTTCGGGTTCTTCAAGGTCGTAAACCCAGGAGTCCGACCCGAACTCATGACTCGTTA 314
Qy 199 GAAAAAGAGGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAGACAGAGCTGCTCC 258
Db 315 GAGCAGGAGGCTATTTGGCTTCTTCGGCTTGCCTCAGTCTCTTAAAAACCGGCGGTCCA 374
Qy 259 CCCGACCTTTTCGGCTATGTTAGCAAGAGGATTTGCCCAAAACGGTGTATGCTGGTGGTTC 318
Db 375 CCGTGAACCGTACGGTTATGTTAAACCGGATTTGACCAAAACCGTGTGCTGGTGGATT 434
Qy 319 GAATACCTTCTCTCAACACCAACCCCTGATGTTATCTCACCACCAATCATTTCGCAATTTTC 378
Db 435 GAGTATCTCTCTCAATGCTAAATCCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 494
Qy 379 CGAGAAAAATCTCTCATCATTTTCAGGCGGCTGTTGGAGAACTACATTACAGCAGTGAAGAAC 438
Db 495 CGTCAAAACCCCTCAAAATTTTCGCTGAGTGGTGGAGGATACATGAAGAGATTAAAGAA 554
Qy 439 ATGTCTATGCGGTTTGGAAATTTGATGCGGAGGGTTGGGATAGGAGGAGGAAATAGC 498
Db 555 GTGTGCTACAAAGTGTTCGAGATGTTCCGAGAAATAGGATAGAGCAAGGACACT 614
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Db 615 CTGAGTAAATGCTGAGAGATGAGAAAGTATGTTGCTTCAGTTCAGTTGAGGAGGAGGAG 674
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Db 675 GC---GGCGGAGGAGAGCGCGGAGGAGGATGTTGAGGAGTGGGTTTGGGAGGAGGAGGAG 731
Qy 619 CCACAGATAATTTCTGTTTAAAGATCTAACAGCAGCATCTGGCTTGCAAAATCTGTTCTACA 678
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Qy 679 GATGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTTTTTCATCATCTTGGTGAC 738
Db 792 GATGGAAGTGGGTCGCTGCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 851
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Db 852 GCTCTTACAGTATGACTAAACCGGAGGTTTCAAGAGTGTAAACACAGGCTTTAGCCGAT 911
Qy 799 ACAACGAAAGTCAAGGTTTATCAATGATCTACTTTGGAGGACCGGCTGAGTGAATAATA 858
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Qy 919 TGTGTAATCAGAAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGGCCCTTTC 978
Db 1032 TCTCAATCAAAATCTTCTGCTTACAAAGTCTAAGTGTGTTATAGACTTGTCTCTT 1091
Qy 979 CAGAAATCTGCTGCTG 994

A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1141)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT The sequences are based on single pass reads.
 Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.
 Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
 URV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length
 http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
 FEATURES
 source location/Qualifiers
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 ORIGIN
 Query Match 42.3%; Score 421.2; DB 4; Length 1141;
 Best Local Similarity 67.3%; Pred. No. 2.5e-117;
 Matches 610; Conservative 0; Mismatches 293; Indels 3; Gaps 1;
 QY 79 ATTCTGTGTCGACCTCAGCACCACCGCATGCCAAGAATCTCATGTGAACCCCTGTAGG 138
 DB 165 ATCCCCGTGTCACCTAGCCGATCCGAAGCGAAGAACCCGAACTCGTAAAGCCCTGCGAG 224
 QY 139 GACTTCGGCTTCTCAAGCTTGTGAACCATGGTGTTCATTTGAGTTAATGGCCAAATTTA 198
 DB 225 GAGTTCGGTCTTCAAGTCTGTAAACCAAGGTCGACCGGAACTCATGACTCGGTTA 284
 QY 199 GAAACGAGGCCCTCAGGTTCTTTAAAAATCTCAGTCCGAGAAACAGAGCTGGTCCC 258
 DB 285 GAGCAGGAGGCTATTGGCTTCTTCGGCTTGCCTCAGTCTCTTAAAAACCGGCGGTCCA 344
 QY 259 CCGGACCTTCGGCTATGTAGCAGAGGATGGCCAAACGGTGATGTCGGTTGGGTC 318
 DB 345 CTGAACCGTACGGTTATGGTAATAACCGGATGGACCAACCGGTGACGTTGGTGGATT 404
 QY 319 GAATACCTCTCTCAACCAACCTGATGTATCTCAACCAAAATCACTTTGCATTTTC 378
 DB 405 GAGTATCTCTCTCAATGCTAATCTCAGTCTCTCTCTTAAACCTCCGCGGTTTC 464
 QY 379 CGAGAAATCTCATCATTTTCAGGGCGGTGGTGGAGAACTACATTACAGATGAAGAAC 438
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 QY 559 CTTTGCCCTGAGTGAAGCACTGAACCGGAATTTGGTTGGGTTTGGGAGCACACAGAC 618

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 QY 979 CAGAAA 984
 DB 1062 GAGAAA 1067
 RESULT 6
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 LOCUS GM880016A20B10 Gm-r1088 Glycine max cDNA clone Gm-r1088-5828 3',
 DEFINITION mRNA sequence.
 ACCESSION BUS49366
 VERSION BUS49366.1 GI:22932227
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 1 (bases 1 to 622)
 Vokhin,L., Shoemaker,R., Keim,P., Retzel,E., Khanna,A., Shealy,R., Clough,S., Thibaud-Nissen,F., Coryell,V., Erpeliding,J., Raph,C., Shoop,B., Stromvik,M., Schweitzer,P., Gong,G. and Liu,L.
 A Functional Genomics Program for Soybean (NSF 9872565) (2002)
 Unpublished (2002)
 Other ESTs: BG881784 corresponding to Gm-cl065-2970 (5')
 Contact: Vokhin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
 Lewin, H. A., Director, Keck Center for Comparative and Functional Genomics
 University of Illinois
 Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
 Tel: (217) 244-6147
 Fax: (217) 333-4582
 Email: l-vokhin@uiuc.edu
 Insert Length: 622 Std Error: 0.00
 Plate: GM880016A20 row: B column: 10
 Seq primer: 5'-TTTTTTTTTTTTTTTTTTT(A/C/G)-3'
 High quality sequence stop: 622.
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 /clone_lib="Gm-r1088"
 /note="The library Gm-r1088 is a sequence-driven, reracked source"

set of 9,216 low redundancy clones selected from cDNA libraries from various tissues and stages of development of soybean that consists of 2,706 cDNAs from germinating cotyledons (source library Gm-cl027); 1,355 cDNAs from immature seed coats (libraries Gm-cl019 and Gm-cl023); 917 cDNAs from tissue culture derived somatic embryos (source libraries Gm-cl036 and Gm-cl075); 3,275 cDNAs from germinating seedlings, shoot tips, or leaves exposed to various stresses (source libraries Gm-cl064, Gm-cl065, Gm-cl066, and Gm-cl067; and Gm-cl068), and 963 cDNAs from young leaves exposed to bacterial and fungal pathogens (source libraries Gm-cl072, Gm-cl073, and Gm-cl074). The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-r1088 and the cDNA clones of the reracked Gm-r1088 library were then sequenced at the 3' end. The unigene selection and 3' sequencing was funded by NSF Plant Genome project #9872565 (http://soybean.genomics.croptci.uiuc.edu/) as part of creation of a low redundancy soybean cDNA set. The source cDNA libraries were constructed by the laboratories of Lila Vodkin, University of Illinois, Randy Shoemaker, Iowa State University, and Paul Keim, Northern Arizona University as part of the Public EST project, http://129.186.26.94/soybeanest.html. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, Randy Shoemaker, Iowa State University, and Paul Keim, Northern Arizona University as part of the Public EST project, http://web.ahc.umn.edu/biodata/nfsboy/. Reracking and 3' sequencing were conducted by services of the University of Illinois Keck Center for Comparative and Functional Genomics http://www.biotech.uiuc.edu/keck.htm. Note: The corresponding 5' EST from each clone in the Gm-r1088 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of the original cDNA library that is also listed under 'OTHER EST'."

ORIGIN

Query Match 42.2%; Score 420.4; DB 5; Length 622;
Best Local Similarity 89.9%; Pred. No. 3.7e-117;
Matches 461; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

QY 487 CAGAGAAATACGTTAGCAGGTTGCTGAAGGATGACAAAGTCATTCGTCCTCAGGTG 546
DB 621 CAGAGAAATGCGTTGATGAGTTGCTGAAGGATGACAAAGTCATTCGTCCTCAGACTT 562

QY 547 AACCACTACCCGCTTGCCCTGAGGTGCAAGCACTGAA---CCGGAATTTGGTTGGTTT 603
DB 561 AACCCNNACCGCATGCCAGAGGTGCAAGCATTCGACGCGAGAAATTTGGTTGGTTT 502

QY 604 GGGAGACACAGACCCACAGATAATTTCTGTCTTAAGATCTAAACAGACATCTGGCTTG 663
DB 501 GGAGAGACACAGACCCACAGATAATTTCTGTCTTGAATCTAAACAGCACCTCAGGCCTG 442

QY 664 CAAATCTGTCACAGATGCACTTGGGTTTCAGTCCACCTGATCAGACTTCTCTTTTC 723
DB 441 CAAATCTGTCACAGATGCACTTGGGTTTCAGTCCACCTGATCAAACTTCTCTTTTC 382

QY 724 ATCAATGTTGGTGACGCTCTACAGGTAAATGACTTAATGGGAGGTTTAAAGTGTAAGCAT 783
DB 381 ATCAATGTTGGTGACACTCTACAGGTGATGACTTAATGGGAGGTTTAAAGTGTAAGCAT 322

QY 784 AGGTTTTGGTGACACAGAAAGTCAAGTTATCAATGATCTACTTTTGGAGACACAGCG 843
DB 321 AGAGTTTTGGTGACCAACCAAGTCAAGTTGTTCAATGATCTACTTTTGGAGGAGCACCC 262

QY 844 TTGAGTGAATAATAGCATTACCTTCAGTCATGTTAAAGGAGAGAGGTTGTTGTAC 903
DB 261 TTGAGTGAATAAGATATCATTACCTTCTTCATGTTTAAAGGAGAAAGAGAGTTTCTAC 202

QY 904 AAAGATTTCATGTTGTGAATACAAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAAT 963

DB 201 AAAGAATTACATGTTGGGAATACAGAAGGCTGCTATGCTCAAGGCTAGCGGATAAT 142
QY 964 AGGCTTGCCCTTTCCAGAAATCTGCTGCTGAT 996
DB 141 AGGCTGCTCCTTTTGAGAAATCTGCTGCTGAT 109

RESULT 7
CNSOABKL 1363 bp mRNA linear HTC 06-FEB-2004
LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
DEFINITION GSLFPGH20Z07 of Hormone Treated Callus of strain col-0 of
Arabidopsis thaliana (thale cress).
ACCESSION BX815974
VERSION BX815974.1 GI:42471555
KEYWORDS HTC; GSLT_cDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 1363)
AUTHORS Castell, V., Aury, J.M., Jallou, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, P., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.
TITLE Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis genome
Annotation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1363)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
COMMENT - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jallou O., Wincker P., Menard M., Cruaud C.,
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/banque_projet_EF/Full
length
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
FEATURES
Location/Qualifiers
1..1363
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="GSLFPGH20Z07"
/tissue_type="Hormone Treated Callus"
/ecotype="Col-0"
/plasmid="pCMVSPORT_6"
1..1363
/gene="Atlg30040"

gene
ORIGIN
Query Match 41.8%; Score 416.4; DB 4; Length 1363;
Best Local Similarity 67.0%; Pred. No. 8e-116;
Matches 607; Conservative 0; Mismatches 296; Indels 3; Gaps 1;

QY 79 ATTCCTGTGGTCGACTCAGCACCGATGCCAAGAATCTCATAGTGAACGCTGTAGG 138
DB 193 ATCCCCGTGTCACCTAGCCGATCGGAGCGAAACCCGATCGTAAAGCCTGCTAG 252
QY 139 GACTTCGGCTTCTCAAGCTTGTGAACCATGTTGTTCCATTGAGTTAATGCCCAATTA 198
DB 253 GAGTTTCGGGTTCTTCAAGGTCGTAACCAACCGAGTCCGACCCGAACTCATGACTCGGTTA 312

QY	199	GAAGAGAGGCGCTCAGGTTCTTTAAATAATCTCAGTCGAGAAAGACAGAGCTGTGTCC	258
Db	313	GAGCAGAGGCTATGCGCTTCTTCGGCTCGCTAGCTCTTTAAATAACCGGCGGTCCA	372
QY	259	CCGAGCCCTTTCGGCTATGGTAGAGAGGATTGGCCAAACGGTGATGTCGGTGGGTC	318
Db	373	CCTGAACCGTATCGGTTATGTAATAAACGATTGGACCAACGGTGACGTTGGTGGATT	432
QY	319	GAATACCTCTCTCAACCAACCGCTGATTTATCTCACCCAAATCACTTTGCAATTTTC	378
Db	433	TAGTATCTCTCTCAATGCTAATCTCTCAGCTCTCTCTCTTAAACCTCCGCGGTTTC	492
QY	379	CGAGAAATCTCTCATATTTTCAGGGCGGTGGTGGAGAACTACATTAACAGCAGTAAGAAC	438
Db	493	CGTCAAAACCCCTCAAAATTTTCGAGTGGTGGAGGAGTACATGAAGAGATTAAAGAA	552
QY	439	ATGTGCTATCGGTTGTGAATGATGGCGGAGGGTTGGGATTAAGGAGAGGATATAG	498
Db	553	GTTCGTACAAGGTGTGGAGATGGTTGCCGAAGAACTAGGGATAGAGCAAGGGACACT	612
QY	499	TTAAGCAGGTCTCTGAAGATGAGAAAGTATCGTGTCTTCAAGTTGAACCACTACCGG	558
Db	613	CTGAGTAAATGCTGAGAGATGAGAAAGTGACTCGTGCCTGAGACTAAACCATTTATCCG	672
QY	559	CCTTGCCTCGAGTGAAGCACTGAACCGCAATTTGGTTGGGTTTGGGAGACACAGAC	618
Db	673	GC----GGCGAGGAGAGCGGAGAGATGGTGAAGTGGGTTTGGGAGACACAAAC	729
QY	619	CCACAGATAATTTCTCTTTAAGATCTAACAGACATCTGGCTTGCATTTCTGTCTACA	678
Db	730	CCACAAATAATCTCAGTTCTAAGATCTAATAACACGCGGGTCTTCAAATCTGTGTGAA	789
QY	679	GATGGCACTTGGGTTTTCAGTCCCACTGATCAGACTTCTTTTTCATCAATGTTGGTAC	738
Db	790	GATGGAAGTTGGTTCGCTGCTCCCTCTGATCTCTTCTTCTTCTTCTTCTTCTTCTT	849
QY	739	GCTCTACAGTATGATTAATGGAGGTTTAAAGGTAAAGCATAGGCTTTTGGCTGAC	798
Db	850	GCTCTTTCAGTTATGATTAACGGAGGTTTCAAGAGTTTAAACAGGCTTTAGCCGAT	909
QY	799	ACAACGAAGTCAAGGTTATCAATGATCTACTTTTGGAGGACCAAGCTTGTAGTGAAATATA	858
Db	910	ACAAGGAGATCGAGGATTTCAATGATATATTTTCGGCGGACCGCAATTGAGCCAGAGATC	969
QY	859	GCACCTTTACCTTCAGTGATGTTAAAGAGAGGAGTGTGTTGACAAAGATTCAATGG	918
Db	970	GCACCAATGCGCATGCTTGTCCCTGAGCAAGATGATTGGCTTTTACAAAGAAATTCATTGG	1029
QY	919	TGTGATACAAGAGGCTCGTACACTTCAAGGCTAGCTGATAATAGGCTTGGCCCTTTC	978
Db	1030	TCTCAATAACAATCTTCTGCTTCAAGTCTAAGCTTGGTGTATTAAGACTTGTCTCTTT	1089
QY	979	CAGAAA 984	
Db	1090	GAGAAA 1095	
RESULT 8			
CNSOAC3R			
LOCUS			
DEFINITION			
Arabidopsis thaliana Full-length cDNA Complete sequence from clone			
GSLT70ZFl of Flowers and buds of strain col-0 of Arabidopsis			
thaliana (thale cress).			
BX814383			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Arabidopsis thaliana (thale cress)			
Arabidopsis thaliana			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;			
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.			
REFERENCE			
1 (bases 1 to 1339)			

AUTHORS		Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
TITLE		Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
JOURNAL		Unpublished
REFERENCE		2 (bases 1 to 1339)
AUTHORS		Genoscope.
JOURNAL		Direct Submission
TITLE		Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT		- Web : www.genoscope.cns.fr The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_FF/Full-length http://www.genoscope.cns.fr/cgi-bin/ggb7source=Arabidopsis. Location/Qualifiers 1..1339 /organism="Arabidopsis thaliana" /mol_type="mRNA" /db_xref="taxon:3702" /clone="GSLT70ZFl1" /tissue_type="Flowers and buds" /ecotype="Col-0" /plasmid="pCMVSPORT_6" 1..1339 /gene="Atlg30040"
FEATURES		source
QY		Query Match 38.8%; Score 386.4; DB 4; Length 1339;
Db		Best Local Similarity 66.9%; Pred. No. 1.3e-106; Matches 581; Conservative 0; Mismatches 281; Indels 6; Gaps 2;
QY		79 ATCTCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTCATAGTGAACGCTGTAGG 138
Db		193 ATCCCCGTCTCAACTAGCCGATCGGAAGCGAAACCCGAATCGTAAAGCCTCGAG 252
QY		139 GACTTCGGTCTTCAAGCTTGTGAACCATGGTTCATTTGGAGTTAATGGCAATTTA 198
Db		253 GAGTTTCGGTCTTCAAGGTCGTAACCAACCGAGTCCGACCCGAACTCATGACTCGGTTA 312
QY		199 GAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAACAGAGAGCTGTCCC 258
Db		313 GAGCAGGAGGCTATTGGCTTCTTCGGCTTTCCTCAGTCTCTTAAAAACCGGCGGTCCA 372
QY		259 CCCGACCCCTTCGGCTATGCTAGCAGAGGATTGGCCCAACCGTGTGCTGGGTC 318
Db		373 CTGAAACCGTACGGTTATGTTAATAACCGATTGGACCAACCGTGACGTTGGTGGATT 432
QY		319 GAATACCTCTCTCAACCAACCAACCTGTATCTCAACCCAAATCACTTTGCATTTTC 378
Db		433 GAGTATCTCTCTCAATGCTAATCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 492
QY		379 CGAGAAATCTCTCATCTTTTCAGGGCGGTGGGAGAACTACATTTACAGCAGTGAAGAAC 438
Db		493 CGTCAAAACCCCTCAAAATTTTCGCTGAGTCCGTTGGAGGATACATGAAGGAGATTAAAGAA 552
QY		439 ATGTGCTATGCGGTTGTGAATTTGATGGCGGAGGGTTGGGATTAAGGAGAGGATATAG 498
Db		553 GTGTGCTACAAGGTGTGGAGATGGTTGCCGAAGAACTAGGATATAGGATAGAGCCAGGACACT 612
QY		499 TTAAGCAGGTTGCTGAAGGATGAGAAAGTGTTCGTGCTTCAAGTTGAGTGTGAGTGTG 558

Db 613 CTGAGTAATATGCTGAGAGATGAGAGAGTACTGCTGCTGAGACTAAACCAATATCCG 672
QY 559 CCTTGCCCTGAGTGAAGCACTGAACCGAAATTTGGTTGGGTTTGGGGAGCACACAGAC 618
Db 673 GC---GGCGGAGGAGAGGCGGAGAGATGGTGAAGTGGGGTTTGGGGAACACACAGAC 729
QY 619 CCACAGATAATTTCTGCTTTAAGATCTAACAGACACATCTGGCTTGGCAATCTGCTTCACA 678
Db 730 CCACAGATAATCTCAGTGTGAAGATCTAATAACACGCGGGCTTCAAAATCTGTGTGAAA 789
QY 679 GATGGCACTTGGGTTTCAGTCCACCTGATACACACTTCTTTTTCATCAATGTTGGTGAC 738
Db 790 GATGGAAGTTGGGTCGCTGCTCTCTGATCATCTTCTTCTTCAATGTTGGAGAT 849
QY 739 GCTCTACAGTAATGACTAATGGAGGTTTAAAGTGAAGCATAGGGTTTGGCTGAC 798
Db 850 GCTCTTTCAGTTATGACTAACGGGAGGTTCAAGAGTGTAAACACAGGGCTTAGCCGAT 909
QY 799 ACAACGAAGTCAAGGTTATCAATGATCTACTTTTGGAGGACCGGTTGAGTGAATAATA 858
Db 910 ACAAGAGATCGAGGATTTCAATGATATATTTCCGGCGGACCGCATTTGAGCCAGAAGATC 969
QY 859 GCACCTTTACCTT---CAGTGATGTTAAAGGAGAGAGTGTGTGACAAAGTTTCACA 915
Db 970 GCACCAATGCAATGCTGTGCTGCTGAGCAAGATGATTTGTGCTTTACAAAGAATTCAT 1029
QY 916 TGGTGTGAATACAAAGAGGCTGGGTACA 943
Db 1030 TGGTCTCAATACAAATCTTCGTTTACA 1057

RESULT 9
BE802903
LOCUS
DEFINITION
sz46c09.y1 Gm-cl051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl051-1097 5' similar to TR:064692 064692 PUTATIVE GA4 PROTEIN.
/, mRNA sequence.

ACCESSION
BE802903
VERSION
BE802903.1 GI:10234015
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE
1 (bases 1 to 612)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)

TITLE
JOURNAL
COMMENT
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 413.

FEATURES
Location/Qualifiers
1..612
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Corolla"
/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl051-1097"
/tissue_type="floral meristematic mRNA"
/lab_host="DH10B"
/clone_lib="Gm-cl051"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from floral
meristematic mRNA provided by Dr. Halina Knap of Clemson
University. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."

ORIGIN

Query Match 37.7%; Score 375.6; DB 2; Length 612;
Best Local Similarity 88.3%; Pred. No. 2.1e-103;
Matches 408; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
QY 1 ATGGTTGTTCTGCTCAGCCAGCATTAACCAAGTTTTCCTCTGAAACCATTCAGTCC 60
Db 151 ATGGTTGTTCTGCTCAGCCAGCATTAACCAAGTTTTCCTCTGAAACCATTCAGTCC 210
QY 61 ACGCCCTTCTTCCAGCGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGATCTC 120
Db 211 ACGCCCTTCTTCCAGCGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGATCTC 270
QY 121 ATAGTGAACGCTGTAGGGACTTCGGCTTCTTCAAGCTTTGTGAACCATTCAGTTC 180
Db 271 ATAGTGAACGCTGTAGGGACTTCGGCTTCTTCAAGCTTTGTGAACCATTCAGTTC 330
QY 181 GAGTTAATGGCAATTTAGAAAACGAGGCCCTCAGTTCCTTTTAAATAATCTCAGTCCGAG 240
Db 331 CAGTTCATGCGCAATTTGGAAAACGAAACCTCGGGTCTTCAAAAACCTCAATCCGAG 390
QY 241 AAAGACAGAGCTGGTCCCGCCGACCTTTCCGCTATGGTAGCAAGAGGATTCGCCCAAC 300
Db 391 AAAGACAGAGCTGGTCCCGCCGACCTTTCCGCTATGGTAGCAAGAGGATTCGCCCAAC 450
QY 301 GGTGATGTCGGTTGGTTCGAATACCTCTCTCAACACCAACCCCTGATGTATCTCACCC 360
Db 451 GCGGATGTCGGTTGGTTCGAATACCTCTCTCAACACCAACCCCTGATGTATCTCACCC 510
QY 361 AAATCACTTTGATTTTCCGAGAAAATCCTCATCTTTCAGGCGGTGTGGAGAACTAC 420
Db 511 AAGTCACAGTTCATTTTTCAGAGAACGTCCTCAGAAATTTTCATGCGGTGGGAGGAATAC 570
QY 421 ATTACAGCAGTCAAGAACATGTGCTATGCGGTGTGGGAATTG 462
Db 571 ATTACAGCAGTCAAGAACATGTGCTATGACGTGGTGGGAATTG 612

RESULT 10

AJ803092
LOCUS
DEFINITION
AJ803092 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
018.5.05.018, mRNA sequence.
ACCESSION
AJ803092
VERSION
AJ803092.1 GI:51118420
KEYWORDS
EST.
SOURCE
Antirrhinum majus (snapdragon)
ORGANISM
Antirrhinum majus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Lamiales; Plantaginaceae; Antirrhineae;
Antirrhinum.
REFERENCE
1 (bases 1 to 785)
Bey, M., Stueber, K., Fellenberg, K., Schwarz-Sommer, Z., Sommer, H.,
Saedler, H. and Zachgo, S.
Characterization of Antirrhinum Petal Development and

Identification of Target Genes of the Class B MADS Box Gene

DEFICIENS
Plant Cell 16 (12), 3197-3215 (2004)
15539471
Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
1. .785
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_5_05_018"
/tissue type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

ORIGIN

Query Match 35.7%; Score 355.8; DB 1; Length 785;
Best Local Similarity 68.4%; Pred. No. 2.7e-97;
Matches 508; Conservative 0; Mismatches 232; Indels 3; Gaps 1;

QY 235 TCCGAGAGACAGAGCTGCTCCCGACCCCTTCGGCTATGCTAGCAAGAGGATTGCG 294
Db 20 TCTGAAAGAGAAACAGGGACCTGACCCCTTTGGCTATGGAATTAAGAAATTGA 79

QY 295 CCAACGGTGTATGCTGGTTCGAATACCTCTCTCAACACCAACCTGATGTTATC 354
Db 80 CGCAATGGCGATGGGATGGTTCGAATACCTCTCTCAACACCTGATGTTATC 139

QY 355 TCACCAATACATTTGCAATTTCCAGAAATCTTCATCATTTCAAGCGGTGTGGAG 414
Db 140 TACAGAAATTTGCATCGCTTTTGGTGAAGCTGCAGAAATTTCAAGTGTATAGTGA 199

QY 415 AACTACATACAGCTGAGACATGCTCTATCGGTGTGGATTTGATGTCGGGAG 474
Db 200 GATTATGTTCTGCAGTAAGAGATGGCGTGTGAGATTTCTGAAATGTGCTGATGAA 259

QY 475 TTGGGATTAAGCAGAGGATAGCTTAAGCAGGTGCTCAAGGATGAGAAATGATTCG 534
Db 260 CTTAAGATTCACAAAGAAAGCTTTTACAACTTTTAATGATGAACAGAGTGAATCT 319

QY 535 TGTCTCAGTTGAACCACTACCGCTTCCTCGGTAGGTCAAGCACTGAACCGGAATTG 594
Db 320 GTTTTCAGGCTAAATCACTATCCATCCCGAATTTCAAGAAATCCAACT--AACTTA 376

QY 595 GTTGGTTGGGAGACACAGACCAACAGATAATTTCTGCTTAAGATCTAACAGCACA 654
Db 377 ATCGGTTTGGTGAACATACGACCGCAATAATATCCGTTTGGAGATCCAAACACT 436

QY 655 TCTGGCTTCAAACTGTCTCAGATGCACCTTGGGTTTCAGTCCACCTGATCAGACT 714
Db 437 TCGGTCTTCAAAATTCGTTGAAGATGGAAATGGAATTTCTATCCCTGATCAAGT 496

QY 715 TCCCTTTTCATCAATGTTGGTGAACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGT 774
Db 497 TCTTTCTTCAATTAATGTTGGTGAACGCTCTACAGGTTATGACTAATGGCAGGTTTAAAGT 556

QY 775 GTAAGCATAGGTTTGGCTGACACACAGAGTCAAGGTTATCAATGATCTACTTTTGA 834
Db 557 GTAAGCACAGGTTTGGTCCAAACAGCTCAAAACCAAGACTTTCAATGATATATTTTGA 616

QY 835 GGACCAAGCTTCAGTGAATATAGCACCTTTACCTTCAGTGTGTTAAAGAGGAGAGAG 894
Db 617 GGACCAACCAATTAAGTGAAGATAGTCTCATTTGCTTCAGTCTAATGAAGAGAGAGAC 676

QY 895 TGTGTTGTAACAAGAGTTTCAATGTTGTAATACAAGAGGCTCGGTACACTTTCAAGGCTTA 954
Db 677 AGCTTGTACAAGAAATTTACTTTGTTTGTAGTACAAAATCTGCTTATTAATCAAGGCTGG 736

QY 955 GCTGATAATAGGCTGCCCCCTTT 977
Db 737 GCTGATAATAGGCTGCTGTTT 759

RESULT 11

CNSOADM7
LOCUS

DEFINITION

1128 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTFB56ZG10 of Flowers and buds of strain col-0 of Arabidopsis
thaliana (thale cress).

ACCESSION

BX814091

VERSION

GI:42474058

KEYWORDS

HTC; GSLT cDNA.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 1128)

AUTHORS

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.

TITLE

A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 1128)

AUTHORS

Genoscope.

JOURNAL

Direct Submission

TITLE

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT

The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
length
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

FEATURES

source

Location/Qualifiers

1..1128

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

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/clone="GSLTFB56ZG10"

/tissue_type="Flowers and buds"

/ecotype="Col-0"

/plasmid="pCMVSPORT 6"

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/gene="Atlg78440"

gene

ORIGIN

Query Match 35.0%; Score 348.6; DB 4; Length 1128;
Best Local Similarity 62.7%; Pred. No. 5e-95;
Matches 581; Conservative 0; Mismatches 334; Indels 12; Gaps 2;

QY 65 CTTTGTTCACGGGATTCCTGTGGTCGACCTCACGCCGCCGATGCCAAGATCTCATAG 124

Db 84 CGGGTCTCTCTAATCCGGTTATAGATATCTCGACCCAGAAATCCAAACATGCCCTCG 143

QY 125 TGAACGCTGTAGGACTTCGGCTTCTCAAGCTTGTGAACCATGGTGTTCATTGGAGT 184

Db 144 TGAAGACATGCGAAGACTTCGGCTTCTTCAAGGTGATCAACCATGGCGTTTCGCGAGAGC 203

QY 185 TAATGCCCAATTTAGAAACGAGGCCCTTCAGGTTCTTTAAAAAATCTCAGTCGAGAAAG 244

Db 204 TAGTCTCTGTTTGAACACAGAGAACGTCGATTTCTTCTCGTTGCCCGAGGTGAGAAAAA 263

QY 245 ACAGAGCTGGTCCCCCGACCCCTTTTCGGCTATGTTAGCAAGAGGATTGCCCCAAACGGTG 304

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QY 836 GACCAGCGTTGAGTGAATAATAGCACTTTTACCTTCAGTGATGTTTAAAGAGAGAGGT 895
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Db 981 CTGATAATAGGCTTCAACAATTCGANA 1007

RESULT 12
BI208568
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BI208568 694 bp mRNA linear EST 11-JUL-2001
EST526608 cTOS Lycopersicon esculentum cDNA clone cTOS17020 5' end,
mRNA sequence.
BI208568
BI208568.1 GI:14686292
EST.
Lycopersicon esculentum (solanum lycopersicum)
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 694)
van der Hoeven,R., Sun,H., Bezzerides,J., Cho,J., Utterback,R.,
Ronning,C. and Tanksley,S.
Generation of ESTs from tomato Suspension Cultures
Unpublished (2001)
Contact: CUGI
Clemson University
Clemson University

100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES
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/db_xref="taxon:4081"
/clone="cTOS17020"
/tissue_type="suspension cultures"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Suspension cultures of L.esculentum E6203 were grown
in Murashige and Skoog based medium, supplemented with 15%
coconut milk (filter sterilized and added after
autoclaving), 2% saccharose, and 1mg/ml 2,4D (pH5.8).
Fresh medium was added every 7 days, and cultures were
grown at 25 C, with 12hrs of light and continuous
shaking."

ORIGIN

Query Match 33.7%; Score 335.4; DB 2; Length 694;
Best Local Similarity 69.6%; Pred. No. 4.8e-91;
Matches 485; Conservative 0; Mismatches 206; Indels 6; Gaps 2;
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Db 361 TCATGTCGAATTTAAGATCAACACACTTCGGGCTCTTCAAAATTTTACTCAAAAATGGCA 420
QY 686 CTGCGGTTTCAGTCCCAACCTGATCAGACTTCCTTTTTTTCATCAATGTTGGTGAAGCTTAC 745
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RESULT 13
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DEFINITION
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    sequence.
ACCESSION
BM893076.1 GI:19348544
VERSION
BM893076.1
KEYWORDS
Glycine max (soybean)
SOURCE
Glycine max
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 567)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through the 'Biogenetic Services', 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stop: 435.
FEATURES
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        from degenerating cotyledons of 9-10 day old etiolated
        seedlings for the cultivar Williams. Complementary DNA was
        synthesized from mRNA using a primer consisting of a
        poly(dT) sequence with a XhoI restriction site. EcoRI
        adapters were ligated to the blunt-ended cDNA fragments
        followed by XhoI digestion. The cDNA fragments were
        directionally cloned into the EcoRI-XhoI restriction site
        of the pBluescript vector. The ligated cDNA fragments
        were transformed into DH10B host cells (GibcoBRL). This
        library was constructed in the laboratory of Dr. Randy
        Shoemaker."
ORIGIN
Query Match 33.6%; Score 334.8; DB 3; Length 567;
Best Local Similarity 88.5%; Pred. No. 6.9e-91;
Matches 363; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 1 ATGGTGTCTCTCAGCCAGCATGACCAAGTTTTCCTCTCGAACCATTCAAGTCC 60
Db 157 ATGGTGTGTTTGTCTCAGCCAGCATTAACCAAGTTTTCCTCTCGAACCATTCAAGTCC 216

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RESULT 14
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    MtBC10E02F1 MtBC Medicago truncatula cDNA clone MtBC10E02 T3, mRNA
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ACCESSION
AL382874
VERSION
AL382874.1 GI:9682625
KEYWORDS
EST.
SOURCE
Medicago truncatula (barrel medic)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 478)
Journet,E.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O.,
Niebel,A., Carreau,V., Chatagnier,O., Kahn,D.,
Gianinazzi-Pearson,V. and Gamas,P.
Medicago truncatula ESTs from endomycorrhizal roots
Unpublished (2000)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
Mt-est@toulouse.inra.fr Website :
http://sequence.toulouse.inra.fr/Mtruncatula.html).
FEATURES
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        /note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2:
        XhoI; M. truncatula sterilised seeds were germinated for
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        : 2/3 calcined Terragreen mix in the presence of onion
        root fragments colonized by the arbuscular mycorrhizal
        fungus Glomus intraradices (Schenck & Smith, isolate
        LPAB). The plants were watered every day and twice a week
        with a modified nutrient Long Ashton solution without

```


Qy	913	ACATGGTGTGAATACAAAGAGGCTGGGTACACTTCAAGGCTAGCTGATAAATAGGCTTGCC	972
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Qy	973	CCTTTCAGAA	984
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Search completed: December 28, 2005, 00:38:46
Job time : 4546.12 secs

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Result No.	Query			DB	ID	Description
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2	827.4	83.1	1359	3	US-09-371-307-62	Sequence 62, Appl
3	424.4	42.6	1237	3	US-09-719-108-7	Sequence 7, Appl
4	421.4	42.1	1352	3	US-09-614-912-13	Sequence 13, Appl
5	419.8	42.1	1365	3	US-09-614-912-5	Sequence 5, Appl
6	418.2	42.0	1403	3	US-09-371-307-64	Sequence 64, Appl
7	381.6	38.3	1008	3	US-09-719-108-9	Sequence 9, Appl
8	362.6	36.4	1473	3	US-09-614-912-7	Sequence 7, Appl
9	356.6	35.8	1318	3	US-09-719-108-5	Sequence 5, Appl
10	354	35.5	1650	3	US-09-614-912-3	Sequence 3, Appl
11	314.2	31.5	1555	3	US-09-614-912-1	Sequence 1, Appl
12	307.8	30.9	783	3	US-09-371-307-67	Sequence 67, Appl
13	166	16.7	811	3	US-09-371-307-71	Sequence 71, Appl
14	155.6	15.6	403	3	US-09-371-307-66	Sequence 66, Appl
15	154.8	15.5	406	3	US-09-371-307-68	Sequence 68, Appl
16	152.4	15.3	966	3	US-09-371-307-58	Sequence 58, Appl
17	120	12.0	426	3	US-09-371-307-70	Sequence 70, Appl
18	112	11.2	450	3	US-09-614-912-9	Sequence 9, Appl
19	103	10.3	210	3	US-09-719-108-3	Sequence 3, Appl
20	101	10.1	199	3	US-09-719-108-4	Sequence 4, Appl
21	79	7.9	595	3	US-09-614-912-15	Sequence 15, Appl
22	75.8	7.6	618	3	US-09-614-912-11	Sequence 11, Appl
23	72.4	7.3	723	3	US-09-371-307-56	Sequence 56, Appl
24	72.4	7.3	4170	3	US-09-371-307-57	Sequence 57, Appl

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RESULT 2

US-09-371-307-62
; Sequence 62, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62

; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Glycine max
US-09-371-307-62
Query Match 83.1%; Score 827.4; DB 3; Length 1359;
Best Local Similarity 89.9%; Pred. No. 3.5e-268;
Matches 898; Conservative 1; Mismatches 97; Indels 3; Gaps 1;
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Qy 361 AAATCACTTTGCAATTTCCGAGAAAATCTCTCATCATTTTCAAGGCGGTGGTGAGACTAC 420
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Qy 778 AAGCATAGGTTTGGTGACACCAACGAAGTCAAGGTTATCAATGATCTACTTTTGAGGA 837
Db 882 AAGCATAGGTTTGGTGACACCAACGAAGTCAAGGTTGATGATCTACTTTTGAGGA 941
Qy 838 CCAGCGTTGAGTGAATAATATAGCACTTTTCACTTCACTGATGTTTAAAGAGAGGAGTGT 897
Db 942 CCACCTTGTGTGAAAAGTAGCACCTTTTACCTTCACTCATGTTTAAAGAGAGAGAGT 1001
Qy 898 TTGTACAAAGAGTTCATGTTGTGNAATACAGAGGCTGCGTACACTTTCAGGCTAGCT 957
Db 1002 TTCTCAAAAGAGTTCATGTTGGTGGGAATACAAAGAGGCTGCGTACGCTCAAGGCTAGCG 1061

QY 958 GATAATAGGCTTGGCCCTTTCCAGAAATCTGCTGCTGAT 996
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Db 1062 GATAATAGACTCGGCCCTTTTCAGAAATCTGCTGCTGAT 1100
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RESULT 3

US-09-719-108-7
; Sequence 7, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/09/719,108
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-719-108-7

Query Match 42.6%; Score 424.4; DB 3; Length 1237;
Best Local Similarity 67.5%; Pred. No. 3.5e-132;
Matches 612; Conservative 0; Mismatches 291; Indels 3; Gaps 1;
QY 79 ATTCTGTGGTGCAGCTCAGCACCGGATGCCAGAAATCTCATAGTGAACCCCTGTAGG 138
|||||
Db 199 ATCCCGCTCGTCAACCTAGCCGATCGGAAGCGAAACCCGAATCGTAAAGCCCTGCGAG 258
|||||
QY 139 GACTTCGGCTTCTCAAGCTTGTGAACCATGGTGTCCATTTGAGTGAATGATGCCAATT 198
|||||
Db 259 GAGTTTCGGGTTCTTCAAGGTCGTAAACCGGAGTCCGACCCGAACTCATGACTCGGTT 318
|||||
QY 199 GAAACGAGGCGCTCAGGTTCTTTAAAAATCTCAGTCCGAGAAAGACAGAGCTGTC 258
|||||
Db 319 GAGCAGAGGCTATTGGCTTCTTCGGCTTGCCTCAGTCTCTTAAAAACGGGCCGCTCA 378
|||||
QY 259 CCGACCCCTTTCGGCTATGATGAGCAAGAGATGGCCCAACCGGTGATGTCGGTGGGTC 318
|||||
Db 379 CCGAACCCTGACGGTTATGGTAAACCGGATGGACCAACGGTGACGTTGGTGGATT 438
|||||
QY 319 GAATACCTCTCTCAACACCAACCTGATGTTATCTACCCCAATCATTTCGATTTTC 378
|||||
Db 439 GAGTATCTCTCTCAATGCTAATCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 498
|||||
QY 379 CGAGAAATCTCTCATCTTTCAGGCGGCTGGGAGAACTACATACAGCAGTGAAGAAC 438
|||||
Db 499 CTTAAACCCCTCAATTTTCGTTGATGCGTGGGAGGATCATGAGAGATTAAGNA 558
|||||
QY 439 ATGTGCTATCGGCTGTGAAATTTGATGGCGGAGGGGTGGGATAGGCGAGGAAATAG 498
|||||
Db 559 GTGTCGTACAGGTTGTGGAGATGGTTGCGGAGAACTAGGATAGAGCAAGGACACT 618
|||||
QY 499 TTAAGCAGGTTGCTGAGATGAGAAAGTATGCTGCTTCAGGTTGAACTACCCG 558
|||||
Db 619 CTGAGTAAATGCTGAGATGAGAGAGTGAATGCTGCTGAGACTAAACCATTTATCG 678
|||||
QY 559 CTTGCGCCCTGAGTGAACACTGAACCGGAATTTGGTTGGTGGGAGGAGCAGACAG 618
|||||
Db 679 GC---GGCGGAGAAAGAGCGGAGAAAGATGGTGAAGTGGGTTGGGGAACACAGAC 735
|||||
QY 619 CCACAGATAAATTTCTGCTCTTAAGATCTTAACAGCACATCTGGCTTGCATATCTGCTCA 678
|||||

Db 736 CCACAGATAATCTCAGTCTTAAGATCTTAATAACACGGCGGGTCTTCAAAATCTGTGATA 795
QY 679 GATGCACCTTGGGTTTCAGTCCACCTGATCAGACTTCTCTTTTTCATCAATTTGGTGAC 738
|||||
Db 796 GATGGAAGTTGGTGGCTGCTCCCTCTGATCACTTCTTCTTCAATTAATGTTGGAGAT 855
QY 739 GCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAAGCATAGGGTTTGGCTGAC 798
|||||
Db 856 GCTCTTCAGGTTATGACTTAACGGGAGGTTCAAGAGTGTAAACACACAGGGTCTTAGCCGAT 915
QY 799 ACAAGGAAGTCAAGGTTATCAATGATCTACTTTTGGAGGACACAGCGCTTGAAGTCAAAATATA 858
|||||
Db 916 ACAAGGAGATCAAGGTTTCAATGATATATTTTCGGCGGACCCCAATGAGCCAGAGATC 975
QY 859 GCACCTTTTACCTTCAGTGTATGTTTAAAGGAGAGGAGTGTTTGTACAAAGAGTTCACATGG 918
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Db 976 GCACCATTTGCCATGCTTGTCCCTGAGCAAGATGATTTGGCTTTTACAAAGATTCACCTTGG 1035
QY 919 TGTGAATACAGAGAGGCTGCGTACACTTCAAGGCTAGCTGATATAGGCTTGGCCCTTTC 978
|||||
Db 1036 TCTCAATACAAATCTTCTGCTTACAAAGTCTAAGCTTGGTGTATATAGACTTGGTCTCTTT 1095
QY 979 CAGAAA 984
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Db 1096 GAGAAA 1101
|||||

RESULT 4

US-09-614-912-13
; Sequence 13, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Cai, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 1352
; TYPE: DNA
; ORGANISM: Glycine max
US-09-614-912-13

Query Match 42.3%; Score 421.4; DB 3; Length 1352;
Best Local Similarity 65.7%; Pred. No. 3.8e-131;
Matches 652; Conservative 0; Mismatches 326; Indels 15; Gaps 2;
QY 1 ATGGTTGTTCTGCTCAGCCAGCATTTGAACCGATTTTCTCTCTGAAACCATTCAGATCC 60
|||||
Db 159 ATGGTGTGTTGTTCCAAAGCAACACAGAACAATACTCTCTCAATTAAGAACTGCATGCCA 218
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QY 61 ACGCCCTTGTTCAACGGGGAFTTCTGTGGTCAGCTCAGCCACCCCGATGCCAAGAATCTC 120
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Db 219 ACCAAATTTCTCAACAATTCCTAGTAGTGACCTCTCCAAACCTGATGCAAGACCCCTT 278
|||
QY 121 ATAGTGAACGCTGTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTG 180
|||
Db 279 ATAGTGAAGGCTGTGTAGGAGTTGGATCTTCAAAGTCATCAATCATGGTGTCTCCATG 338
|||
QY 181 GAGTTAATGGCCAAATTAGAAACGAGGCGCTCAGGTTCTTTAAAAATCTCAGTCCGAG 240
|||
Db 339 GAAGCTATATCCGAATTTGGAATATGAAGCCTTCAAAATCTTCTATGTCACTCAATGAA 398
|||
QY 241 AAAGACAGAGCTGGTCCCCCGACCTTTCGGCTATGTAGCAAGAGGATTTGGCCCCAAAC 300
|||
Db 399 AAGGAAAAGTAGGACTCCCAATCAATTTGGGTATGTAGCAAGAAAATTTGACACAAT 458
|||
QY 301 GGTGATGTGGTGGTTCGAATACCTCTCTCAACACCAACCCCTGATGTATCTCACCC 360
|||
Db 459 GGGGACGTTGGTGGATTTGATACCTTCTTCAACACCAATCAAGAACACAACT---- 513
|||
QY 361 AATCACTTTGCATTTTCCGAGAAATCCTCATCTTTCAGGCGGTGTGGAGAACTAC 420
|||
Db 514 -----TCTCTGTTTATGGGAAAAACCCCTGAGAAATTCAGGTGTCTGTGGAACAGTTAC 566
|||
QY 421 ATTACAGCAGTGAAGAACATGTCTATGCGGTGTGGAATTTGATGCGGAGGGTTGGG 480
|||
Db 567 ATGCTCTCTGTGAGGAAGATGGCATGTGAGATCTTGTGATGATGCAAGGGTTGAAG 626
|||
QY 481 ATAAGCAGAGGAATACGTTAAGCAGTGTCTGAAGGATGAGAAAAGTGAATCTGTCCTTC 540
|||
Db 627 ATTACAGAAAAGGATGTTTGTAGCAAGCTTCTAATGGATAAACAAAGTGACTCTATTTTC 686
|||
QY 541 AGTTGAACCACTACCGGCTTGCCTGAGTGTGCAAGCACTGAACCGGAATTTGGTGG 600
|||
Db 687 AGGGTGAATCATTAACCTGCTGTGCTGTAATGACTCTGAATGATCAGAACTTGATTGGG 746
|||
QY 601 TTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGC 660
|||
Db 747 TTTGGAGAACACACAGACCCACAAATCATCTCTGTGTAAGATCCAAACACTTCAGGC 806
|||
QY 661 TTGCAATCTGTCTCAGATGGCACTTGGGTTTTCAGTCCCACTGATCAGACTTCCTTT 720
|||
Db 807 CTTTCAGATTTATCTTAGAGATGGAATTTGATTTTCACTCCACCATGACAAATCTTT 866
|||
QY 721 TTTCAATGTTGGTGAACGCTCTACAGGTAAAGTAACTAATGTGGAGGTTTAAAGTGAAG 780
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Db 867 TTTTATTAACGTTGGTGAATTTCTCTCAGGTTATGACAAATGGAAGTTCCGAAGTGTGAG 926
|||
QY 781 CATAGGTTTGGCTCACACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCA 840
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Db 927 CACAGAGTTGGCAAAATGGGTTCAAGTCCAGGCTTTCATGATTTTACTTTGGAGTCCA 986
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QY 841 GGGTTGAGTGAATAATAGCACCTTTACCTTTCAGTGTATTAAGGAGGAGAGTGTGTTG 900
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Db 987 CTTTGGTGTGAGAAATAGACCACTTATCTCTCTCATG---AAGGAAAAGAAAGTCTA 1043
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QY 901 TACAAAGAGTTACATGGTGTGAATACAAAGAGGCTGCGTACACTTTCAAGGCTAGCTGAT 960
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Db 1044 TATAAAGAGTTTACCTGTTTGAAGTACAAAAAATCAATCTACGGTTCAAGATTTATCTAAA 1103
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QY 961 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGCT 993
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Db 1104 AATAGACTTGAACATTTTGAAGAATTGCAGCT 1136
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RESULT 5

US-09-614-912-5

; Sequence 5, Application US/09614912

; Patent No. 6677502

; GENERAL INFORMATION:

; APPLICANT: Allen, Steve

; APPLICANT: Rafaleski, Antoni

```
; APPLICANT: Orozco, Buddy
; APPLICANT: Milao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Caimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Glycine max
US-09-614-912-5
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Query Match 42.1%; Score 419.8; DB 3; Length 1365;

Best Local Similarity 65.6%; Pred. No. 1.3e-130;

Matches 651; Conservative 0; Mismatches 327; Indels 15; Gaps 2;

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QY 1 ATGGTGTGTTCTCTCAGCCAGCATTTGAACCACTTTTCTCTCTGAAACCATTTCAAGTCC 60
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Db 166 ATGGTGTGTTCTCCAAAGCAACACAGAACATCTCTACATTAAGAACTGCGATGCCA 225
|||
QY 61 ACGCCCTTGTTCACGGGGATTCCTGTGTCGACCTCACGCACCCCGATGCCAAGAAATCTC 120
|||
Db 226 ACCAAATTTTCTCAACAATTTCCCATAGTGGACCTCTCCAAACCTGATGCCAAGACCCCTT 285
|||
QY 121 ATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTG 180
|||
Db 286 ATAGTGAAGGCTGTGTAGGAGTTTGGATTTCTTCAAAGTCATCAATCATGGTGTCTCCATG 345
|||
QY 181 GAGTTAATGGCCAAATTTAGAAAAACGAGGCGCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240
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Db 346 GAAGCTATATCCGAATTTGGAATATGAGCCTTCAAATTTCTTCTATGTCACTCAATGAA 405
|||
QY 241 AAAGACAGAGCTGGTCCCCCGACCTTTTCGGCTATGTAGCAAGAGGATTTGGCCCCAAAC 300
|||
Db 406 AAGGAAAAGTAGGACCTCCCAATCCATTTGGGTATGTAGCAAGAAAATTTGACACAAT 465
|||
QY 301 GGTGATGTGGTGGTTCGAATACCTCTCTCAACACCAACCCCTGATGTATCTCACCC 360
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Db 466 AGGGACGTTGGTGGATTTGAGTACCTTCTTCAACACCAATCAAGAACACAACT----- 520
|||
QY 361 AAATCACTTTGCATTTTCCGAGAAAATCCTCATCAATTTTCAGGCGGTGTGGAGAACTAC 420
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Db 521 -----TCTCTGTTTATGGCAAAAACCCCTGAGAAATTCAGGTGTCTGTGACAGTTAC 573
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QY 421 ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTGTGGAATTTGATGCGGAGGGTTGGGG 480
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Db 574 ATGTCTTCTGTGAGGAAGATGTCATGTGAGATTTCTTGTAGTTGATGGCAAGAGGTTGAAG 633
|||
QY 481 ATAAGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATCTGTCCTTC 540
|||
Db 634 ATTCAGCAAAAGGATGTGTTTATAGCAAGCTTCTAATGGATTAACAAAGTCACTCTATTTTC 693
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QY 541 AGGTTGAACCACTACCCGCGCTTTGCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGG 600
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RESULT 6
US-09-371-307-64
; Sequence 64, Application US/09371307A
; Patent NO. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT-216
; CURRENT APPLICATION NUMBER: US/09/371.307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Glycine max
US-09-371-307-64

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RESULT 7
US-09-719-108-9
; Sequence 9, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.097000
; CURRENT APPLICATION NUMBER: US/09/719,108
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8

; PRIOR FILING DATE: 1998-06-12									
; PRIOR APPLICATION NUMBER: GB 9815404.0									
; PRIOR FILING DATE: 1998-07-15									
; NUMBER OF SEQ ID NOS: 16									
; SOFTWARE: Patent In Ver. 2.1									
; SEQ ID NO 9									
; LENGTH: 1008									
; TYPE: DNA									
; ORGANISM: Arabidopsis thaliana									
US-09-719-108-9									
Query Match 38.3%; Score 381.6; DB 3; Length 1008;									
Best Local Similarity 64.7%; Pred. No. 8.5e-118;									
Matches 586; Conservative 0; Mismatches 314; Indels 6; Gaps 1;									
QY	79	ATTCTGTGGTGCACCTCAGCAGCCCGATGCCAAGATCTCATAGTGAACCCCTGTAGG	138						
DB	79	ATCCCTGTTATAGACTTAACCGACTCAGATGGCCAAACCCAAATCGTCAAGGATGTGAA	138						
QY	139	GACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTGGAGTTAATGGCCAAATTA	198						
DB	139	GAGTTTGGTCTTCAAGATCATCAACCATGGGTCCGACCCGATCTTTGACTCAGTTG	198						
QY	199	GAAACGAGCCCTCAGTCTTAAAAAATCTCAGTCCGAGAAAGACAGAGCTGTGCC	258						
DB	199	GAGCAAGAAGCCATCAACTTCTTTGCTTGTGCATCACTCTCTCAAGACAAAGCGGTCCA	258						
QY	259	CCGACCCCTTCGGCTATGGTAGCAGAGATGGCCCAACGGTCACTCGGTGGGTC	318						
DB	259	CCTGACCCCTTGGTGTACGCTAATAAAGATTTGGACCCCAATGGTGACCTTGGCTGCTT	318						
QY	319	GAATACCTCTCTCAACACCAACCTCGATGTATCTCAACCAAAATCACTTTGCAATTTTC	378						
DB	319	GAGTACATCTCTTAATGCTATCTTTGCTTGAAGTCTCAAAACACCCGCAATTTTC	378						
QY	379	CGAGAAAAATCTCATCATTTCAAGGCGGTGGTGAGAACTACATTAACAGCAGTGAAGAC	438						
DB	379	CGGCACACCCCTGCAATTTTCAGAGAGGAGTGAAGAGTACATTAAGAGATGAAGAGA	438						
QY	439	ATGTGCTATCGGTGTGGAATGTATGGCGGAGGGTGGGATAGGCAGGAGGATAG	498						
DB	439	ATGTGAGCAAAATTTCTGGAATGGTAGAGAGAGCTAAGATAGAGCCAAAGGAGAG	498						
QY	499	TTAAGCAGGTGTGTGAAGATGAGAAAGTGAATTCGTGCTTCAAGTTGAACCACTACCCG	558						
DB	499	CTGAGCGGTTTGTGAAAGTGAAGAAAGTGAATTCGTGCTGAGATGAACCACTACCCG	558						
QY	559	CTTGGCCCTGAGGTGCAAGACCTGAACCCGAAATTTGGTGGGTTTGGGAGCACACAGAC	618						
DB	559	-----GAGAAAGGAGAGACTCCGGTCAAGGAAGAGATTGGGTTCCGTGAGCACACTGAT	612						
QY	619	CCACAGATAATTTCTCTTATAGATCTAACNGACATCTGGCTTGCAAATCTGTCTACA	678						
DB	613	CCACAGTTGATATCACTGCTCAGATCAAAACGACACAGAGGGTTGCANAATCTGTGTCAA	672						
QY	679	GATGGCACTTGGGTTTCAGTCCACCTGATCAGACTTCTTTTTCATCAATGTTGTGTAC	738						
DB	673	GATGGAACATGGGTTGATGTTACACCTGATCACTCTCTTCTTCTTCTTGTGCGAGAT	732						
QY	739	GCTCTACAGTAATGACTAATGGGAGGTTTAAAGTGTAAAGCATAGGGTTTGGCTGAC	798						
DB	733	ACTCTTCAGTGTATGACAAACGGAAGATTCAAGAGTGTGAACATAGAGTGGTGACAAAT	792						
QY	799	ACNACGAAGTCAAGTTATCAATGATCTACTTTGGAGGACCAGCTTGTAGTGAATATA	858						
DB	793	ACAAAGAGGTCAAGSATATCGATGATCTACTTCGACAGGTCCTCTTTGAGCGAAGATTT	852						
QY	859	GCACCTTTTACTCTCAGTGTATTTAAAGGAGAGAGGTGTTGTACAAAGAGTTCACATGG	918						
DB	853	GCACCAATATCATGCCTTGTGCCAAAGCAAGATGATGCTTTTATATGATTTACTTGG	912						
QY	919	TGTGAATACAAGAAGCTCGGTACATCTCAAGGCTAGCTGATTAATAGGCTTGCCTTTTC	978						
; Sequence 7, Application US/09614912									
; Patent No. 6677502									
; GENERAL INFORMATION:									
; APPLICANT: Allen, Steve									
; APPLICANT: Rafalski, Antoni									
; APPLICANT: Orozco, Buddy									
; APPLICANT: Miao, Gou-Hau									
; APPLICANT: Famodu, Omolayo O.									
; APPLICANT: Lee, Jian Ming									
; APPLICANT: Sakai, Hajime									
; APPLICANT: Weng, Zude									
; APPLICANT: Caimi, Perry G									
; APPLICANT: Anderson, Shawn									
; TITLE OF INVENTION: Plant Metabolism Genes									
; FILE REFERENCE: BBI378 US NA									
; CURRENT APPLICATION NUMBER: US/09/614,912									
; CURRENT FILING DATE: 2000-07-12									
; PRIOR APPLICATION NUMBER: 60/143,401									
; PRIOR FILING DATE: 1999-07-12									
; PRIOR APPLICATION NUMBER: 60/143,412									
; PRIOR FILING DATE: 1999-07-12									
; PRIOR APPLICATION NUMBER: 60/146,650									
; PRIOR FILING DATE: 1999-07-30									
; PRIOR APPLICATION NUMBER: 60/170,906									
; PRIOR FILING DATE: 1999-12-15									
; PRIOR APPLICATION NUMBER: 60/172,959									
; PRIOR FILING DATE: 1999-12-21									
; PRIOR APPLICATION NUMBER: 60/172,946									
; PRIOR FILING DATE: 1999-12-21									
; NUMBER OF SEQ ID NOS: 204									
; SOFTWARE: Microsoft Office 97									
; SEQ ID NO 7									
; LENGTH: 1473									
; TYPE: DNA									
; ORGANISM: Triticum aestivum									
US-09-614-912-7									
Query Match 36.4%; Score 362.6; DB 3; Length 1473;									
Best Local Similarity 61.5%; Pred. No. 2.8e-111;									
Matches 603; Conservative 0; Mismatches 369; Indels 9; Gaps 1;									
QY	2	TGTTGTTCTGTCTCAGCCAGCATTGAACAGTTTTTCTCTCTGAAACCATTCAGTCCA	61						
DB	128	TGTTCTGCCAGACGCCCGCGTCGATCATCCGCTCTCTCAGTGC CGCGACCCG	187						
QY	62	CGCCCTTGTTCACGGGATTCCTGTGTGTCGACCTCACGCCCCCGATGCCAAGAATCTCA	121						
DB	188	GGGACTACTTCTCGGCATGCCGTGGTGCAGCTCTCCAGCCCTGCGCGCGCGGCCA	247						
QY	122	TAGTGAACCCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTTTCCATTGG	181						
DB	248	TCGCCAGCGCTGCGAGCGCTTCGGGTTCTTCAAGCTCTCAACCCAGGGGTGCCCGCG	307						
QY	182	AGTTAATGCCAATTTAGAAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGA	241						
DB	308	ACAGATGGACAGGCTCGAGTCGAGGCGCGTCAGGTTCTTCTCGTCCGCGAGCGCGACA	367						
QY	242	AAAGACAGAGCTGGTCCCGCCGACCCCTTTCGGCTATGGTAGCAAGAGATTGGCCCAACG	301						
DB	368	AGGACCGCTCCGCGCGCGCTACCCGTTCCGGCTACGGCAGCAAGCGCATCGGGCTCAATG	427						
QY	302	GTGATGTGGTGGTTCGATACCTCTCTCAACACCAACCCCTGATGTTATCTCACCCA	361						
DB	428	CGACATGGGGTGGTTCGAGTACCTGCTCTCTGGCGGTGACTCCGCTCTCCGCGG	487						

QY 362 AATCATCTTGCATTTTCGAGAAATCCTCATCTTTCAGGGGGTGGTGGAGAACTACA 421
 Db 488 CTTGCGCCCTCCGCTCTCG-----CGCTCTTCGCGGGCGGCTGAAACGAGTACA 538
 QY 422 TTACAGCAGTGAAGAACATGTCTATGCGGTGTGGAATTTGATGGCGGAGGGTGGGGA 481
 Db 539 TCGCGCGGTGCGGAAGTGGCGGTGCGGTGATGAGCGCATGGCGHGGGGCTGGGCA 598
 QY 482 TAAAGCAGAGGAATACGTTAAGCAGGTGTCTGAAGGATGAGAAAAGTGAATCGTGTTCA 541
 Db 599 TTGCGGCGCTGAGCGGCTGAGCGGATGTTGACGCGGAGGGGAGCGACAGGTGTTCC 658
 QY 542 GGTGAAACACTACCGGCTTGGCTGAGGTGAAGCACTGAACCGGAATTTGGTGGGT 601
 Db 659 GGGTGAACACTACCGCGCTGCCACGCGCTGCGAGGGCTGGGCTGCGAGCGCCACCGGCT 718
 QY 602 TTGGGAGGACACAGACCCACAGATAATTTCTGTTTAAAGATCTAACAGCACATCTGGCT 661
 Db 719 TCGGCGAGCACAGGACCGCGAGCTCATCTCGTGTGCGCTCCAAACGCGCATCGCGCC 778
 QY 662 TCAAAATCTGTCTCAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTCTTTT 721
 Db 779 TCGAGATCGCTCCAGAACGGGAGTGGTGTGCGTCCCTCGGACCGGAGCTTCT 838
 QY 722 TCATCAATGTTGGTGACGCTCTACAGGTAAATGACTAATGGGAGGTTTAAAGTGTAAGC 781
 Db 839 TCGTCAACCTCGCGCACTGTTGCGAGTGTGACCAACCGGAGGTTCAAGAGCGTGAAGC 898
 QY 782 ATAGGGTTTGGCTGACACACGAAAGTCAAGGTATCATGATCTACTTTGAGGACCG 841
 Db 899 ACAGGGTGGTGCCCAACAGCTTAAAGTCTAGGGTTTCCATGATCTACTTTGAGGGCC 958
 QY 842 CTTGAGTCAAAATATAGCACCTTACCTTACCTTCACTGATGTAAAGAGAGGAGTGTGTT 901
 Db 959 CAATGACACAGAGATGACCAATTCGCCAGCTGCTGGCGCGGAGGAGGAGGCTGT 1018
 QY 902 ACAAGAGTTCACTGTTGTAATACAAAGAGGCTGCGTACACTTCAAGGCTAGCTGATA 961
 Db 1019 ACAAGAGTTCACTGTTGTAATACAAAGAGGCTGCGTACAACTCCAGGCTCGGGACA 1078
 QY 962 ATAGGCTTGGCTTTCGAGA 982
 Db 1079 ACAGGCTGCTCAGTTCACCA 1099

RESULT 9

US-09-719-108-5
 ; Sequence 5, Application US/09719108
 ; Patent No. 6670527
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Stephen G
 ; APPLICANT: Hadden, Peter
 ; APPLICANT: Phillips, Andrew L
 ; TITLE OF INVENTION: Gibberellin 2-Oxidase
 ; FILE REFERENCE: 0623.0970000
 ; CURRENT APPLICATION NUMBER: US/09/719,108
 ; CURRENT FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: PCT/GB99/01857
 ; PRIOR FILING DATE: 1999-06-11
 ; PRIOR APPLICATION NUMBER: GB 9812821.8
 ; PRIOR FILING DATE: 1998-06-12
 ; PRIOR APPLICATION NUMBER: GB 9815404.0
 ; PRIOR FILING DATE: 1998-07-15
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 1318
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1243, 1265)

OTHER INFORMATION: unidentified residue
 US-09-719-108-5

Query Match 35.8%; Score 356.6; DB 3; Length 1318;
 Best Local Similarity 63.2%; Pred. No. 2.8e-109;
 Matches 586; Conservative 0; Mismatches 329; Indels 12; Gaps 2;
 QY 65 CTTGTTTCAACGAGGATTTCTGTTGGTGCACCTCAGCACCCTCGATGCCAAGAATCTCATAG 124
 Db 78 CCGGGTTCTCTTAATCCGGTTATAGATATGTGACCCAGAAATCCAAATGATCCCTCG 137
 QY 125 TGAACGCTGTAGGACTTCGGCTTCTCAAGCTTGTGAACCATGGTGTTCATTGGAGT 184
 Db 138 TGAAGATGCGAAGACTTTCGGCTTCTCAAGGTGATCAACCATGGCTTTCGAGAGC 197
 QY 185 TAATGCCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTTAAAAAATCTCAGTCCGAGAAAG 244
 Db 198 TAGTCTCTGTTTAAACACAGAGACCGTCGATTTCTCTCGTTGCCAAGTCAGAGAAA 257
 QY 245 ACAGAGTGGTCCCCCGACCCCTTTCGGCTATGTTAGCAAGAGATTTGGCCCAACGGTG 304
 Db 258 CCCAAGTCG---CAGGTTATCCCTTCGGATACGGGAAACAGTAAGATTGGTCGGAATGGTG 314
 QY 305 ATGTGCTGGTGGTGAATACCTCTCTCAACACCAACCCCTGATGTATCTCACCCAAAT 364
 Db 315 ACGTGGGTGGGTGAGTACTTGTGATGAACGCTTAATCATGATTCGGGTTCCGCTCCAC 374
 QY 365 CACTTTGCAATTTTCGAGAAAATCCTCATCTTCAGGGCGGTGGTGGAGAACTACATTA 424
 Db 375 TATTTCCAGTCTTCTCAAAAGCCCGGAACTTTTCAGAAAACGATTTGGAAGAGTACACA 434
 QY 425 CAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAAATGATGGCGGAGGGTGGGGATAA 484
 Db 435 CATCAGTGAGAAAATGACATTCGATGTTTGGAGAGATCACAGATGGGTAGGGATCA 494
 QY 485 GCGAGAGAAATACGTTAAGCAGGTGCTGAAGGATGAGAAAAGTGAATTCGTCCTCAGGT 544
 Db 495 AACCGAGGAACACACTTAGCAAGCTTGTCTCGACCAAAACACGAGCTCGATATTGAGAC 554
 QY 545 TGAACCACTACCGGCTTTCGCTGAGGTGCAAGCACTGAAC-----CGGAATTCG 595
 Db 555 TTAATCACTATCCACCATGCTCTTAGCAATAAGAAAACCAATGGTGGTAAAGATGTGA 614
 QY 596 TTGGGTTTGGGAGCACACAGACCCACAGATAATTTCTGTTTAAAGATCTAACAGACAT 655
 Db 615 TTGGTTTGGTGAACACACAGATCTCAAAATCATCTCTGCTTTAAGATCTAACACACTT 674
 QY 656 CTGGCTTGCATAATCTGCTCAGATGGCACTTGGGTTTCAGTCCACCTGATCAGACTT 715
 Db 675 CTGGTCTCCAAATTAATCTAAATGATGGCTCATGGATCTCTGCTCCCTCCGATCACACTT 734
 QY 716 CTTTTCATCAATGTTGGTGAAGCTCTACAGGTAATGACTAATGAGGTTTAAAGTG 775
 Db 735 CTTCTTCTTCAACGTTGGTGACTCTCTCAGGTTGATGACAAATGGGAGTTCAAGAGCG 794
 QY 776 TAAAGCATAGGGTTTGGCTGACACACAGAACTCAAGGTATCAATGATCTACTTTGGAG 835
 Db 795 TGAGCATAGGGTTTGTAGTAACTGTAATAAATCTAGGGTTCTATGATTTACTTTGCTG 854
 QY 836 GACCAAGCTTGAAGTAAATATAGCACTTTACCTTTCAGTGTATGTTAAAGAGAGGAGT 895
 Db 855 GACCTTCATTGACTCAGAGAAATCGTCCGTTGACATGTTTGTATAGCAATGAGGACGAGA 914
 QY 896 GTTTGTACAAAGAGTTTCACTGGTGTGAATACAAAGAGGCTGCGTACACTTCAAGGCTAG 955
 Db 915 GGTGTACGAGGAGTTTACTTGGTCTGAATCAAAAACTCTACCTACAACTCTAGATTGT 974
 QY 956 CTGATAATAGGCTTCCCTTTCCAGA 982
 Db 975 CTGATAATAGGCTTCAACAATTCGAAA 1001

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US-09-614-912-3
; Sequence 3, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Caimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-614-912-3

Query Match      35.5%; Score 354; DB 3; Length 1650;
Best Local Similarity 60.9%; Pred.No.2.4e-108;
Matches 598; Conservative 0; Mismatches 375; Indels 9; Gaps 1;

QY      2  TGGTGTCTCTGCTCAGCCAGCATTGAACACAGTTTTCCTCTGAAACCAATCAAGTCCA 61
DB      132 TGGTGTCTCGTGGCCGCCCGCGTGCATCACAATCCCGTGTCTGAGGTGCGCGACCCCG 191

QY      62  CGCCCTTGTTCAGGGGATCTCTGTGTGTCGACTCAGCACCCCGATGCCAAGATCTCA 121
DB      192 GCGACGTCTTCTCCGGCGTCCCGTCTGCGACCTCGCGCAGCCCGCGCGGAGGCGG 251

QY      122 TAGTGAACCCCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTTTCCATTGG 181
DB      252 TGGTGACGCTCGAGCGGTACGGGTCTTCAAGGTGCTCAACCAACGCGGTGGCCACGG 311

QY      182 AGTTAATGGCCAATTTAGAAAAAGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGA 241
DB      312 ACAGATGACAGAGCGGAGTCCGAGCGCGTCAAGTCTTCTCCAGACGACCGCGACA 371

QY      242 AAGACAGAGTGTGTCCCGCCGACCTTTCGGCTATGTTAGCAAGAGATTGGCCCAACG 301
DB      372 AGGACCGCTCCGCGCGGCTACCCGCTTCGGGTACGCGCAGCAAGCGGATCGGGTTCAATG 431

QY      302 GTGATCTCGGTGGGTGCAATACCTCTCTCAACCAACCAACCTGATGTTATCTCACCCA 361
DB      432 GCACATGCGGTGGGTGCAATACCTCTCTCGCCCTGACGACGCGTCTCGCGACG 491

QY      362 AATCACTTTGCAATTTCCGAGAAAAATCTCATCATTTTCAGGGCGGTGGTGAGAACTACA 421
DB      492 CCTGCAACCGTCCGTCTCTCG-----CGGTCTTCCGGCGGCTCTGAACGAGTACA 542

QY      422 TTACAGAGTGAAGAACATGTGCTATGCGGTGTTGGAATTTGATGGCGAGGGGTGGGGA 481
DB      543 TCTCGGGGTGCGAAGGTGGCGGTGCGGTGATGGAGGCGATGTCCGAGGGGCTGGGCA 602
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RESULT 11
US-09-614-912-1
; Sequence 1, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Caimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1555
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QY      482 TAAGCAGAGGAATACGTTAAGCAGGTTGCTGAAGAGATGAGAAAAAGTATTCGTGCTTCA 541
DB      603 TTGCGCAGCGCGACGCGCTGAGCGCGCTGAGCGCGAGGAGCGACCGAGGTGTTCC 662

QY      542 GGTTCAAACCACTACCGCGCTTGCCTGAGGTGCAAGCACTGAACCGGATTTGGTTGGGT 601
DB      663 GCGTGAACCACTACCGCGCTTGCCTGAGGTGCAAGCACTGAACCGGATTTGGTTGGGT 722

QY      602 TTGGGAGCAGACAGACCCACAGATAAATTTCTGTCTTAAGATCTAACAGCAATCTGGCT 661
DB      723 TCGGCGAGCAGACCCAGCCGCGAGCTCGTCTCGTGTCTCGCTCAAAACGCGACGTCGCGCC 782

QY      662 TGCAAAATCTGTCTCAGAGATGGCACTTGGGTTTTCAGTCCCACTGATCAGACTTCTCTTT 721
DB      783 TGCAGATCGCGCTCCGCGACGCGCCAGTGGGTGTCGTCGCTCCGACCGCGACTCTCTTCT 842

QY      722 TCATCAATGTGTGTCAGCGCTCTACAGGTAAATGACATAATGGGAGGTTTAAAGTGTAAAGC 781
DB      843 TCGTCAACGTCGCGCACTCGTTGCAAGTCTGACCAATGGGAGGTTCAAGAGCGGTGAAGC 902

QY      782 ATAGGGTTTTGGCTGACACAACGAAATCAAGGTATCAATGATCTACTTTGGAGGACCAAG 841
DB      903 ACAGGGTGGTGCCCAACAGCCTTAAAGTCTAAGGTTTCTCTCATCTACTTTGGAGGCGCAC 962

QY      842 CGTTGAGTGAAATATATAGCACCTTTTACCTTTCAGTGATGTTAAAAAGGAGAGGAGTGT 901
DB      963 CGTTAGCAGAGAGGATTCACCATTTGCCACAGCTGCTGGGGGAGGAGAGCAGAGCCTGT 1022

QY      902 ACAAGAGTTTCATGTGTGTAATACAGAAAGGCTGCGTACACTTCAAGGCTAGCTGATA 961
DB      1023 ACAAGAGTTTCATGTGTGTAATACAGAAAGGCTGCGTACAAATCAAGGCTTGGAGACA 1082

QY      962 ATAGGCTTGCCCTTTCCAGAA 983
DB      1083 ACAGGCTGGCCAGTTTGAA 1104
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; TYPE: DNA
 ; ORGANISM: Zea mays
 US-09-614-912-1

Query Match	31.5%	Score 314.2	DB 3	Length 1555
Best Local Similarity	59.3%	Pred. No. 6.3e-95		
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Qy	16	CAGCCAGCATTTGAACACAGTTTTTCTTCTGTAAACCATTTCAAGTCCACGCGCTTGTGTTCCACG	75	
Db	136	CCGCTGTGTCGACACAGATCCCGCTCTGCGGTCCCGGGCCCGACGGACAGCTTCTCG	195	
Qy	76	GGGATTCCTGTGGTGCACCTCACGCACCCCGATGCCAAGAATCTCATAGTGAACCGCTGT	135	
Db	196	GGAGTCGCGGTGCTGCGACTGTCAGCCACGCGCGCGCGGGCGATCGTCGACGCGCTGC	255	
Qy	136	AGGACATTCGGCTTCTTCAGACTTGTGAACCATGGTGTTCATTTGGAGTTAATGGCCAAAT	195	
Db	256	GAGCGCTTCGGGTTCCTCAAGGTGCTCAACCAACGCGGTGGCGCGGCCACCATGGAAGG	315	
Qy	196	TTAGAAAAAGAGCGCCCTCAGGTTCTTTTAAAAAATCTCAGTCCGAGAAAGACAGAGCTGGT	255	
Db	316	GCCGAGTCCGAGGCGGTGAGTTCTTCGCGCAGCGCAGCGGACCAAGACCCGCGCGGG	375	
Qy	256	CCCCCGACCCCTTCGGGTATGTGTAGCAGAGAGATTTGGCCCAACCGGTGATGTGCGTTGG	315	
Db	376	CCGCGGTACCGGTTTCGGGTACGGCAGCAAGCGGATCGGGTCTCAATGCGGACATGGGGTGG	435	
Qy	316	GTCCGAATACCTTCCTCCTCAACACCAACCCCTGATGTTATCTCACCCAAATCACTTTGCAAT	375	
Db	436	CTCGAGTACCTTCCTTCCTCGCGTGCAGCGCGCTCGTCTCCGACGCTGCCCGCTGCC	495	
Qy	376	TTCCGAGAAAAATCCTCATCATTTTCAGGCGCGGTGTGTGAGAACTACATTTACAGCAGTGAAG	435	
Db	496	TCCAGCG-----CCGCGTTCCGAGCGCGCTGAACGAGTACGTCGCGCGCTGCGG	546	
Qy	436	AACATGTGTATGCGGTGTGGAAATTCATGCGCGAGGGGTGGGGATAAGCAGAGCAAT	495	
Db	547	AAGTGGCGGCGGTGTGCTGGAGCGATGCGGAGGGCTTGGGCAATTCGGGACCGCGAC	606	
Qy	496	ACGTTAAGCAGGTTGCTGAAGGATGAGAAAAAGTGAATTCGTCTTCAGGTTGAACCACTAC	555	
Db	607	GCGCTGAGCTCCATGTTGAGCGCGCGCGGAGCGCACGAGGTGTTCCGCGTGAACCACTAC	666	
Qy	556	CGGCTTGCCTTGAGGTGCAAGCACTGAACCGGAATTTGGTGTGGGTTGGGAGCACACA	615	
Db	667	CGGCTTGCCTTGCCTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCGCTGAGGCGCACACC	726	
Qy	616	GACCCACAGATAATTTCTGCTTAAAGATCTAAACAGCACATCTGCTTGCCTTGCCTGCTC	675	
Db	727	GACCCGAGATTCATCTCGTGCTCGCTCCAAACGCGACCTCCGCGCTGCGATCGCGCTC	786	
Qy	676	ACAGATGGCAC---TTGGGTTTCAGTCCCACCTGATCAGACTTCCTTTTTCATCAATGTT	732	
Db	787	CGCGACGCGCGAGTGGGTCTCGGTGCGCTCCGACCGCGACGCTCTCTCGTTAAGCTC	846	
Qy	733	GGTGACGCTCTACAGGTAATGCACTAAATGGGAGGTTTAAAGTGTAAAGCATAGGTTTGG	792	
Db	847	GGCGACTCGTTGAGGTTGCTACCAACCGGAGGTTTCAGGACGCGTGAAGCACCGGGTGGT	906	
Qy	793	GCTGACACAAAGAGTCAAGGTTATCAATGTATCTACTTTTGAGGACACAGCGTTGAGTGA	852	
Db	907	ACCAAGCCTCAAGTCCAGAGTTTCCTTCATCTACTTCGCGGGCGCGCGCTGGGGCAG	966	
Qy	853	AATATAGCACCTTTACCTTCAGTGAATGTAAAGGAGGAGGAGTGTGTGTACAAAGAGTTC	912	
Db	967	CGGATCGCGCGCGCTGCCGACAGTGTCTGCGGAGGGAGGAGAGCCTGTGTACAAAGGAGTTC	1026	
Qy	913	ACATGGTGTGAATAACAAGAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCC	972	
Db	1027	ACGTGGGGCGAGTACAAGAGGCGCGGTACAAGACGAGGCTTCGGGCAACACAGGCTGCGC	1086	
Qy	973	CTTTTCCAGAA	983	

Db 1087 CAGTTTGAGAA 1097

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RESULT 12
US-09-371-307-67
; Sequence 67, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 67
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (726)
; OTHER INFORMATION: n = a, c, g, or t
US-09-371-307-67

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Query Match	30.9%;	Score 307.8;	DB 3;	Length 783;
Best Local Similarity	70.2%;	Pred. No. 5.8e-93;		
Matches 436;	Conservative 0;	Mismatches 167;	Indels 18;	Gaps 1;
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DB	52	CAAACTTTGAGGGTGGCTTTGAAATAATATATGAATCAGTAAGAANAATGGCGTGTGAG	111	
QY	451	GTGTTGGAAATTGATGGCGGAGGGGTTGGGATTAAGGCAGAGGAATACTGTTAAGCAGGTTG	510	
DB	112	ATACTTGAATGATGGCTGATGGTTGAAGATACAACCCAGGAATGTGTTGAGCAAGCTG	171	
QY	511	CTGAAGGATGAGAAAAGTGATTCGTGCTTCAGGTTGAACCACTACCCGCGCTTGCCCTGAG	570	
DB	172	TTGATGATGAAGAGAGTGACTCTGTGTTTTCAGGGTGAATCATTTACCCACCATGCCCTTAAT	231	
QY	571	GTGCAAGCACTG-----AACCGGAATTTGGTTGGGTTTGGGAGCAC	612	
DB	232	GTTCAACCTTTGAGTGTGTAATGGCAATGGCAATGGGGATGTGATTTGGTGAACAC	291	
QY	613	ACAGACCCACAGATAAATTTCTGTCTTTAAGATCTAAACAGCACATCTGGCTTGCAAATCTGT	672	
DB	292	ACTGATCCACAATTAATCTCAGTGTGAGATCTAAACAACACTCTGGTCTTCAAATCTCT	351	
QY	673	CTCACAGATGGCACTTGGGTTTCAGTCCCACTCGATCAGACTTCTCTTTTTTCATCAATGTT	732	
DB	352	CTAAGAAGAAGAAGCTGGATTTTCAGTGCACCTGACCAAACTCATTTCTTCATCAATGTT	411	
QY	733	GGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTPAAAGCATAGGGTTTGG	792	
DB	412	GGTGACTCTCTTACAGGTAATGACCAATGGAAGGTTTAAAGTGTAAACAATAGGGTAGTG	471	
QY	793	GCTGACACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACACAGGTTTGAGTGAA	852	
DB	472	ACCAACAGTGTGAATCAAGGCTATCAATGATTTATTTTGGTGGACCACTTGAGTGAG	531	
QY	853	AATATAGCACTTTTACCTTCAGTGTATGTTTAAAGGAGGAGGTGTTTGTACAAAGATTTC	912	
DB	532	AAAATAGCACCTTTTGCCATCTTTTATGAGAGGTTGATCAACAAAGCTTATATAAAGAAATTT	591	


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; Sequence 68, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (306)
; OTHER INFORMATION: n = a, c, g, or t
US-09-371-307-68

Query Match      15.5%; Score 154.8; DB 3; Length 406;
Best Local Similarity 66.6%; Pred. No. 1.7e-41;
Matches 279; Conservative 0; Mismatches 113; Indels 27; Gaps 3;

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QY 307 GTCGGTGGGTGGAATACCTCTCTCAACACCAACCCCTGATGTTATCTCACCCAAATCA 366
Db 62 GTTGGTGGGTGGAATATCTTCTCTCAACCAACCAAG-----ACCCGAATCT 111
QY 367 CTTTGCATTTCCGAGAAATCCTCATCTTTCAGGGCGGTGGTGAGNACTACATTACA 426
Db 112 CTTTGGAACT-----GAAACCCAGAGAGTTTCAGGATTGCTTTGGATAATTATATGGCA 166
QY 427 GCAGTGAAGACATGTGCTATGCGGTGTTGGAATTGATGGCGAGGGGTTGGGGATAAGG 486
Db 167 GCAGTGAAGAAATGGCATGTGAGATACCTTGAATGATAGCTGTGGCTAAAGGTTGAG 226
QY 487 CAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAGTATTCGTTCAGGTTG 546
Db 227 CCAAGAAATGCTTAAGTAAAGCTGATGATGGATGAACAGAGTGACTCTGTTTTCAAGGCTG 286
QY 547 AACCACTACCCGCTTGCCCTGAGG-----TGCAGCACTGNAACCGGAATTG 594
Db 287 AACCAATTACCTCCGTCGCCNAGAGGTGTTTCAGTCCCTTGAATGGAACGAGCAGTAATGTG 346
QY 595 GTTGGGTTTGGGGAGCACACACACAGATAATTTCTGCTTAAGATCTTAACAGCAC 653
Db 347 ATTGGATTCCGGTGAACACACTGACCCCAAAATCAITTTTCAGTCTTAAGATCCAAACAC 405
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OM nucleic - nucleic search, using sw model

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Title: US-10-670-454-1_COPY_68_1063

Perfect score: 996

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Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

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- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	996	100.0	999	8	US-10-821-711-3	Sequence 3, Appli
2	996	100.0	1318	8	US-10-670-454-1	Sequence 1, Appli
3	827.4	83.1	1359	3	US-09-371-307-62	Sequence 62, Appli
4	827.4	83.1	1359	6	US-10-401-321-62	Sequence 62, Appli
5	424.4	42.6	1026	3	US-09-938-842A-1350	Sequence 1350, Ap
6	424.4	42.6	1026	3	US-09-938-842A-1350	Sequence 1350, Ap
7	424.4	42.6	1237	8	US-10-670-454-7	Sequence 7, Appli
8	418.2	42.0	1403	3	US-09-371-307-64	Sequence 64, Appli
9	418.2	42.0	1403	6	US-10-401-321-64	Sequence 64, Appli
10	388.2	39.0	1390	7	US-10-424-599-21951	Sequence 21951, A
11	381.6	38.3	1008	8	US-10-670-454-9	Sequence 9, Appli
12	356.6	35.8	1318	7	US-10-670-454-5	Sequence 5, Appli
13	354	35.5	984	7	US-10-392-325-3	Sequence 3, Appli
14	354	35.5	1260	7	US-10-437-963-78659	Sequence 78659, A
15	314.2	31.5	1611	8	US-10-425-115-69575	Sequence 69575, A
16	307.8	30.9	783	3	US-09-371-307-67	Sequence 67, Appli
17	307.8	30.9	783	6	US-10-401-321-67	Sequence 67, Appli
18	301.6	30.3	831	7	US-10-425-114-6183	Sequence 6183, Ap
19	285	28.6	927	6	US-10-259-194A-141	Sequence 141, Appl
20	278.8	28.0	591	7	US-10-424-599-9278	Sequence 9278, Ap
21	272.6	27.4	860	7	US-10-424-599-129307	Sequence 129307,
22	272.6	27.4	860	7	US-10-425-114-7861	Sequence 7861, Ap
23	203.2	20.4	1008	7	US-10-437-963-16086	Sequence 16086, A

24	201.8	20.3	847	8	US-10-425-115-159585	Sequence 159585,
25	188.6	18.9	1322	7	US-10-425-114-4257	Sequence 4257, Ap
26	188	18.9	1327	8	US-10-425-115-103352	Sequence 103352,
27	187	18.8	1271	7	US-10-437-963-1288	Sequence 1288, Ap
28	183.6	18.4	415	7	US-10-424-599-128562	Sequence 128562,
29	181.2	18.2	608	7	US-10-424-599-101563	Sequence 101563,
30	172.2	17.3	919	7	US-10-425-114-34429	Sequence 34429, A
31	169.6	17.0	802	8	US-10-425-115-177171	Sequence 177171,
32	166	16.7	811	3	US-09-371-307-71	Sequence 71, Appl
33	166	16.7	811	6	US-10-401-321-71	Sequence 71, Appl
34	156.2	15.7	504	6	US-10-259-194A-614	Sequence 614, App
35	155.6	15.6	403	3	US-09-371-307-66	Sequence 66, Appl
36	155.6	15.6	403	6	US-10-401-321-66	Sequence 66, Appl
37	154.8	15.5	406	3	US-09-371-307-68	Sequence 68, Appl
38	154.8	15.5	406	6	US-10-401-321-68	Sequence 68, Appl
39	152.4	15.3	966	3	US-09-371-307-58	Sequence 58, Appl
40	152.4	15.3	966	6	US-10-401-321-58	Sequence 58, Appl
c	150.4	15.1	537	6	US-10-259-194A-453	Sequence 453, App
42	146.4	14.7	322	7	US-10-424-599-67680	Sequence 67680, A
43	140.4	14.1	2478	7	US-10-437-963-20123	Sequence 20123, A
44	128.4	12.9	457	7	US-10-424-599-42166	Sequence 42166, A
45	127.4	12.8	597	7	US-10-424-599-108868	Sequence 108868,

ALIGNMENTS

RESULT 1
US-10-821-711-3
; Sequence 3, Application US/10821711
; Publication No. US20040237142A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Larry A
; APPLICANT: Krieger, Elysia K
; APPLICANT: Ye, Xudong
; APPLICANT: Zhang, Wanggen
; TITLE OF INVENTION: DNA CONSTRUCTS AND METHODS TO ENHANCE THE PRODUCTION OF
; FILE REFERENCE: 38-21(52967)B
; CURRENT APPLICATION NUMBER: US/10/821,711
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: 60/461,459
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 3
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Phaseolus coccineus
US-10-821-711-3

Query Match	100.0%	Score	996	DB	8	Length	999
Best Local Similarity	100.0%	Pred. No.	0	Mismatches	0	Indels	0
Matches	996	Conservative	0	0	0	Gaps	0
Qy	1	ATGTTGTTCTGTTCTCAGCCAGCATTTGAACAGATTTTCTTCTGAAACCACTTCAAGTCC	60				
Db	1	ATGTTGTTCTGTTCTCAGCCAGCATTTGAACAGATTTTCTTCTGAAACCACTTCAAGTCC	60				
Qy	61	ACGCCCTTGTTCAGGGGATTCCTGTGTGTCAGCTCAGCACCCTGATGCCAAGATCTC	120				
Db	61	ACGCCCTTGTTCAGGGGATTCCTGTGTGTCAGCTCAGCACCCTGATGCCAAGATCTC	120				
Qy	121	ATAGTGAACGCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGNAACCATGGTTCATG	180				
Db	121	ATAGTGAACGCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGNAACCATGGTTCATG	180				
Qy	181	GAGTTAATGGCCAATTTAGAAAAAGAGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG	240				
Db	181	GAGTTAATGGCCAATTTAGAAAAAGAGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG	240				
Qy	241	AAAGACAGAGCTGTGTCCTCCCGACCTTTCGGCTATGTAGCAAGAGATTGGCCCAAC	300				
Db	241	AAAGACAGAGCTGTGTCCTCCCGACCTTTCGGCTATGTAGCAAGAGATTGGCCCAAC	300				

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QY 301 GGTGATGTCGGTTGGGTGGAATACCTCCTCAACACCAACCTCGATGTTATCTCACCC 360
DB 301 GGTGATGTCGGTTGGGTGGAATACCTCCTCAACACCAACCTCGATGTTATCTCACCC 360

QY 361 AAATCACTTTGCAATTTCCGAGAAATCTCATCATTTTCAGGCGGTGTGAGAACTAC 420
DB 361 AAATCACTTTGCAATTTCCGAGAAATCTCATCATTTTCAGGCGGTGTGAGAACTAC 420

QY 421 ATTACAGCATGAGAACATGTCTATGCGGTGTTGGAATTCATGCGGAGGGTTGGG 480
DB 421 ATTACAGCATGAGAACATGTCTATGCGGTGTTGGAATTCATGCGGAGGGTTGGG 480

QY 481 ATAAGGCAGAGGAATACGTTTAAGCAGTTGCTGAAGGATGAGAAAAGTCAATTCGTGCTTC 540
DB 481 ATAAGGCAGAGGAATACGTTTAAGCAGTTGCTGAAGGATGAGAAAAGTCAATTCGTGCTTC 540

QY 541 AGGTTGAACCACTACCCGCTTGCCTGAGGTGCAAGCACTGAACCGGAAATTTGGTTGG 600
DB 541 AGGTTGAACCACTACCCGCTTGCCTGAGGTGCAAGCACTGAACCGGAAATTTGGTTGG 600

QY 601 TTTGGGGACACACAGACCCACAGATAATTTCTGCTTAAGATCTTAACAGCACATCTGGC 660
DB 601 TTTGGGGACACACAGACCCACAGATAATTTCTGCTTAAGATCTTAACAGCACATCTGGC 660

QY 661 TTGCAAAATCTGCTCACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCCTTT 720
DB 661 TTGCAAAATCTGCTCACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCCTTT 720

QY 721 TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGAGGAGGTTTAAAAAGTGAAG 780
DB 721 TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGAGGAGGTTTAAAAAGTGAAG 780

QY 781 CATAGGGTTTGGCTGACACAGAGTCAAGGTTATCAATGATCTACCTTCGAGGAGCA 840
DB 781 CATAGGGTTTGGCTGACACAGAGTCAAGGTTATCAATGATCTACCTTCGAGGAGCA 840

QY 841 GCGTTGAGTGAATAATAGCACCTTTACCTTCAGTGTATGTTAAAAAGAGAGAGTGTG 900
DB 841 GCGTTGAGTGAATAATAGCACCTTTACCTTCAGTGTATGTTAAAAAGAGAGAGTGTG 900

QY 901 TACAAAGAGTTCACATGTTGTAATACAAAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 960
DB 901 TACAAAGAGTTCACATGTTGTAATACAAAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 960

QY 961 AATAGGCTTGCCTTTCAGAAATCTGCTGTGAT 996
DB 961 AATAGGCTTGCCTTTCAGAAATCTGCTGTGAT 996
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RESULT 2

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US-10-670-454-1
; Sequence 1, Application US/10670454
; Publication No. US20040229357A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/10/670,454
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
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; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Phaseolus coccineus
US-10-670-454-1

Query Match 100.0%; Score 996; DB 8; Length 1318;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 996; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTTGTTCTGTCTCAGCCAGCATTTGAACCAAGTTTTTCTTCTGAAACCATTTCAAGTCC 60
DB 68 ATGGTTGTTCTGTCTCAGCCAGCATTTGAACCAAGTTTTTCTTCTGAAACCATTTCAAGTCC 127

QY 61 AGCCCTCTTGTTCACCGGGATTCCTGTGTGCGACCTTCAGGCACCCCGATGCCAAGAATCTC 120
DB 128 AGCCCTCTTGTTCACCGGGATTCCTGTGTGCGACCTTCAGGCACCCCGATGCCAAGAATCTC 187

QY 121 ATAGTGAACGCGCTGTAGGGACCTTCGGCTTCTTCAAGCTTTGTGAACCATGTGTTCAATTG 180
DB 188 ATAGTGAACGCGCTGTAGGGACCTTCGGCTTCTTCAAGCTTTGTGAACCATGTGTTCAATTG 247

QY 181 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240
DB 248 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 307

QY 241 AAAGACAGAGCTGGTCCCGCCCGACCTTTTGGCTATGTGTAGCAAGAGGATTTGGCCCAAC 300
DB 308 AAAGACAGAGCTGGTCCCGCCCGACCTTTTGGCTATGTGTAGCAAGAGGATTTGGCCCAAC 367

QY 301 GGTGATGTCGGTTGGGTGGAATACCTCTCTCAACCAACCTGATGTTATCTCACCC 360
DB 368 GGTGATGTCGGTTGGGTGGAATACCTCTCTCAACCAACCTGATGTTATCTCACCC 427

QY 361 AAATCACTTTGCAATTTCCGAGAAATCTCTCATCATTTTCAGGCGGTGTGAGAACTAC 420
DB 428 AAATCACTTTGCAATTTCCGAGAAATCTCTCATCATTTTCAGGCGGTGTGAGAACTAC 487

QY 421 ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTTGGAAATTCATGCGGAGGGTTGGGG 480
DB 488 ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTTGGAAATTCATGCGGAGGGTTGGGG 547

QY 481 ATAAGGCAGAGGAATACGTTTAAGCAGAGTGTCTGAAGGATGAGAAAAGTGAATTCGTGCTTC 540
DB 548 ATAAGGCAGAGGAATACGTTTAAGCAGAGTGTCTGAAGGATGAGAAAAGTGAATTCGTGCTTC 607

QY 541 AGGTTGAACCACTACCCGCTTGCCTGAGGTGCAAGCACTCAACCGGAAATTTGGTTGGG 600
DB 608 AGGTTGAACCACTACCCGCTTGCCTGAGGTGCAAGCACTCAACCGGAAATTTGGTTGGG 667

QY 601 TTTGGGGAGCACACAGACCCACAGATAATTTCTGCTTTAAGATCTAAACAGCACATCTGGC 660
DB 668 TTTGGGGAGCACACAGACCCACAGATAATTTCTGCTTTAAGATCTAAACAGCACATCTGGC 727

QY 661 TTGCAAAATCTGCTCACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCCTTT 720
DB 728 TTGCAAAATCTGCTCACAGATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCCCTTT 787

QY 721 TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGAGGAGGTTTAAAAAGTGAAG 780
DB 788 TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGAGGAGGTTTAAAAAGTGAAG 847

QY 781 CATAGGGTTTGGCTGACACAGAGTCAAGGTTATCAATGATCTACCTTTGGAGGACCA 840
DB 848 CATAGGGTTTGGCTGACACAGAGTCAAGGTTATCAATGATCTACCTTTGGAGGACCA 907

QY 841 GCGTTGAGTGAATAATAGCACCTTTACCTTCAGTGTATGTTAAAAAGAGAGAGTGTG 900
DB 908 GCGTTGAGTGAATAATAGCACCTTTACCTTCAGTGTATGTTAAAAAGAGAGAGTGTG 967

QY 901 TACAAAGAGTTCACATGTTGTAATACAAAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 960
DB 968 TACAAAGAGTTCACATGTTGTAATACAAAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 1027
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QY 961 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGCTGAT 996
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Db 1028 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGCTGAT 1063
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RESULT 3

US-09-371-307-62
; Sequence 62, Application US/09371307A
; Patent No. US20020053095A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Glycine max
US-09-371-307-62

Query Match 83.1%; Score 827.4; DB 3; Length 1359;
Best Local Similarity 89.9%; Pred. No. 1.7e-270;
Matches 898; Conservative 1; Mismatches 97; Indels 3; Gaps 1;
QY 1 ATGGTTGTTCTGCTCAGGCGATTTGAACAGTTTTCCTTCTGAAACCATTCAGTCC 60
|||
Db 102 ATGGTTGTTCTGCTCAGGCGATTTGAACAGTTTTCCTTCTGAAACCATTCAGTCC 161
|||
QY 61 AGCCCTTGTCTCAGGCGATTTCTGTGTCGACCTCAGCACCCCGATGCCAAGATCTC 120
|||
Db 162 AGCCCTTGTCTCAGGCGATTTCTGTGTCGACCTCAGCACCCCGATGCCAAGATCTC 221
|||
QY 121 ATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTGTTCCATTG 180
|||
Db 222 ATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTGTTCCATTG 281
|||
QY 181 GAGTTAATGGCCAAATTAGAAACGAGGCCCTCAGGTTCTTTAAATAATCTCAGTCCGAG 240
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Db 282 CAGTTTCATGGCCAAATTGGAACACGAAACCTCGGGTTCTTCAAAAAACCTCAATCCGAG 341
|||
QY 241 AAAGCAGAGCTGGTCCCGCCGACCTTTTCGGCTATGTAGCAAGAGGATTCGCCCAAC 300
|||
Db 342 AAAGCAGAGCTGGTCCCGCCGACCTTTTCGGCTATGTAGCAAGAGGATTCGCCCAAC 401
|||
QY 301 GGTGATGTCGGTTCGAAATACCTCTCTCAACACCAACCTGATGTTATCTCACCC 360
|||
Db 402 GCGGATGTCGGTTCGAAATACCTCTCTCAACACCAACCTGATGTTATCTCACCC 461
|||
QY 361 AAATCACTTTGATTTTCAGAGAAATCTCATCATTTTCAGGCGGTGTGAGAACTAC 420
|||
Db 462 AAGTCACAGTTTCATTTTCAGAGAAAGTCTCAGAAATTTTCAGGCGGTGTGAGAACTAC 521
|||
QY 421 ATTACAGCAGTCAAGAACTGCTATGCGGTGTTGGAATTCATGCGGAGGGTGGG 480
|||
Db 522 ATTACAGCAGTCAAGAACTGCTATGCGGTGTTGGAATTCATGCGGAGGGTGGG 581
|||
QY 481 ATAAGCAGAGAAATACGTTTAAGCAGGTTGCTGAAGGATGAGAAAGTATTCGTCCTC 540
|||
Db 582 ATAAACGAGAGAAATGTTGTTAGTAGTTGCTGAAGGATGAGAGNGTATTCGTCCTC 641
|||
QY 541 AGGTTGAACCACTACCCGCTTGCCTCAGGTCAGGTCAGCACTGAAC---CGGAATTTGGTT 597
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Db 642 AGACTTAACCACTACCCGCCCATGCGGAGGTGCAAGCAATTGAACGGAAGAAATTTGGTT 701
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QY 598 GGGTTTGGGAGACACACAGACCCACAGATAAATTTCTGTCTTTAAGATCTAAACAGCACTCT 657
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Db 702 GGAATTTGGAGAGCACACAGACCCACAGATAAATTTCTGTCTTTGAGATCTAAACAGCACTCA 761
|||
QY 658 GGCCTTGAATCTGTCTCAGAGATGGCACTTTGGGTTTCAGTCCCACTGATCAGACTTCC 717
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Db 762 GGCCTTGAATCTGTCTCAGAGATGGCACTTTGGGTTTCAGTCCCACTGATCAAACTTCC 821
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QY 718 TTTTTCATCAATGTTGGTGACGCTCTCAGAGTAATGACTTAATGCGAGGTTTAAAAAGTGA 777
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Db 822 TTTTTCATCAATGTTGGTGACACTCTTCAGGTAATGACTTAATGCGAGGTTTAAAAAGTGA 881
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QY 778 AAGCATAGGGTTTGGCTTGACACCAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGCA 837
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Db 882 AAGCATAGAGTTTGGCTTGACCAACCAAGTCAAGGTTTGTCAATGATCTACTTTGGAGCA 941
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QY 838 CCAGGTTGAGTGAATAATATAGCACTTTACCTTCAGTGTATGTTTAAAAAGGAGAGTGT 897
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Db 942 CCACCTTGTGTGAAGATAGACCTTTACCTTCAGTGTATGTTTAAAAAGGAGAGAGT 1001
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QY 898 TTGTACAAAGAGTTTCAATGTTGTAATACAAAGAGGCTGCTACACTTCAAGGCTAGCT 957
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Db 1002 TTGTACAAAGAGTTTCAATGTTGTAATACAAAGAGGCTGCTACACTTCAAGGCTAGCT 1061
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QY 958 GATAATAGGCTTGGCCCTTTCCAGAAATCTGCTGCTGAT 996
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Db 1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCTGAT 1100
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RESULT 4

US-10-401-321-62
; Sequence 62, Application US/10401321
; Publication No. US20030233679A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Baerson, Scott R.
; APPLICANT: Baerson, Scott R.
; TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
; FILE REFERENCE: 11899.0216.DVUS01 (MOBT:216--1)
; CURRENT APPLICATION NUMBER: US/10/401,321
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Glycine max
US-10-401-321-62

Query Match 83.1%; Score 827.4; DB 6; Length 1359;
Best Local Similarity 89.9%; Pred. No. 1.7e-270;
Matches 898; Conservative 1; Mismatches 97; Indels 3; Gaps 1;
QY 1 ATGGTTGTTCTGCTCAGGCGATTTGAACAGTTTTCCTTCTGAAACCATTCAGTCC 60
|||
Db 102 ATGGTTGTTCTGCTCAGGCGATTTGAACAGTTTTCCTTCTGAAACCATTCAGTCC 161
|||
QY 61 AGCCCTTGTCTCAGGCGATTTCTGTGTCGACCTCAGCACCCCGATGCCAAGAAATCTC 120
|||
Db 162 AGCCCTTGTCTCAGGCGATTTCTGTGTCGACCTCAGCACCCCGATGCCAAGAACTC 221
|||
QY 121 ATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTGTTCCATTG 180
|||
Db 222 ATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTGTTCCATTG 281
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Db 928 TCTCAATCAAAATCTTCCTTACAAGCTTAAGCTTGGTGTATATAGACTTGGTCTCTTT 987
Qy 979 CAGAAA 984
Db 988 GAGAAA 993

RESULT 6

US-09-938-842A-1350
; Sequence 1350, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1350
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1350

Query Match 42.6%; Score 424.4; DB 3; Length 1026;
Best Local Similarity 67.5%; Pred. No. 4,7e-133;
Matches 612; Conservative 0; Mismatches 291; Indels 3; Gaps 1;

Qy 79 ATTCTGTGGTGCACCTCAGCCGCCGATGCGAAGAAATCTCATAGTGAAGCCCTGTAGG 138
Db 91 ATCCCGTGTCAACTAGCCGATCGGAGGAAACCCGATCTGAAGCCCTGCCAG 150
Qy 139 GACTTCGGCTTCTCAAGCTTGTGAACCATGGTGTTCATATGGAGTTAATGCCCAATTA 198
Db 151 GAGTTCGGCTTCTCAAGCTGTGAACCATGGTGTTCATATGGAGTTAATGCCCAATTA 210
Qy 199 GAAACGAGGCCCTCAGGTTCTTTAAATCTCAGTCGAGAAACAGAGCTGGTCCC 258
Db 211 GAGCAGGAGGCTATTGGCTTCTTCGGCTTGCCTCAGTCTCTTAAACCCGCGGTCCA 270
Qy 259 CCGGACCTTTCGGCTATGTAGCAAGAGATTGGCCAAACGGTGATGTGGTGGGTG 318
Db 271 CTGAAACGTCGATGTATGTATGAACGATGACCAACGGTGAGCTTGGTGGATT 330
Qy 319 GAATACCTCTCTCAACCAACCACTGATGTATCTCAACCAATCACTTTGCAATTTTC 378
Db 331 GAGTATCTCTCTCAATCTAATCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 390
Qy 379 CGAGAAATCTCATCATTTTCAAGCGGTGTGGAGAACTACATTTACAGAGTGAAGAAC 438
Db 391 CGTCAACCCCTCAAAATTTTCGTCGAGTCGGTGGAGAGTACATGAAGAGATTAAAGAA 450
Qy 439 ATGTCTATGCGGTGTGGAAATGTATGGCGGAGGGTGGGGATAGCAGAGGAATACG 498
Db 451 GTGTCTCAAGAGTGTGGAGATGTGGCCGAAGAACTAGGGATAGAGCCAGGACACT 510
Qy 499 TTAACGAGGTTCTCAAGGATGAGAAAGTATTCGTCTTCAAGTTCAACCACTATCCCG 558
Db 511 CTGATTAATGCTGAGAGATGAGAGAGTGTCTGTGCTGAGACTAATCACTATTCG 570
Qy 559 CCTTCGCTGAGGTGCAAGCACTGAACCCGAAATTTGGTGGTGGTGGGAGCACAGAC 618

Db 571 GC---GGCGAGGAAGCGGCGGAGAGATGCTGAAGTGGGGTTTGGGGAACACACAGAC 627
Qy 619 CCACAGATAAATTTCTGTCTTAAGATCTAAACAGACATCTGGCTTGCAAAATCTGTCTACA 678
Db 628 CCACAGATAAATCTCAGTGTCTAAGATCTAAATACACGCGGGTCTTCAAATCTGTGTGAAA 687
Qy 679 GATGGCACTTGGGTTTCAGTCCCACTGATCAGACTTCTTTTTCATCAATGTTGGTGAC 738
Db 688 GATGGAAGTTGGGTCGCTGCTCCCTCTGATCACTCTTCTTCTTCAATTAATGTTGGAGAT 747
Qy 739 GCTCTACAGGTAATGACTAATGGGAGGTTTAAAGCTTAAAGCATAGGGTTTGGCTGAC 798
Db 748 GCTCTCAGGTTATGACTAAACGAGGTTCAAGAGTGTAAACACAGAGGCTCTTAGCCGAT 807
Qy 799 ACAACGAGTCAAGGTTATCAATGATCTACTTTTGGAGGACGAGCGTTGAGTGAATAATA 858
Db 808 ACAAGGAGATCGAGGATTTCAATGATATATTTCCGCGGACCGCCATTCAGCCAGAAGATC 867
Qy 859 GCACCTTTACCTTCAGTGTATTAAGGAGAGGAGTGTTTGTACAAAGAGTTACATGG 918
Db 868 GCACCATTTGCCATGCTTGTCCCTTGAGCAAGATGATTTGGCTTTACAAAGAAATTCACTTGG 927
Qy 919 TGTGAATACAAGAGGCTGCGTACACTTCAAGGCTAGCTGATATAATAGGCTTGCCTTTC 978
Db 928 TCTCAATACAATCTTCTGCTTACAAGTCTAAGCTTGGTGTATATAGACTTGGTCTCTTT 987
Qy 979 CAGAAA 984
Db 988 GAGAAA 993

RESULT 7

US-10-670-454-7
; Sequence 7, Application US/10670454
; Publication No. US20040229357A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/10/670,454
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-670-454-7

Query Match 42.6%; Score 424.4; DB 8; Length 1237;
Best Local Similarity 67.5%; Pred. No. 5.3e-133;
Matches 612; Conservative 0; Mismatches 291; Indels 3; Gaps 1;
Qy 79 ATTCCTGTGGTGCACCTCAGCCGCCGATGCGAAGAAATCTCATAGTGAAGCCCTGTAGG 138
Db 199 ATCCCGTGTCAACTAGCCGATCGGAGGAAACCCGATCTGAAGAGCTTGGAG 258
Qy 139 GACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTTGGAGTTAATGCCCAATTA 198
Db 259 GAGTTCGGGTTCTTCAAGTGTGAACCATGGAGTCCGAGTCCGACCCGAACTCATGACTCGGTTA 318
Qy 199 GAAACGAGGCCCTCAGGTTCTTTTAAATAATCTCAGTCCGAGAAAGACAGAGCTGGTCCC 258

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Db 319 GAGCAGAGGCTATTGGCTCTTTCGGCTTGGCTCAGTCTCTTAAACCCGGCCGGTCCA 378
QY 259 CCGAGCCCTTTTCGGCTATGCTAGCAGAGGATTTGGCCCAACGGTGTATGCTGGTTGGGTC 318
Db 379 CTTGAACCGTACGGTTATGTTAATAACCGATTGGACCAACGGTACGTTGGTTGGATT 438
QY 319 GAATACCTCTCTCTCAACCAACCCCTGATTTATCTCACCCCAAAATCACTTTGGCAATTTTC 378
Db 439 GAGTATCTCTCTCAATCTAATCTCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 498
QY 379 CGAGAAAATCTCATCATTTTCAGGCGGTTGGGAGAACTACATTACAGCAGTGAAGAAC 438
Db 499 CGTCAAAACCCCTCAAAATTTTCGGTGAAGTGGTGGAGAGTACATGAAGAGAGATTAAAGAA 558
QY 439 ATGTGCTATGCGGTGTTGGAATTTGATGGCGGAGGGGTTGGGATAGAGGAGGAGGATAGC 498
Db 559 GTGTCTGTAACAGGTGTTGAGATGTTGTCGCGAAGAACTAGGAGATAGGCAAGGGACACT 618
QY 499 TTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTCGTGCTTCAGGTTGAACCACTACCCG 558
Db 619 CTGAGTAAATGCTGAGAGATGAGAGAGTGAATTCGTGCTTCAGGTTGAACCACTATTCGG 678
QY 559 CTTGCGCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGGTTGGGAGGAGCACACAGAC 618
Db 679 GC---GGCGGAGGAGGCGGAGAGATGTTGAAGTGGGGTTTGGGGAACACACAGAC 735
QY 619 CCACAGATAATTTCTCTCTTAAGATCTAACAGCACACTCTGGCTTGCAAAATCTGCTCACA 678
Db 736 CCACAGATAATCTCAGTGTCTAAGATCTAATAACACGGCGGGTCTTCAAAATCTGTGTGAAA 795
QY 679 GATGGCACTTTGGTTCAGTCCCACTGATCAGACTTCTCTTTTCAATCAATGTTGGTGAC 738
Db 796 GATGAAGTTGGTTCGCTGCTGCTCTGATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 855
QY 739 GCTCTACAGTAATGACTAATGGGAGGTTTAAAGTGTAAAGCAATGAGGTTTGGCTGAC 798
Db 856 GCTCTTTCAGGTTATGACTAAACGGGAGGTTCAAGAGTGTAAACACAGGGTCTTAGCCGAT 915
QY 799 ACAACCAAGTCAAGGTTATCAATGATCTACTTTGGAGGACGAGCTTGAGTGAATAATA 858
Db 916 ACAGAGATTCAGAGGATTTCAATGATATATTTTCGGCGGACCGCATTTGAGCCAGAGATC 975
QY 859 GCACCTTTTACCTTCAGTGTATGTTAAAGGAGAGGAGTGTGTTGACAAAGATTTCAATGG 918
Db 976 GCACCAATGCCATGCTTGTCCCTGAGCAAGATGATTTGGCTTTTACAAAGATTTCACTTGG 1035
QY 919 TGTGAATACAAGAGCGTGGTACACTTCAAGGCTAGCTGATTAATGAGGCTTGGCCCTTTTC 978
Db 1036 TCTCAATACAAATCTTCTGCTTACAAAGTCTAAGCTTGGTGAATTAAGACTTGTGCTCTTT 1095
QY 979 CAGAAA 984
Db 1096 GAGAAA 1101

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RESULT 8

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US-09-371-307-64
; Sequence 64, Application US/093711307A
; Patent No. US20020053095A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOST:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10

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; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Glycine max
; US-09-371-307-64

Query Match      42.0%; Score 418.2; DB 3; Length 1403;
Best Local Similarity 66.2%; Pred. No. 7.4e-131;
Matches 657; Conservative 0; Mismatches 318; Indels 18; Gaps 3;

QY 1 ATGGTGTGTTCTGCTCAGCCAGCATTTGAACCACTTTTCTCTCTGAAACCAATTCAGATCC 60
Db 149 ATGGTGTGTTCTCCAGGCAACAACAGAACAAATACTCTCTACATCAAGAACTACATGCCA 208
QY 61 AGCCCTTTGTTCAACGGGGAATTCCTGTGTGAGACTTCAAGCAACCCGATGCCAAGAAATCTC 120
Db 209 ACGGCATTTCTCTCAACAAATTCCTCGTAGTGGACCTCTCCAAACCAAGATGCCAAGACCCTC 268
QY 121 ATAGTGAACGCGCTGTAGGGAATTCGCGCTTCTTCAAGCTTGTGAACCATGCTTCCATTTG 180
Db 269 ATAGTGAAGGCTGTGTGAGGAATTTGGAATTTCTTCAAGTCATCAACCATGTTCCCATG 328
QY 181 GAGTTAAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240
Db 329 GAAACTATATCCCAATTTGGAATCTCAAGCTTCTCAAGTCTCTCTATGCCACTCAATGAG 388
QY 241 AAAGACAGAGCTGTGTCCTCCCGACCTTTTCGCTATGTGTAGCAAGAGATTGGCCCAAC 300
Db 389 AAGGAAAAAGTAGGGCCCTCCCAACCATATGGGTATGGTAGCAAGAAAATTTGGACACAAT 448
QY 301 GGTGATGTGCGTTGGTGTGATACCTCTCTCAACCAACCCCTGATGTTTATCTCACCC 360
Db 449 GGGGATGTTGGTGTGATGATCTCTCTCAACCAACCATGAGTGTGTTTCAAGTGTGTTT 503
QY 361 AAATCACTTTGCAATTTTCGAGAAAATCTCTCATCTATTTTCAGGGCGGTGGTGAGAACTAC 420
Db 504 -----TCTCTGTTTATGGCAAAAACGCTGAGAAAATTTAGGTGTTGTTGAAACAGTTAC 556
QY 421 ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAAATGATGCGGAGGGGTTGGG 480
Db 557 ATGTCTCTCTGTGAGGAAAATGCGCATGTGAGATTTCTTGAGCTGATGGCAGAGGATTTGAAG 616
QY 481 ATAAGCAGAGCAATACGTTAAGCAGGTTGCTGAAGAGATGAGAAAAGTGAATTCGTGCTTC 540
Db 617 ATACAACAAAAATGTTGTTTAGCAAGCTTCTTATGAGATAAAGAGAGTGAATCTGTTT 676
QY 541 AGGTTGAACCACTACCCGCTTTGCCCTGAGGTGCAAGCACTGAACCCGGAATTTGGTTGGG 600
Db 677 AGGGTGAATCACTACCTGCTTGGCTGAACTT---GTGAATGGTCAAAAACATGATAGGG 733
QY 601 TTTGGGAGACACACAGACCCACAGATAATTTCTGTCTTAAAGATCTTAAAGCAATCTGGC 660
Db 734 TTTGGAGAAACACACAGGACCCACAAAATCATTTCTCTACTTAGGTCCAACAAATCTTCAGGC 793
QY 661 TTGCAAAATCTGCTCACAGATGCGACTTGGGTTTTCAGTCCCACTGATCAGACTTCTCTTT 720
Db 794 CTTCAAGTTTTTCTTAGAGATGAAACTGGATTTTCAGTCCCACTGATCAGAAATCTTTC 853
QY 721 TTTCAATCAATTTGGTGAGCGCTCTACAGGTAATGACTTAATTTGGGAGGTTTAAAAAGTGAAG 780
Db 854 TTTCAATAATTTGGTGATTTCTCTTCAGGTTATGACCAATGGAAGGTTTTCGAAGTGTGAAA 913
QY 781 CATAGGTTTGGCTGACACAAAGCAAGTCAAGGTTATCAATGATCTACTTTTGGAGGACCA 840
Db 914 CACAGAGTTTGTGACAAAATGGATTTAAGTCTAGACTCTCAATGATTTACTTTGGAGGTCCA 973
QY 841 GGGTTGAGTGAATAATATAGCACCTTTTACCTTCAGTGTGATGTTTAAAGAGGAGGAGTCTTTG 900
Db 974 CCAATTGAGTGAGAAAATAGTACATTTTCTTCACTTATG---AAAGGAAAAGAAAGCTTA 1030
QY 901 TACAAAGAGTTTCATGTTGTGAATACAAAGAGGCTGGGTACACTTCAAGGCTAGCTGAT 960

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Db 1031 TACAAAGAGTTACGGTTCAGATATAAAATTTAAACCTATGCTTCAAGATTGGCTGAT 1090
QY 961 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGCT 993
Db 1091 AATAGGCTTGGACATTTTGAGAGAAATTTGTTGCT 1123

RESULT 9
US-10-401-321-64
; Sequence 64, Application US/10401321
; Publication No. US20030233679A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Pillier, Kenneth J.
; APPLICANT: Kilshore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; APPLICANT: Baerson, Scott R.
; TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
; FILE REFERENCE: 11899.0216.DVUS01 (MOB:216--1)
; CURRENT APPLICATION NUMBER: US/10/401,321
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Glycine max
US-10-401-321-64

Query Match 42.0%; Score 418.2; DB 6; Length 1403;
Best Local Similarity 66.2%; Pred. No. 7.4e-131;
Matches 657; Conservative 0; Mismatches 318; Indels 18; Gaps 3;

QY 1 ATGGTTGTTCTCTCAGCCAGCATTTGAACCAAGTTTTCCTTCTGAAACCACTTCAAGTCC 60
Db 149 ATGGTTGTTCTCTCAGCCAGCATTTGAACCAAGTTTTCCTTCTGAAACCACTTCAAGTCC 208

QY 61 AGCCCTTGTTCACGGGATTCCTGTGTCGACCTCAGCACCCGATGCCAAGAAATCTC 120
Db 209 AGCGCATTCCTCAACAAATCCCGTAGTGGACCTCTCAACACCAAGATGCAAGACCTC 268

QY 121 ATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTTCATG 180
Db 269 ATAGTGAAGGCTGTGAGGAATTTGGAATTTCTTCAAAAGTCATCAACCATGGTTCCTCC 328

QY 181 GAGTTAATGGCCAAATTTAGAAACGAGCCCTCAGGTTCTTTAAATAATCTCAGTCCGAG 240
Db 329 GAACTATATCCAAATTTGGAATTTCAAGCTTCAAGTTCTTCTCTATGCCACTCAATGAG 388

QY 241 AAAGACAGAGCTGTGTCCTCCCGACCTTTCGGCTATGTTAGCAAGAGGATGGCCCAAC 300
Db 389 AAGGAAAAGTAGGCGCTCCCAACCATATGTTGTTAGTGGTATGTCAGCAAGAAATTTGACAC 448

QY 301 GGTGATGTGGTGGTGGATGCAATACCTCTCTCAACCAACCCCTGATGTTATCTCAACC 360
Db 449 GGGGATGTGGTGGTGGTGGATGCAATACCTCTCTCAACCAACCCCTGATGTTATCTCAACC 503

QY 361 AAATCACTTTCATTTTCGAGAAATCTCATCATTTTCAGGGCGGTGGTGGAGAACTAC 420
Db 504 -----TCTGTTTATGCGCAAAACCGTGAATAATTTAGGTTGTTGTTGAACAGTTAC 556

QY 421 ATTACAGCAGTGAAGAAATATGCTGATGCGGTGTTGGAATTCATGCGGAGGGGTTGGG 480
Db 557 ATGCTCTTGTGAGGAAATGCGATGTGAGATTTCTTGAGTGTATGCGGAGAGGATTTGAAG 616

QY 481 ATAAGCGAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAGTGAATTCGTGCTTC 540

Db 617 ATACAAACAAAAATGTGTTTAGCAAGCTTCTTATGGATAAAGAGAGTGACTCTCTTTT 676
QY 541 AGGTTGAACCACTACCCGCCCTTGCCTCAGGTGCAAGCACTGAACCCGAAATTTGGTTGG 600
Db 677 AGGTGATCACTACCTCTGCTTGCCTGAACTT---GTGAATGGTCAAAACATGATAGG 733
QY 601 TTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAAGATCTAAACGACATCTGCG 660
Db 734 TTGGAGAACACACGGAACCCCAAAATCATTTCTTACTTAGGTCCAACAAATCTTCAGGC 793
QY 661 TTGCAAAATCTGCTCACAGATGGCACTTGGGTTTTCAGTCCCACTGATCAGACTTCCCTT 720
Db 794 CTTCAAGATTTTCTTAGAGATGGAACTGGATTTTCAGTCCCACTGATCAGAAATCTTTC 853
QY 721 TTCAATCAATGTTGGTGAACGCTCTACAGGTAATGACTAATGGAGGTTTAAAGTGTAAAG 780
Db 854 TTCAATGTTGGTGAATTTCTTTCAGGTTATGACCAATGGAGGTTTTCGAAGTGTGAA 913
QY 781 CATAGGTTTGGTGCACACAAAGAGTCAAGGTTATCAATGATCTACTTTGGAGGACCA 840
Db 914 CACAGAGTTTGGACAAATGGATTTAAGTCTAGACTCTCAATGATTTACTTTGGAGGTCCA 973
QY 841 GGGTTAGTGAATAATATAGCACCTTTACCTTCAGTGATGTTAAAGAGAGAGGAGTGTG 900
Db 974 CCAATGAGTGAATAATATAGTACCAATTTATCTTCACTTATG---AAAGGAAAGAAAGCTTA 1030
QY 901 TACAAAGAGTTTCAATGCTGTAATACAAAGAGGCTGCTGATCCTTCAAGGCTAGCTGAT 960
Db 1031 TACAAAGAGTTTACGTTGCGAGTATATAAAATTTAACTATGCTTCAAGTGTGCTGAT 1090
QY 961 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGCT 993
Db 1091 AATAGGCTTGGACATTTTGGAGAGAAATTTGTTGCT 1123

RESULT 10
US-10-424-599-21951
; Sequence 21951, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kowalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 21951
; LENGTH: 1390
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_119826C.1
US-10-424-599-21951

Query Match 39.0%; Score 388.2; DB 7; Length 1390;
Best Local Similarity 64.1%; Pred. No. 1.3e-120;
Matches 637; Conservative 0; Mismatches 343; Indels 13; Gaps 3;

QY 1 ATGGTTGTTCTGCTCAGCCAGCATTTGACCAAGTTTTCCTTCTGAAACCACTTCAAGTCC 60
Db 175 ATGGTTGTTCTGCTCAAAAGCAACACAGAACTACTCTCATCAAGAACTTACATGCCA 234

QY 61 ACGCCCTTGTTCAGGGGATTCCTGTGTGCTCAGCTCAGCAACCCGATGCCAAGAAATCTC 120
Db 235 ACTGATCTCTCTCAACAAATTTCCATAGTGAACCTCTCCAAACCTGATGCAAGACCCTT 294

QY 121 ATAGTGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTTGAACTGGTTCATG 180
Db 295 ATAGTGAAGGCTTGTGAGGAGTTTGGATTTCTTCAAGTTCATCAACCATGGTGTGCCCAT 354


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QY 181 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTTAAAAATCTCAGTCCGAG 240
|||
Db 355 GAAGCTATATCCAAATGGAAATGAGGCTTCAAACTTCTCTA--TGCACCTCAAT 412
|||
QY 241 AAAGACAGAGTGGTCCCCCGACCTTTGGCTATGTTAGCAAGAGGATTTGCCCAAC 300
|||
Db 413 GAGAAAAAGTAGGACCTCCCAATCCATTTGTTGGGTGTAGCAAGAAATTTGACACAAT 472
|||
QY 301 GGTGATGTCGGTGGTGGTGAATACCTCTCCCTCAACACCAACCTGATGTTATCTCACCC 360
|||
Db 473 GGGGACGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 524
|||
QY 361 AAATCACTTTGCAATTTTCCGAGAAAATCTCATCATTTTCAAGGCGGTGGTGGAGAACTAC 420
|||
Db 525 CACAACTTCTCTGTTTATGGCAAAACGCTGAGAAATTCAGGTGCTGTGTGAACAGTTAC 584
|||
QY 421 ATTACAGCAGTGAAGAACATGTCTATGCGGTGTTGGAATGATGGCGAGGGGTTGGG 480
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Db 585 ATGCTCTCTGTGAGGAAGATGGCATGTGAGATTTCTTGAGTTGATGCGAAGGGTTGAAG 644
|||
QY 481 ATAAGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAGTGAATTCGTGCTTC 540
|||
Db 645 ATTACGCAAAAGGATGTTTGAAGAGCTTCTAATGGATANAACAAAGTGAATCTATTTTC 704
|||
QY 541 AGGTTGAACCACTACCGCGCTTCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTGGG 600
|||
Db 705 AGGTTGAATCATTAAGCTGCTGCTGCTGAATGACTCTGAATGATCAGAACTTGATGGG 764
|||
QY 601 TTTGGGAGCACACAGACCCACAGATAATTTCTGCTTAAGATCTAAACAGCACATCTGCC 660
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Db 765 TTTGGAGAACACACAGACCCACAAATCATCTCTCTGTTAAGATCCAAACAACTTCAGGC 824
|||
QY 661 TTGCAAACTGCTCAGAGATGGCACTTGGGTTTCACTGCCAGCTGATCAGACTTCCCTTT 720
|||
Db 825 CTTCAAGATTTATCTTAGAGATGGAATTTGAATTTCACTGCCACAGCTCGAGCCGCTTTT 884
|||
QY 721 TTCAATCAATTTGCTACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAAG 780
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Db 885 TTTATTAAGTTGGTGAATCTCTTCAAGTTATGACAAATGGAAGTTTCGAAGTGTGAGA 944
|||
QY 781 CATAGGTTTGGCTGACACAAAGAGTCAAGGTTTCAATGATCTATCTTTGGAGGACCA 840
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Db 945 CACAGAGTGTGGCAAAATGGTTTCAAGTCCAGGCTTCAATGATTTTACITTTGGAGTCCA 1004
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QY 841 GCGTTCAAGTCAAAATATAGCACCTTTACCTTCAGTGAATGTTAAAGGAGAGGTTGTG 900
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Db 1005 CCTTTCAGTGAGAAAAATGCAACCATTTATCTCTCATG---AAAGGAAAGAAAGTCTTA 1061
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QY 901 TACAAAGAGTTCAATGGTGTGAATACAAAGAGGCTGGCTACACTTTCAAGGCTAGCTGAT 960
|||
Db 1062 TATAAAGAGTTTACCTGGTTGGTGAACAAAATCAATCTACGGTTCAAGATTAATCTAAA 1121
|||
QY 961 AATAGGCTTTGCCCTTTTCCAGAAATCTGCTGCT 993
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Db 1122 AATAGACTTTGAACATTTTGAAGAAATTCAGCT 1154
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RESULT 11

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US-10-670-454-9
; Sequence 9, Application US/10670454
; Publication No. US20040229357A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/10/670,454
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
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; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-10-670-454-9
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Query Match 38.3%; Score 381.6; DB 8; Length 1008;

Best Local Similarity 64.7%; Pred No. 1.9e-118;

Matches 586; Conservative 0; Mismatches 314; Indels 6; Gaps 1;

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QY 79 ATTCTGTGTGTCGACCTCAOGCACCCCGATGCGCAAGAAATCTCATAGTGAACCCCTGTAGG 138
Db 79 ATCCCTGTTATAGACTTTAACCAGCTCAGATGCCAAAACCCAAATCGTCAAGCATGTGAA 138
|||
QY 139 GACITTCGGCTTCTTCAAGCTTGTGAACCATGCTGTTTCCATTTGGAGTTAATGCGCAATTA 198
|||
Db 139 GAGITTTGGGTTCTTCAAAAGTCAACAACCATGCGGGTCCGACCCGATCTTTTGACTCAGTTG 198
|||
QY 199 GAAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAACAGAGCTGGTCCC 258
|||
Db 199 GAGCAAGAAGCATCAACTTTCTTTGCTTGTGATCACTCTCTCAAGACAAAGGGGTCCA 258
|||
QY 259 CCCGACCCCTTTCCGGCTATGTTAGCAAGAGGATTTGCCCAACCGGTGATGTCGGTTGGGTC 318
|||
Db 259 CTTGACCCCGTTTGGTTACGGTACTAAAGGATTTGGACCAATGGTGACCTTGGCTGGCTT 318
|||
QY 319 GAATACCTCTCTCAACACCAACCTGATGTTATCTCAACCAATCACTTTGCAATTTTC 378
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Db 319 GAGTACATTTCTCTTAATGCTAATCTTTGCCCTTGAGTCTCAAAAACCCACCCCAATTTTC 378
|||
QY 379 CGAGAAAAATCTCATCATTTTCAAGGCGGTGGTGGAGAACTACATTTACAGCAGTGAAGAAC 438
|||
Db 379 CGGCAACCCCTGCAATTTTCAAGAGGCGATGGAAGAGTACATTTAAAGAGATGAAGAGA 438
|||
QY 439 ATGTCGTATGCGGTGTGGAAATTTGATGGCGGAGGGTTGGGGATAGGCGAGGAAATACG 498
|||
Db 439 ATGTCGAGCAAAATTTCTGNAATGTTAGAGGAAGAGCTAAAGATAGAGCCAAAGAGAGAG 498
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QY 499 TTAAGCAGGTTGCTCAAGGATGAGAAAGTGAATTCGTGCTTCAAGTTGAAACCACTACCCG 558
|||
Db 499 CTGAGCCGTTTGGTGAAGAGTGAAGAAAGTGAATTCGTGCTGAGAAATGAACCATTAACCCG 558
|||
QY 559 CCTTCCCTCGAGTGCAGACACTGAACCGGAATTTGGTTGGGTTTGGGGAGCACACAGAC 618
|||
Db 559 -----GAGAAGGAAGACTCCGGTCAAGGAAGAGATTTGGGTTGGTGGGACACTGAT 612
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QY 619 CCACAGATAAATTTCTGTCTTAAGATCTAAACAGCATCTGGCTTGCAAAATCTGTCTCA 678
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Db 613 CCACAGTTGATATCACTGCTCAGATCAAAACGACACAGAGGGTTTGCAAAATCTGTGTCAA 672
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QY 679 GATGCACTTGGGTTTCACTCCCACTGATCAGATTCCTTTTTCATCAATGTTTGGTGAC 738
|||
Db 673 GATGGAACATGGGTTGATGTTTACCTGATCACTCTCTCTTCTTCTTGTGCGAGAT 732
|||
QY 739 GCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAAGCATAGGGTTTTTGGCTGAC 798
|||
Db 733 ACTCTTCAGGTGATGACAAAACGGAAGATTTCAAGAGTGTGAACATAGAGTGGTGACAAAT 792
|||
QY 799 ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCGGTTGAGTGAATAATA 858
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Db 793 ACAAGAGGTCAAGGATATCGATGATCTACTTCGAGGTCCTCTCTTTGAGCGAGAAGATT 852
|||
QY 859 GCACCTTTACCTTCAGTGAATGTTAAAGGAGGAGGATGTTTGTACAAAGAGTTCAATGG 918
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Db 853 GCACCAATTTATCATGCTTTGTGCAAGAGCAAGATGATGCTTTTATAATAGTATTACTTGG 912
|||
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QY 919 TGTGAATACAGAGGCTCGTACACTTCAAGGCTAGCTGATGATTAAGGTTGCCCTTTC 978
Db 913 TCTCAATACAGTTATCTGCTTACAAAATAAGCTTGGTGAATATAGGCTTGGTCTCTTT 972
QY 979 CAGAAA 984
Db 973 GAGAAA 978

RESULT 12
US-10-670-454-5
; Sequence 5, Application US/10670454
; Publication No. US20040229357A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.097000
; CURRENT APPLICATION NUMBER: US/10/670,454
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1243, 1265)
; OTHER INFORMATION: unidentified residue
US-10-670-454-5

Query Match 35.8%; Score 356.6; DB 8; Length 1318;
Best Local Similarity 63.2%; Pred. No. 7.5e-110;
Matches 586; Conservative 0; Mismatches 329; Indels 12; Gaps 2;

QY 65 CCTGTGTTACGGGGATTCTCTGTGGTCGACCTCAACGACCCCGATGCGAAGATCTCATAG 124
Db 78 CCGGTTCTCTAATCCGGTTATAGATATGTCTGACCCAGATCAACATCCAAACATGCCCTCG 137
QY 125 TGAACGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTTGTCATTTGGAGT 184
Db 138 TGAAGCATGCGAAGACTTCGGCTTCTTCAAGGTGATCAACCATGCGTTTCCGCGAGAGC 197
QY 185 TAAATGCCAATTTAGAAAAGAGGCGCTCAGTCTTTAAAAAATCTAGTCCGAGAAG 244
Db 198 TAGTCTCTGTTTAGAACAAGAGCGTGCATTTCTCTCTGTTGCCCAAGTCAGAGAAA 257
QY 245 ACAGAGCTGTTCCCGGACCTTTCCGCTATGTGTAGCAAGAGGATTGCGCCCAACGGTG 304
Db 258 CCAAGTCG---CAGTTATCCCTTCGGATACGGAAACAGTAAGATTGTCGGAATGGTG 314
QY 305 ATGTGGTTGGGTGCAATACCTCCTCTCAACACCAACCCCTGATGTTATCTCACCCAAT 364
Db 315 AGTGGTTGGGTGAGTACTTGTGATGAACGCTAATCATGATTCGGGTCGGGTCCAC 374
QY 365 CACTTTGCATTTCCGAGAAAATCTCATCTATTCAGGGCGGTGGTGGAGAACTACATTA 424
Db 375 TATTTCCAGTCTTCTCAAAAGCCCGGAACTTTTCAGAAAACGCAATTCGAAGAGTACAAA 434
QY 425 CAGCAGTAGAACACTGTCTATCGGTGTTGCAATTTGATGCGGAGGGGTTGGGGATTA 484
Db 435 CATCAGTAGAANAATGCAATTCGATGTTTGGAGAAGATCACAGATGGGCTAGGGATCA 494

QY 485 GCGAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAATTCGTGCTTCAGGT 544
Db 495 AACCGAGAACACACTTTAGCAAGCTTGTGTCTGACCAAAACACGCGACTCGATATTTGAGAC 554
QY 545 TGAACCACTACCGCTTGCCTGAGGTGCAAGCACTGAAC-----CGAAATTTGG 595
Db 555 TTAATCACTATCCACCATGTCTCTTAGCAATAGAAAACCAATGGTGAAGATGTGA 614
QY 596 TTGGGTTTGGGAGCACACAGACCCACAGATAAATTTCTGTCTTAAGATCTAACACACAT 655
Db 615 TTGGTTTGGTGAACACACAGATCTCAATCATCTCTGTCTTAAGATCTAACACACAT 674
QY 656 CTGGCTTCAAAATCTGTCTCACAGATGCGACTTGGGTTTCAGTCCCACTGATCAGACT 715
Db 675 CTGGTCTCCAAATTAATCTAAATGATGGCTCATGGATCTGTCTCCCTCCCGATCACACT 734
QY 716 CTTTTTCATCAATGTTGGTGACGCTCTACAGGTAAATGACATAATGGGAGTTTAAAAAGTG 775
Db 735 CTTCTTCTTCAACGTTGGTGACTCTCTCAGGTGATGACAAATGGGAGGTTCAAGAGCG 794
QY 776 TAAAGCATAGGTTTGGCTCAACACAAAGTCAAGGTTATCAATGATCTACTTTGGAG 835
Db 795 TGAGGCATAGGTTTGTAGCTAACTGTAATAAATCTAGGGTTTCTATGATTTACTTTCGCTG 854
QY 836 GACCAAGCTTCAAGTAAATATAGCACCTTTACCTTCACTGATGTTTAAAGAGAGGAGT 895
Db 855 GACCTTCATTCAGTCAAGAAATCGCTCCGTTGACATGTTTGTATAGACAAATGAGGACGGA 914
QY 896 GTTTGTACAAAGAGTTTCATGTTGTAATACAGAGGCTGCGTACACTTCAAGGCTAG 955
Db 915 GTTGTACAGAGGTTTACTTGGTCTGAATACAAAACCTTACCTACAACTCTAGATTGT 974
QY 956 CTGATAATAGGCTTGCCCTTTTCCAGA 982
Db 975 CTGATAATAGGCTTCAACAAATTCGAAA 1001

RESULT 13
US-10-392-325-3
; Sequence 3, Application US/10392325
; Publication No. US2004006080A1
; GENERAL INFORMATION:
; APPLICANT: Tanaka, Hiroshi
; APPLICANT: Kayano, Toshiaki
; APPLICANT: Matsuoaka, Makoto
; APPLICANT: Kobayashi, Masatomo
; APPLICANT: Saito, Tamio
; APPLICANT: Sakamoto, Tomoaki
; APPLICANT: Sakai, Miho
; TITLE OF INVENTION: GIBBERELLIN 2-OXIDASE GENE, FUNCTIONS AND USES THEREOF
; FILE REFERENCE: SH2-014
; CURRENT APPLICATION NUMBER: US/10/392,325
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 7
; PRIOR APPLICATION NUMBER: JP 2002-276051
; PRIOR FILING DATE: 2002-09-20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(984)
; OTHER INFORMATION:
US-10-392-325-3

Query Match 35.5%; Score 354; DB 7; Length 984;
Best Local Similarity 60.9%; Pred. No. 4.8e-109;
Matches 598; Conservative 0; Mismatches 375; Indels 9; Gaps 1;

QY 2 TGGTTGTTCTGTCTCAGCCAGCAATTAAGCCAGTTTTCCTTCTTGAAACCAATCAAGTCCA 61

Db 5 TGGTCTCGTGGCCGCCCGCTCGATCACATCCCGTGTGAGGTCGCGGACCCCG 64
Qy 62 CGCCCTTGTTACGGGGATTCCTGTGTCGACTACGACCCCGGATGCCAAGATCTCA 121
Db 65 GCGACGCTCTTCGCGCGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 124
Qy 122 TAGTGAACCCCTGTAGGAGCTTCGGCTCTCTCAAGCTTGTGAACCAATGCTTCAATGG 181
Db 125 TGGTGACGCCCTCGAGACGCTACGGGTTCTTCAAGGTCGTCAACCAACGCGGTGGCCACGG 184
Qy 182 AGTTAATGCCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAATCTCAGTTCGAGA 241
Db 185 ACACGATGACAAAGCGGAGTCGGAGCGCGTCAGGTTCTTCTCCACAGACGACCGCACA 244
Qy 242 AAGACAGAGCTGTCTCCCGCCCGCTTCGCGCTATGTTAGCAAGAGGATGGCCCAAGCG 301
Db 245 AGACCGCTCCGCGCGGCTACCGGTTCCGGTACGGCAGCAAGCGGATCGGGTTCAATG 304
Qy 302 GTGATGTCGGTTGGGTGCAATACCTCTCTCAACCAACCCCTGATGTTATCTCACCCA 361
Db 305 GCGACATGGGTGGCTCGAGTACCTCTCTCGCCCTCGACGACGCTCGCTCGCGACG 364
Qy 362 AATCACTTTGCAATTTCCGAGAAAATCCCTCATCATTTACGGCGGTGTTGAGAACTACA 421
Db 365 CTTGCAACCGTCCGCTCTCTCG-----CGTCTTCGCGGCGCTCTGAACGAGTACA 415
Qy 422 TTACAGCAGTGAAGACATGCTATGCGGTGTGGAATGTATGGCGGAGGGTTGGGA 481
Db 416 TCTCGGGGTGCGAAAGGTGGCGGTGCGGGTGATGAGCGGATGTTCGAGGGGCTGGGA 475
Qy 482 TAAGGACAGAGGAATACGTTAAGCAGGTGTCTGAAGGATGAGAAAAGTATGTTGTTCA 541
Db 476 TTGCGCAGCGGACGCGCTGAGCGCGCTGTGACGCGGAGGAGCGACAGGTGTTCC 535
Qy 542 GGTGAACCACTACCCGCTTCGCCCTGAGGTGCAAGCACTGAACCCGGAATTTGGTTGGGT 601
Db 536 GGTGAACCACTACCCGCGGTGCGCGCGCTGCGAGGGGCTCGGCTGCAAGCGTCAACGGCT 595
Qy 602 TTGGGAGACACACAGACCCACAGATAATTTCTGTCTTTAAGATCTAACACACATCTGGCT 661
Db 596 TCGCGAGACACACGACCCGCGAGCTCGTCTCGGTGCTCCGCTCAAAACGACGCTCGGCC 655
Qy 662 TGCAATCTGTCTCAAGATGGCAGCTTGGGTTCAGTCCCACTGATCAGACTTCCTTTT 721
Db 656 TGCAGATCGGCTCCGCGACGCGCAGTGGGTGTCGTGCGCTCCGACCCGCACTCTCTCT 715
Qy 722 TCATCAATGTTGGTGAAGCTCTACAGGTAAAGCTAATGGGAGGTTTAAAGTGTAAAGC 781
Db 716 TCGTCAACGTCGGCGACTCGTTGCAAGTTCTGACCAATGGGAGGTTCAAGAGCGTGAAGC 775
Qy 782 ATAGGGTTTGGCTGACACACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCA 841
Db 776 ACAGGGTGGTGGCCAAACGCTTAAAGTCTAGGGTTTCCTTCACTTTGAGGGCCAC 835
Qy 842 CGTTGAGTGAAAATATAGCACCTTTTACCTTCAGTGTATGTTTAAAGGAGGAGTGTGTTGT 901
Db 836 CGTTACCAAGAGGATTTGACCAATTCACAGCTGCTGGGGGAGGAGAGCAGGCTGT 895
Qy 902 ACAAGAGTTCAATGGTGTGAATACAAAGGCTCGGTACACTTCAAGGCTAGCTGATA 961
Db 896 ACAAGAGTTCAATGGGATGAGTACAAAGGCTGCCTACAAATCAAGGCTTGGAGACA 955
Qy 962 ATAGGCTTGCCCTTTCCAGAA 983
Db 956 ACAGGCTGGCCCGAGTTTGAGAA 977

RESULT 14

US-10-437-963-78659
; Sequence 78659, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 78659
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_78444C.1
US-10-437-963-78659

Query Match 35.5%; Score 354; DB 7; Length 1260;

Best Local Similarity 60.9%; Pred. No. 5.6e-109; Mismatches 375; Indels 9; Gaps 1;
Matches 598; Conservative 0;

Qy 2 TGGTTGTTCTGTCTCAGCCAGCATTTGAACCAAGTTCCTCTCTGAAACCATTTCAAAGTCCA 61
Db 144 TGGTTCTCGTGGCCGCCCGCGTGCATCATATCCCGTGTGTAGGTCGCCGACCCCG 203
Qy 62 CGCCCTTGTTACGGGGATTCCTGTGTCGACTCACGCACCCCGATGCCAAGAATCTCA 121
Db 204 GCGACGCTCTTCGCGCGTGCCTGCTCGACTCGGAGCCCGCGCGGAGGGCG 263
Qy 122 TAGTGAACCCCTGTAGGAGCTTCGGCTTCCTCAAGTGTGAACTGTTGATGTTCCATTGG 181
Db 264 TGGTGACGCTTCGAGCGGTACGGGTTCTTCAAGGTCGTCAACCAACGCGGTGGCCACGG 323
Qy 182 AGTTAATGCCAATTTAGAAAACGAGGGCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGA 241
Db 324 ACACGNTGGACAAAGCCCGAGTCGGAGGCGCTCAGGTTCTTCTCCAGAGCGACCCGACA 383
Qy 242 AAGACAGAGCTGGTCCCCCGACCTTTCGGCTATGTTAGCAAGAGGATTTGGCCCAACG 301
Db 384 AGGACCGCTCCCGCGCGCTACCGGTTTCGGGTACGCGAGCAAGCGGATTCGGGTTCAATG 443
Qy 302 GTGATGTCGGTTGGTTCGAACTACCTCCTCAACACCAACCTCTGATGTTATCTCACCCA 361
Db 444 GCGACATGGGGTGGCTTCGAGTACCTCCTCGCCCTCGACGACGCGTCTCGCCGACG 503
Qy 362 AATCACTTTGCAATTTCCGAGAAAATCCTCATCATTTTCAGGGCGGTGGTGGAGAACTACA 421
Db 504 CTTGACACCGTCCGCTCTGCG-----CGTCTTCGCGGCGCTCTGACGAGTACA 554
Qy 422 TTACAGCAGTGAAGAACATGTGCTATGCGGTGTGGAATTTGATGCGGAGGGGTTGGGA 481
Db 555 TCTCGGGGTGCGAAGGTGGCGGTGATGAGGCGATGTGCGAGGGGCTGGGCA 614
Qy 482 TGAAGCAGAGGAATAGTTAAGCAGGTTGCTGAAAGATGAGAAAGTGTGTTGTTGTTCA 541
Db 615 TTGCGCAGGCGACGCGCTGAGCGCGGTGTCACGCGGAAGGAGCGACCAAGGTGTTCC 674
Qy 542 GGTGGAACCACTTACCCGCTTCCTCTGAGGTGCAAGCACTGAAACCGGAATTTGGTTGGGT 601
Db 675 GGTGGAACCACTTACCCGCGCTGCGCGCGCTGACAGGGGCTCGGCTGACGCGTCAACGGCT 734
Qy 602 TTGGGAGACACAGACCCACAGATAATTTCTGTCTTAAAGATCTTAACAGACATCTGGCT 661
Db 735 TCGGGAGACACACCGACCGCAGCTGCTCGGTGTCGCGCTCAAAACGCGCAGCTCGGCGC 794
Qy 662 TGCNAATCTGTCTCAGATGCGACTTGGGTTTCAGTCCCACTGATCAGACTTCCTTTT 721
Db 795 TGCAGATCGCGCTCCGCGACCGCCAGTGTTGGTGTGTCGTGCTCCCGACCGGACTCTCTT 854

QY 722 TCATCAATGTTGGTACCGTCTACAGGTAAATGACTAAATGGGAGGTTTAAAGTGTAAAGC 781
DB 855 TCGTCAACGTCGGCGACTCGTTGCGAGGTTCTGACCAATGGGAGGTTCAAGAGCGTGAAGC 914
QY 782 ATAGGTTTGGCTGACACAAAGAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAAG 841
DB 915 ACAGGTTGGTGGCCAAACAGCCTAAAGTCTAGGGTTCTCTCATCTACTTTGGAGGGCCAC 974
QY 842 CGTTGAGTGAANAATATAGCACCTTTACCTTTCAGTGTATGTTAAAGGAGGAGGAGTGTGT 901
DB 975 CGTTAGCACAGAGGATTGCACATTGCCACAGCTGCTGGGGGAGGAGAGCAGACCTGT 1034
QY 902 ACAAGAGTTACATGGTGTGAATACAGAGGCTGCGTACACTTCAAGGCTAGCTGATA 961
DB 1035 ACAAGGAGTTACATGGGATGATGACAGAGGCTGCCTACAAATCAAGGCTTGGAGACA 1094
QY 962 ATAGGCTTGGCCCTTTCCAGAA 983
DB 1095 ACAGGCTGGCCAGTTTGAA 1116

RESULT 15

US-10-425-115-69575
; Sequence 69575, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 69575
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MR14577_163444C.1
US-10-425-115-69575

Query Match 31.5%; Score 314.2; DB 8; Length 1611;
Best Local Similarity 59.3%; Pred. No. 2.5e-95;
Matches 576; Conservative 0; Mismatches 383; Indels 12; Gaps 2;

QY 16 CAGCCAGCATTAAGACAGATTTTCTCTCTGAACCAATTCAGTCCAGCCCTTGTTCAG 75
DB 193 CGGCTGTCTGACAGATCCGCTCTCTGCGGTCCCGGGCCCAAGGACAGCTTCTCG 252
QY 76 GGGATTCGTGCTGACCTCAGCACCCGATGCCAAGATCTCATAGTGAACGCTGT 135
DB 253 GGAGTGCCGGTCTGACCTGTCTCAGCCAGCGCGCGGGCGGATCTCAGCCCTGC 312
QY 136 AGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGTTCTTCCATTGGAGTTAATGGCCAAT 195
DB 313 GAGCGCTTCGGGTTCTTCAAGGTGCTCAACACGGGTGCGCGGCCACCATGGACAGG 372
QY 196 TTAGAAAACAGAGCCCTCAGGTTCTTTAAANAATCTCAGTCCGAGAAAGACAGAGTGTGT 255
DB 373 GCGAGTCCGAGCCGCTCAGGTTCTTCGGCGAGGCGCAGGCGGACAAAGGACCGCGGGG 432
QY 256 CCCCCGAGCCCTTCGGCTATGGTAGCAGAGGATGGCCCAACGGTATGTCGGTTGG 315
DB 433 CCGGCGTACCGGTTTCGGGTACGCGACAGCGGATCGGGCTCAATGGCGACATGGGGTGG 492
QY 316 GTCGAATACCTCTCTCAACACCAACCTGATGTTATCTCACCCAAATCACTTTGCATT 375
DB 493 CTCGAGTACTCTCTCTCGCGGTGACGCGCGGTGCTCTCCGACGCTGCCCGTGGCC 552
QY 376 TTCCGAGAAAATCCTCATCTTTCAGGGCGGTGGTGGAGAACTACATTAACAGCAGTGAAG 435

DB 553 TCCAGCG-----CGCGGTTCCGGAGCCGCTGAACGAGTACGTCCGCGCCGTGGG 603
QY 436 AACATGTCTATGCGGTGTGGAAATTGATGCGGAGGGTTGGGATTAAGGACAGAGGAAT 495
DB 604 AAGGTGGCGCGCGTGTGCTGAGGCGATGCGGAGGSCCTGGGCATTTCGCGACCGGAC 663
QY 496 AGTTAAGCAGGTTGCTGAAAGATGAGAAAGTGTATGCTGCTTCAAGTTGAGGTTGAACACTAC 555
DB 664 CGCTGAGCTCATGCTGAGCGCGCGGAGCGCACAGGTTGTTCCGCTGAACACTAC 723
QY 556 CGGCTTCCGCTGAGGTCGAAGCACTGAACCGGAATTTGGTTGGGAGGAGCACACA 615
DB 724 CGGCTTCCGCGCTGAGGCTGCGAGGCTGCGAGCGCCACGCGCTTCGCGAGGACAC 783
QY 616 GACCCACAGATAAATTTCTTAAAGATCTAACAGCACATCTGGCTTGCATAATCTGTCTC 675
DB 784 GACCGCAGATCACTCTCGTGTCTCGCTCCAAACGCGACCTCCGCGCTCGAGATCGGCTC 843
QY 676 ACAGATGGCAC---TTGGGTTTCAGTCCACCTGATCAGACTTCTTTTTCATCAATGTT 732
DB 844 CGCGACGCGCGAGTGGGTCTCGGTGCCCTCCGACCGCGACGCGCTTCTTGGTTAACGTC 903
QY 733 GGTGACGCTCTACAGGTAATGACTAATGCGGAGGTTTAAAGTGTAAAGCATAGGCTTTTG 792
DB 904 GCGGACTCGTTGACAGGTCTGACCAACGCGGAGGTTTCAGGAGCGTGAAGCACCGGGTGGTG 963
QY 793 GCTGACACACAGAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAAGCGTTGAGTGAA 852
DB 964 ACCAACAGCCTCAAGTCCAGAGTTTCTTTCATCTACTTCGCGGGCGCGCGCTGGGCGAG 1023
QY 853 AATATAGCACCTTTACCTTCAAGTGTATGTTAAAGAGAGAGGAGTGTGTGTACAAAGATTC 912
DB 1024 CGGATCGCGCGCTGCGCGAGGTGCTGCGGAGGAGGAGAGGCTGTGTACAAAGGATTC 1083
QY 913 ACATGTTGTGAATACAAGAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCC 972
DB 1084 ACGTGGGCGAGTACAAGAGGCGCGGTACAGAGCGAGGCTCGCGGACAAACAGGCTGGCC 1143
QY 973 CTTTCCAGAA 983
DB 1144 CAGTTTGAA 1154

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Job time : 939.171 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2005, 18:17:41 ; Search time 179.487 Seconds
(without alignments)
2879.764 Million cell updates/sec

Title: US-10-670-454-1_COPY_68_1063

Perfect score: 996
Sequence: 1 atggtgtgtctgtctcagcc.....tcagaaaatctgtgtgat 996

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 8336576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/2/pubpna/PCT NEW PUB.seq.*
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10: /cgn2_6/ptodata/2/pubpna/US60 NEW PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56.4	5.7	1017	7	US-11-152-892-5
2	40	4.0	1011	7	US-11-152-892-3
3	39.2	3.9	3861	7	US-11-152-892-2
C 4	38.8	3.9	150437	7	US-11-112-908-44
C 5	38.8	3.9	182314	7	US-11-112-908-45
6	36	3.6	2171	7	US-11-152-892-1
7	35	3.5	3770	7	US-11-174-166-19
8	33.2	3.3	611587	7	US-11-117-187-209
C 9	33	3.3	921	7	US-11-112-908-140
C 10	33	3.3	180862	7	US-11-112-908-40
C 11	32.2	3.2	163317	7	US-11-117-187-212
C 12	31.6	3.2	1138	6	US-10-750-185-56890
C 13	31.6	3.2	101786	7	US-11-117-187-199
14	31.4	3.2	167116	7	US-11-121-086-44
C 15	31.4	3.2	187786	6	US-10-995-561-13474
C 16	31.4	3.2	187986	6	US-10-995-561-13252
C 17	31.2	3.1	1596	6	US-10-750-185-49342
18	31.2	3.1	2701	6	US-10-750-185-58921
19	31	3.1	1866	6	US-10-750-185-59097
C 20	31	3.1	3109	6	US-10-750-185-45757
C 21	31	3.1	193363	7	US-11-112-908-32
C 22	31	3.1	380749	6	US-10-995-561-13216
23	30.8	3.1	1464	6	US-10-750-185-27149

24	30.8	3.1	1595	6	US-10-750-185-34358	Sequence 34358, A
25	30.8	3.1	4173	7	US-11-063-343-16	Sequence 16, Appl
26	30.8	3.1	241805	6	US-10-995-561-13215	Sequence 13215, A
C 27	30.6	3.1	868	6	US-10-750-185-50973	Sequence 50973, A
C 28	30.4	3.1	987	6	US-10-750-185-44904	Sequence 44904, A
C 29	30.4	3.1	1898	6	US-10-750-185-34003	Sequence 34003, A
C 30	30.4	3.1	2761	6	US-10-995-561-298	Sequence 298, App
C 31	30.4	3.1	2911	6	US-10-750-185-31364	Sequence 31364, A
C 32	30.4	3.1	43943	6	US-10-995-561-13466	Sequence 13466, A
C 33	30.4	3.1	96539	6	US-10-995-561-13289	Sequence 13289, A
34	30.4	3.1	101001	6	US-10-995-561-13255	Sequence 13255, A
35	30.4	3.1	173995	6	US-10-995-561-13277	Sequence 13277, A
C 36	30.2	3.0	1788	6	US-10-750-185-51119	Sequence 51119, A
C 37	30.2	3.0	2639	6	US-10-750-185-53993	Sequence 53993, A
C 38	30.2	3.0	135019	6	US-10-849-438-11	Sequence 11, Appl
C 39	30.2	3.0	150468	7	US-11-112-908-56	Sequence 56, Appl
C 40	30.2	3.0	193789	7	US-11-112-908-55	Sequence 55, Appl
41	30	3.0	12756	6	US-10-995-561-13434	Sequence 13434, A
C 42	30	3.0	96539	6	US-10-995-561-13289	Sequence 13289, A
C 43	30	3.0	200628	7	US-11-121-086-62	Sequence 62, Appl
C 44	30	3.0	1125000	6	US-10-995-561-13286	Sequence 13286, A
C 45	29.8	3.0	755	6	US-10-750-185-32477	Sequence 32477, A

ALIGNMENTS

RESULT 1

US-11-152-892-5
; Sequence 5, Application US/11152892
; Publication No. US20050251883A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M.
; APPLICANT: Schomburg, Fritz M.
; APPLICANT: Michaels, Scott D.
; APPLICANT: Bizzell, Colleen M.
; FILE OF INVENTION: Dwarfism Genes and Dwarf Plants
; CURRENT APPLICATION NUMBER: US/11/152,892
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US/10/155,435
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Arabidopsis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1014)
US-11-152-892-5

Query Match 5.7%; Score 56.4; DB 7; Length 1017;
Best Local Similarity 55.7%; Pred. No. 4.6e-09;
Matches 108; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy	674	TCACAGATGGCACTGGGTTTCAGTCCACCTGATCAGACTTCCTTTTCATCAATGTTG	733
Db	704	TCAAAGACAATAGATGGATCGCTGTTAAACCTTAATCTCAATATCAATATG	763
Qy	734	GTGACGCTCTACAGGTAATGACTAATGGAGGTTTAAAGTGTAAAGCATAGGTTTTCG	793
Db	764	GTGACTTATTTTCAGCATGGAGCATGGCAATGTCACAAAGTGTGAACACCGTGTATCA	823
Qy	794	CTGACACACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACAGCGTTGAGTAA	853
Db	824	CGAACCCAAAGGTGGAGAGATTCTCAACGGCTTATTTTATGTGTCCATCATACGACGCG	883
Qy	854	ATATAGACCTTTA	867
Db	884	TTATAGATGTTTCA	897


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; LENGTH: 182314
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-45

Query Match      3.9%; Score 38.8; DB 7; Length 182314;
Best Local Similarity 58.8%; Pred. No. 0.24;
Matches 67; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 769 AAAAGTGTAAAGCATAGGCTTTTGGCTGACACAAAGTCAAGGTATCAATGATCTAC 828
Db 65032 ACAAATAAAGCAAGAGTGTAGTTGATACAAATAATCAATCAATTTTACAGTATGAT 64973

QY 829 TTTGAGGACCAAGCGTGTAGTGAATAATATAGCACCTTTTACCTTCAGTGTGTTA 882
Db 64972 GATTTAGGAGTAATGATGATGATGATATACAAATTTTATTTATTTATTTA 64919

RESULT 6
US-11-152-892-1
; Sequence 1, Application US/11152892
; Publication No. US20050251883A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M.
; APPLICANT: Schomburg, Fritz M.
; APPLICANT: Michaelis, Scott D.
; APPLICANT: Bizzell, Colleen M.
; TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
; FILE REFERENCE: 960296.97605
; CURRENT APPLICATION NUMBER: US/11/152,892
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US/10/155,435
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2171
; TYPE: DNA
; ORGANISM: Arabidopsis
US-11-152-892-1

Query Match      3.6%; Score 36; DB 7; Length 2171;
Best Local Similarity 49.5%; Pred. No. 0.11;
Matches 93; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 114 GAATCTCATAGTAAGCGCTGTAGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGT 173
Db 180 GAACAATAATGGTTGAGCTGCGAAGAGGTGGGGATTTTTTCAANTTGTGAACCATGGAAT 239

QY 174 TCCATTGGAGTTAATGGCCAAATTAGAAAACGAGGCCCTCAGGTCTCTTTAAAAAATCTCA 233
Db 240 TCCAAAGACGCTTTTGAGATGATGCTCTCGAAGAGAAGAACTCTTTGACCAACCTTT 299

QY 234 GTCCGAGAAGACAGAGCTGGTCCCCCGACCCCTTTCGGCTATGGTAGCAAGAGATTGG 293
Db 300 TTCTGTGAAAGTCAGAGAACGTTTTTCGGACTTATCGAAGATAGTTACCGTTGGGGAA 359

QY 294 CCCAAACG 301
Db 360 CCCTAGCG 367

RESULT 7
US-11-174-166-19
; Sequence 19, Application US/11174166
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Kirsch, Wolff M.
; APPLICANT: Lennart, Anton
; APPLICANT: Kellin, Wayne J.
; APPLICANT: Kang, Dae-Kyung
; APPLICANT: Levine, Rodney L.
; APPLICANT: Rouault, Tracey
```

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; TITLE OF INVENTION: IRON REGULATING PROTEIN-2 (IRP-2) AS
; TITLE OF INVENTION: A DIAGNOSTIC FOR NEURODEGENERATIVE DISEASE
; FILE REFERENCE: LOMAU.140C1
; CURRENT APPLICATION NUMBER: US/11/174,166
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: 60/222,863
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 3770
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-11-174-166-19

Query Match      3.5%; Score 35; DB 7; Length 3770;
Best Local Similarity 57.9%; Pred. No. 0.35;
Matches 62; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 783 TAGGTTTTGGCTGACACAAAGTCAAGGTATCAATGATCTACTTTGGAGGACCGC 842
Db 1691 TGGAGTGTTCACCTACCTTACCTAGCAAGCTAGCGTTTGAATAGTTGGCTATGGATGTTCAAC 1750

QY 843 GTTGAGTGAATAATAGCACCTTTACCTTCAGTGTATTAAGAGGAG 889
Db 1751 CTGTGTAGGAAATACAGCACCTTTATCAGAAGCAATTTTGAATGCAG 1797

RESULT 8
US-11-117-187-209
; Sequence 209, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 209
; LENGTH: 611587
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-209

Query Match      3.3%; Score 33.2; DB 7; Length 611587;
Best Local Similarity 61.6%; Pred. No. 50;
Matches 53; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 851 AAAATATAGCACCTTTACCTTCAGTGTATGTTAAAAAGGAGAGGAGTGTTTGTACAAAGACT 910
Db 108621 AAAAAAAGAGCTTCTCTACAGTCAAGATATAAAGAAAGAAATGGGTTAAGAAAGACT 108680

QY 911 TCACATGCTGTGAATACAAAGAGGCT 936
Db 108681 TCAAAAGATTATGAATGCAAAAGGCT 108706

RESULT 9
US-11-112-908-140/c
; Sequence 140, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
```

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; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 140
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-140

Query Match      3.3%; Score 33; DB 7; Length 921;
Best Local Similarity 51.0%; Pred. No. 0.66;
Matches 78; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 381 AGAATCTCATCTTCATTTAGGCGCGTGTGGAGACTACATTACAGCAGTGAAGACAT 440
DB 834 ATATAAGATGACATTTTCAATTCAGTTGTGGACAAAGTAGATTATTCATAAAGGCTGCT 775
QY 441 GTGCTATGCGGTGTTCGAATTGATGCGGAGGGGTGGGGATAAGCAGCAGCAATACGTT 500
DB 774 GAATTAAGTACTTAAGTAAAGGTAGGAGCCGGGATGGGGATGAGGCTAAGGAGGTGTT 715
QY 501 AAGCAGGTTGCTGAAGGATGAGAAAAGTGATTC 533
DB 714 GAATAGTTATATCACACACACCAAAAATAAATTC 682

RESULT 10
US-11-112-908-40/c
; Sequence 40, Application US/11/112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40
; LENGTH: 180862
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-40

Query Match      3.3%; Score 33; DB 7; Length 180862;
Best Local Similarity 51.0%; Pred. No. 26;
Matches 78; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 381 AGAATCTCATCTTCATTTAGGCGCGTGTGGAGAACTACATTACAGCAGTGAAGACAT 440
DB 138122 ATATAAGATGACATTTTCAATTCAGTTGTGGACAAAGTAGATTATTCATAAAGGCTGCT 138063
QY 441 GTGCTATGCGGTGTTCGAATTGATGCGGAGGGGTGGGGATAAGCAGCAGCAATACGTT 500
DB 138062 GAAATAACTAGTTAACTAAGGGGTAGGAGCCGGGATGGGGATGAGGCTAAGGAGGTGTT 138003
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QY 501 AAGCAGGTTGCTGAAGGATGAGAAAAGTGATTC 533
DB 138002 GAATAGTTATATCACACACACCAAAAATAAATTC 137970

RESULT 11
US-11-117-187-212
; Sequence 212, Application US/11/117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 212
; LENGTH: 163317
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-212

Query Match      3.2%; Score 32.2; DB 7; Length 163317;
Best Local Similarity 57.4%; Pred. No. 45;
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 768 TAAAGTGTAAGCATAGGTTTTCGCTGACACACGAAGTCAAGTTATCAATGATCTA 827
DB 104835 TAAAAAGGAAAGACTAGTTTTTTTTTATTACACACCTCAACACCAATGATCTC 104894
QY 828 CTTTGGAGGACCAGCGTTTGAGTGAAAAATATAGCACTTTAC 868
DB 104895 CAAGTGAGAACCAACCCACACAGAAAAAATTGAAACCTTAC 104935

RESULT 12
US-10-750-185-56890/c
; Sequence 56890, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56890
; LENGTH: 1138
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-56890

Query Match      3.2%; Score 31.6; DB 6; Length 1138;
Best Local Similarity 47.9%; Pred. No. 2.3;
Matches 91; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 427 GCAGTGAAGAACATGTGCTATCGGTTGGAATTGATGCGGAGGGGTTGGGGATAAG 486
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32089  GGCCCTCTGTTTATGATGACGGGAGATCTGACAGAGGTGGGACGCTTGGCTT  32097
DD

Search completed: December 28, 2005, 01:30:14
Job time : 183.487 secs

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Alignment Scores:

[illegible]

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Pred. No.: 2,26e-155 Length: 999
Score: 1748.00 Matches: 331
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-670-454-2 (1-331) x CQ899251 (1-999)

QY 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
Db 1 ATGGTTGTTCTGCTCAGCAGCAATTTGAACAGTTTCTTCTGTAACCAATTCAGAGTCC 60
QY 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
Db 61 ACGCCCTTGTTCACGGGGATTCCTGTGTGCGACTCAGCACCCCGATGCCAAGATCTC 120
QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
Db 121 ATAGTGAACGCCCTGTAGGACATTCGGCTTCTTCAAGCTTGTGAACCAATCGTGTCCATTG 180
QY 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
Db 181 GAGTTAATGGCCAAATTTAGAAAACGAGGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240
QY 81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
Db 241 AAAGACAGAGCTGTCCCCCGACCTTTCGGCTATGTAGCAGAGGATTTGGCCCAAC 300
QY 101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
Db 301 GGTGATGTCGGTGGTTCGAATACCTCTCTCAACACCAACCTCATGTATCTCAGCC 360
QY 121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
Db 361 AAATCACTTTCGATTTTCGAGAAAATCTCATCATTTCAGGCGGTGTGGAGAACTAC 420
QY 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
Db 421 ATTACAGCAGTGAAGAACATGTCTATGCGTGTGGATTTGATGCGCGGGGTGGGG 480
QY 161 IleArgLysArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
Db 481 ATAAGGCAGAGGAATACGTTAAGCAGGTTCCTAAGGATGAGAAAAGTGAATCGTCTTC 540
QY 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
Db 541 AGGTTGAACACACTACCCGCTTTCCTGAGGTGCAAGCACTGAACCGGAATTTGGTGGG 600
QY 201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGly 220
Db 601 TTTGGGGAGCACACAGCCCAACAGATTAATTTCTGTCTTAAGATCTTAACAGCACATCTGC 660
QY 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhe 240
Db 661 TTGCAAAATCTGCTCACAGATGCACTTGGGTTTCACTCCACCTCATCAGACTTCCTTT 720
QY 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
Db 721 TTCATCAATTTGGTGACCTCTACAGGTAATGACTAATGGGAGGTTTAAAAAGTGAAG 780
QY 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
Db 781 CATAGGGTTTGGCTGACACACAGAGTCAAGGTTATCATGATCTACTTTGGAGAGCCA 840
QY 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
Db 841 GCGTTGAGTGAATAATAGCACCTTTACCTTCAGTGTATGTTAAAGAGAGAGGAGTGTGG 900
QY 301 TyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp 320
Db 901 TACAAAGAGTTTCAATGGTGTGAATCAAGAAGGCTGCGTACACTTCAAGGCTAGCTGAT 960
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QY 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
Db 961 AATAGGCTTGGCCCTTTCCAGAAATCTGCTGCT 993

RESULT 2
BD243009 1318 bp DNA linear PAT 17-JUL-2003
LOCUS Enzyme.
DEFINITION BD243009
ACCESSION BD243009
VERSION BD243009.1 GI:33052779
KEYWORDS JP 2002518005-A/1.
SOURCE Phaseolus coccineus
ORGANISM Phaseolus coccineus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.
REFERENCE 1 (bases 1 to 1318)
AUTHORS Thomas,S.G., Hedden,P. and Phillips,A.L.
TITLE Enzyme
JOURNAL Patent: JP 2002518005-A 1 25-JUN-2002;
THE UNIVERSITY OF BRISTOL
COMMENT OS Phaseolus coccineus (scarlet runner bean)
PN JP 2002518005-A/1
PD 25-JUN-2002
PP 11-JUN-1999 JP 2000554838
PR 12-JUN-1998 GB 9812821.8,15-JUL-1998 GB 9815404.0 PT
STEPHEN GREGORY THOMAS,PETER HEDDEN,ANDREW LEONARD PHILLIPS PC
C12N9/04,A01H5/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10, PC
C12N15/09,
PC C12N5/00,C12N5/00,C12N15/00
CC Enzyme
FH Key Location/Qualifiers
FT source 1..1318
FT /organism='Phaseolus coccineus (scarlet runner
bean)'
FEATURES
source
Location/Qualifiers
1..1318
/organism="Phaseolus coccineus"
/mol_type="genomic DNA"
/db_xref="taxon:3886"

ORIGIN

Alignment Scores:
Pred. No.: 3,17e-155 Length: 1318
Score: 1748.00 Matches: 331
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-670-454-2 (1-331) x BD243009 (1-1318)

QY 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
Db 68 ATGGTTGTTCTGCTCAGCAGCAATTTGAACAGTTTCTTCTGTAACCAATTCAGAGTCC 127
QY 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
Db 128 ACGCCCTTGTTCACGGGGATTCCTGTGTGCGACTCAGCACCCCGATGCCAAGAAATCTC 187
QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
Db 188 ATAGTGAACGCCCTGTAGGACATTCGGCTTCTTCAAGCTTGTGAACCAATCGTGTCCATTG 247
QY 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
Db 248 GAGTTAATGGCCAAATTTAGAAAACGAGGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 307
QY 81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
Db 308 AAAGACAGAGCTGGTCCCGACCTTTTCGGCTATGGTAGCAAGAGGATTTGGCCCAAC 367
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Db      1028 ATAGGCTGGCCCTTCCAGAAATCTGCTCT 1060
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RESULT 4
AX008671
LOCUS      AX008671             1318 bp    DNA        linear    PAT 06-SEP-2000
DEFINITION Sequence 1 from Patent WO9966029.
ACCESSION AX008671
VERSION   AX008671.1   GI:9996195
KEYWORDS  .
SOURCE    Phaseolus coccineus
ORGANISM  Phaseolus coccineus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Phaseolus.
REFERENCE 1
AUTHORS   Phillips,A.L., Hedden,P. and Thomas,S.G.
TITLE     Enzyme
JOURNAL   Patent: WO 9966029-A 1 23-DEC-1999;
          PHILLIPS ANDREW LEONARD (GB); HEDDEN PETER (GB); UNIV BRISTOL (GB);
          THOMAS STEPHEN GREGORY (GB)
FEATURES  source
            1..1318
            /organism="Phaseolus coccineus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:3886"

ORIGIN
Alignment Scores:
Pred. No.:      3 17e-155      Length:      1318
Score:          1748.00      Matches:      331
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              6              Gaps:      0

US-10-670-454-2 (1-331) x AX008671 (1-1318)
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|||||
Db      68 ATGGTTGTTCTGCTCAGCCAGCATTCGAACAGTTTTCCTCTCTGAAACCATTCAGAGTCC 127
|||||
Qy      21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
|||||
Db      128 ACGCCCTTGTTTCAGCGGGATCTCTGTGTGACCTCAGCCACCCCGATGCCAAGATCTC 187
|||||
Qy      41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
|||||
Db      188 ATAGTGAACGCTGTAGGACTTCGGCTTCTTCAGCTTGTGAACCATTCGTTCCATTG 247
|||||
Qy      61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
|||||
Db      248 GAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 307
|||||
Qy      81 LysAspArgAlaGlyProProAspProPheGlyTyrClySerLysArgIleGlyProAsn 100
|||||
Db      308 AAAGACAGAGCTGTGTCCTCCCGACCCCTTCGGCTATGTGTAGCAAGAGGATGTGCCCAAC 367
|||||
Qy      101 GlyAspValGlyTrpValGlyTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
|||||
Db      368 GGTGATGTCGGTGGGTGCAATACCTCTCTCACACCAACCCCTGATGTATCTCACCC 427
|||||
Qy      121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
|||||
Db      428 AATACATCTTTGCATTTTCCGAGAAAATCCTCATCATTTTCAGGCGGTGTGGAGAACTAC 487
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Qy      141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluMetAlaGluGlyLeuGly 160
|||||
Db      488 ATTACAGCAGTGAAGAACATGTGCTATGCCGTGTGGAATGTATGCGCGAGGGGTGGGG 547
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Qy      161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
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548 ATAAGGCACAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAAGTGATTCGTGCTTC 607
181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
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608 AGGTTGAACCACTACCCCGCTTGCCCTGAGGTGCAAGCACTGAACCGAATTTGGTTGGG 667
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201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGly 220
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668 TTGGGGAGCACACAGACCCACAGATATTTCTGCTTAAGATCTTAACAGCACATCGGC 727
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221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSerPhe 240
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728 TTGCAAAATCTGCTCACAGATGGCACTTGGGTTTCAGTCCACCTGATCAGACTTCTTT 787
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241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
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788 TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAG 847
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261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
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848 CATAGGGTTTGGCTGACACACGAAGTCAAGTTATCAATGATCTACTTTCGAGGACCA 907
|||||
281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
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908 GCGTTGAGTGAAAATATATAGCACCTTTACCTTCAGTGTATGTTAAAAGGAGGAGTGTGG 967
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301 TyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp 320
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968 TACAAAGAGTTTACATGGTGTGAATACAAAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 1027
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321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
|||||
1028 ATAGGCTTGGCCCTTTCAGAAATCTGCTCT 1060

RESULT 5
PCO132438      1318 bp    mRNA        linear    PLN 20-APR-1999
LOCUS          Phaseolus coccineus mRNA for GA 2-oxidase, gene ga2ox1.
DEFINITION    AJ132438
ACCESSION     AJ132438
VERSION       AJ132438.1   GI:4678585
SOURCE        GA 2-oxidase; ga2ox1 gene.
KEYWORDS      Phaseolus coccineus
ORGANISM      Phaseolus coccineus
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                Phaseolus.
REFERENCE 1
AUTHORS       Thomas,S.G., Phillips,A.L. and Hedden,P.
TITLE         Molecular cloning and functional expression of gibberellin 2-
                oxidases, multifunctional enzymes involved in gibberellin
                deactivation
JOURNAL       Proc. Natl. Acad. Sci. U.S.A. 96 (8), 4698-4703 (1999)
PUBMED        10200325
REFERENCE 2   (bases 1 to 1318)
AUTHORS       Phillips,A.L.
TITLE         Direct Submission
JOURNAL       Submitted (18-JAN-1999) Phillips A.L., Plant Sciences, IACR Long
                Ashton Research Station, Long Ashton Research Station, Bristol,
                BS41 9AP, UK
FEATURES      Location/Qualifiers
                1..1318
                /organism="Phaseolus coccineus"
                /mol_type="mRNA"
                /db_xref="taxon:3886"
                /issue_type="Embryo"
                /dev_stage="Late developing seeds"
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                /gene="ga2ox1"
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 VQWVEYLLNTNPVISPKSLISIFRESPHFRAVVENYITAVKMCYAVLELMSGLG
 IQRNTLRLLKDEKSDSCFRNLHYPPCPVEQALNRLNVGFGEHTDPOIISVLRNST
 SGLQICLDGTGTVSPDQTSFFINVGDALQVMTNGFRKFSVKHRVLADITKSLSMY
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 ORIGIN

Alignment Scores:

Pred. No.: 3,178-155 Length: 1318
 Score: 1748.00 Matches: 331
 Percent Similarity: 100.00% Conservativity: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 15 Gaps: 0

US-10-670-454-2 (1-331) x PCOI32438 (1-1318)

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 QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
 DB 198 ATAGTGAACGCTGTAGGACTTCGGCTCTTCAAGCTTGTAACCATGTTCCATTG 247
 QY 61 GluLeuMetAlaAsnLeuGlnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
 DB 248 GAGTTAATGGCCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTTAAAAAATCTCAGTCCGAG 307
 QY 81 LysAspArgAlaGlyProProAspProPheGlyTyGlySerLysArgIleGlyProAsn 100
 DB 308 AAAGCAGAGCTGTGTCCTCCCGACCTTTCGGCTATGTAGCAAGAGATTGGCCCAAC 367
 QY 101 GlyAspValGlyTrpValGluTyLysLeuLeuLeuAsnThrAsnProAspValLysSerPro 120
 DB 368 GGTGATGTCGGTGGTGCATACCTCTCTCTCAACCAACCTGATGTTATCTCACCC 427
 QY 121 LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValAluGluAsnTy 140
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 DB 548 ATAAGCAGAGGATAGCTTAAGCAGGTGCTGTAAGGATGAGAAAAGTGAATTCGTGCTTC 607
 QY 181 ArgLeuAsnHisTyProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
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 QY 201 PheGlyGluHisThrAspGlnIleLysValLeuAsnSerValLeuAsnSerThrSerGly 220
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 QY 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhe 240
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 QY 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
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QY 261 HisArgValLeuAlaAspThrThyLysSerArgLeuSerMetIleTyPheGlyGlyPro 280
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 RESULT 6
 AB181372
 LOCUS
 DEFINITION Vigna angularis VAGA20xAl mRNA for gibberellin 2-oxidase, complete cds.
 ACCESSION AB181372
 VERSION AB181372.1 GI:67077811
 KEYWORDS
 SOURCE Vigna angularis (adzuki bean)
 ORGANISM Vigna angularis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Vigna.
 REFERENCE 1
 AUTHORS Park,S., Nakajima,M., Xu,Z., Tomioka,K., Sakane,M. and Yamaguchi,I.
 TITLE Gibberellin 2-oxidases from adzuki bean hypocotyl
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1360)
 AUTHORS Nakajima,M., Xu,Z., Park,S., Tomioka,K., Sakane,M. and Yamaguchi,I.
 TITLE Direct Submission
 JOURNAL Submitted (08-JUN-2004) Masaotoshi Nakajima, The University of
 Tokyo, Dept. Appl. Biol. Chem., Fac. of Agriculture, 1-1-1 Yayoi,
 Bunkyo, Tokyo, 113-8657, Japan
 (E-mail:nkjmp@grl.ch.a.u-tokyo.ac.jp, Tel:81-3-5841-5192,
 Fax:81-3-5841-8025)
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Best Local Similarity: 94.24%		Mismatches: 12
Query Match: 93.54%		Indels: 0
DB: 15		Gaps: 0
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QY	21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysLeu 40	
DB	143 ACGCCCTTGTTCACGGGGATTCCTGTGTGTCGATCTTCAGGCACCCCGATGCCAAGAACCTC 202	
QY	41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60	
DB	203 ATAGTGGAGCCCTGTAGGACCTACGGCTCTTCAAGCTCGTGAACCATGTGTTCATTTG 262	
QY	61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80	
DB	263 GAGTTAGTGGCCAAATTAGAAAACGAAGCCCTCAGGTTCTTCAAAAAATCTCAGTCAGAG 322	
QY	81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100	
DB	323 AAAGACAGGGCTGGTCCCGCCGACCTTTCCGGCTACGCTAGCAAGGGGATTTGGCCCAAC 382	
QY	101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120	
DB	383 GCGCATGTGGTTGGTTCGAATACCTCTCTCAACACCAACCCCTGAGGTCAATCTCACCC 442	
QY	121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140	
DB	443 AAATCACTCTCCATTTTCCGTGAAGTCTCTCATCTTCAGGGCGGTGGTGAGAACTAC 502	
QY	141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160	
DB	503 ATTACAGCAGTAAAGAACATGTGTTATGCGGTGTTGGAATTGATGGCAGAGGGTTGGGG 562	
QY	161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180	
DB	563 ATAGCCGAGAGGAATACCTTAAGCAGGTGCTGAAGGATGAAGGATGAAAAAGTGAATCATGCTTC 622	
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DB	623 AGGATCAACCACTACCCGCGGTGCCAGAGGTGCCAGCACTGAACCGGAATTTGGTTGGG 682	
QY	201 PheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly 220	
DB	683 TTTGGGGAGCACACAGACCCACAGATAAATTTCTGTCTTAAGATCTAATAGCACATCAGGC 742	
QY	221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSerPhe 240	
DB	743 TTGCAAAATCTGCTCCGACATGGCACTTGGGTTCAGTCCCACTGATCAGACTTCCTTT 802	
QY	241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260	
DB	803 TTCATCAATGTTGGTGATGCTCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAAG 862	
QY	261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280	
DB	863 CATAGGGTTTGGCTGACACACGAAGTCAAGGTTATCAATGATATACATTTTGGAGGACCA 922	
QY	281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluCysLeu 300	
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QY	301 TyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp 320	
DB	983 TACAAAGATTTCATGTTGGGTAATACAGAGGCTGGGTACACTTCAAGGCTAGTGTAT 1042	
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RESULT 7	
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LOCUS	AR528429 1359 bp DNA linear PAT 08-OCT-2004
DEFINITION	Sequence 62 from patent US 6723897.
ACCESSION	AR528429
VERSION	AR528429.1 GI:53916494
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 1359)
AUTHORS	Brown, S.M., Ellich, T.D., Heck, G.R., Kishore, G.M., Logusch, E.W., Logusch, S.J., Piller, K.J., Rao, S., Ream, J.E. and Baerson, S.R.
TITLE	Methods for controlling gibberellin levels
JOURNAL	Patent: US 6723897-A 62 20-APR-2004;
FEATURES	Monsanto Technology, LLC; St. Louis, MO
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Percent Similarity:	90.36% Conservative: 4
Best Local Similarity:	89.16% Mismatches: 31
Query Match:	87.56% Indels: 1
DB:	6 Gaps: 1
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QY	21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysLeu 40
DB	162 AGCCCTTGTTCGCGGGATTCCTGTGTGTCGACTCAGGACCCCGATGCCAAGACCCAC 221
QY	41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
DB	222 ATAGTCAATGCTCGAGGACTTCGGCTTCTTCAAGCTCGTGAACCCACCGGTGTTCGGTTA 281
QY	61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
DB	282 CAGTTTCATGGCCCAATTTGGAAAAACGAAACCCCTCGGGTTCTTCAAAAAACCTCAATCCGAG 341
QY	81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
DB	342 AAAGACAGGGCTGGTCCCTGACCTTTTGGCTACGGCAGCAAGAGGATTTGGCCCTAAC 401
QY	101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
DB	402 GCGCATGTGGTTGGTTCGATACCTCTTCTCAACCAACCCCTGATGTCATCTCCCC 461
QY	121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
DB	462 AAGTCAAGTTCATTTTCAGGAAGTCTCTCAGAAATTTTCAGGGCGGTGGTGGAGGAATAC 521
QY	141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
DB	522 ATTAGACGGTGAAGAACATGTCTATGAGGTGTGGATTTGATGCTCAGGGATTGGGG 581
QY	161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
DB	582 ATAACGCAAGGAATGTGTGATGAGTTGCTGAGGATCGAAGGATGAGAAGAGTGTATCTTC 641
QY	181 ArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsn--ArgAsnLeuVal 199
DB	642 AGACTTAACTACCTACCCCATGCCCGGAGGTGCAAGCATTTGAACGAAGGAATTTGGTT 701

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QY 200 GlyPheGlyGluHisThrAspProGlnIlelleSerValLeuArgSerAsnSerThrSer 219
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QY 240 PhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerVal 259
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QY 280 ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluCys 299
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Db 1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCT 1097

RESULT 8
AY594292 1245 bp mRNA linear PLN 30-APR-2005
LOCUS Neriium oleander GA 2-oxidase 2 mRNA, complete cds.
DEFINITION AY594292
ACCESSION AY594292
VERSION AY594292.1 GI:51011365
KEYWORDS Neriium oleander (common oleander)
SOURCE Neriium oleander
ORGANISM Neriium oleander
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Gentianales; Apocynaceae; Apocynoidae;
Wrighteae; Neriium.
REFERENCE 1 (bases 1 to 1245)
Ubeda-Tomas,S., Garcia-Martinez,J.L. and Lopez-Diaz,I.
Isolation, characterization and multi-site polyadenylation of GA
20-oxidases and GA 2-oxidases in Neriium oleander
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1245)
Ubeda-Tomas,S., Garcia-Martinez,J.L. and Lopez-Diaz,I.
Direct Submission
TITLE Submitted (08-APR-2004) Instituto de Biologia Molecular y Celular
de plantas, Consejo Superior de Investigaciones Cientificas (CSIC),
Universidad Politecnica de Valencia, Avda. de los Naranjos s/n,
Valencia 46022, Spain
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ORIGIN
Alignment Scores:

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Pred. No.: 7.65e-100 Length: 1245
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Query Match: 66.42% Indels: 2
DB: 15 Gaps: 2

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Db 1 ATGGTGGTCTTGTCCAAACCCAGCAATGGAAACAGTTCTGCTTAGTCAAGAACTGTTAAGCT 60
QY 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
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QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
Db 121 CTTGTTAAGGCGCTGTCAAGAGTTTGGATTTTCAAGATCATTAATCAGCGTGTTCACCAC 180
QY 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysSerGlnSerGlu 80
Db 181 GAATTCATCACCAACTTGAGTCTGAAGCTGTCAAAATCTTCTCTTCCCTCCCTTCCGAT 240
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QY 101 GlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
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Db 958 GATAACAGACGTGCTGCTGTTGAGAAATGCTGCC 993

RESULT 9
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LOCUS Nicotiana tabacum GA20x1 mRNA for gibberellin 2-oxidase 1, complete
DEFINITION cds.
ACCESSION AB125232
VERSION AB125232.1 GI:46849528
KEYWORDS Nicotiana tabacum (common tobacco)
SOURCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
ORGANISM Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE
AUTHORS Sakane, M., Nakajima, M. and Yamaguchi, I.
TITLE Molecular cloning of GA 2-oxidase in BY-2
JOURNAL Unpublished
AUTHORS Sakane, M., Nakajima, M. and Yamaguchi, I.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-2003) Masayuki Sakane, University of Tokyo,
Applied Biological Chemistry; Yayoi 1-1-1, Bunkyo-ku, Tokyo
113-0032, Japan (E-mail: m-sakane@gr1.ch.a.u-tokyo.ac.jp,
URL: http://pgr1.ch.a.u-tokyo.ac.jp/, Tel: 81-3-5841-5158 (ex. 25158),
Fax: 81-3-5841-8025)
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Alignment Scores:
Pred. No.: 4,37e-97 Length: 1292
Score: 1132.00 Matches: 213
Percent Similarity: 78.92% Conservative: 49
Best Local Similarity: 64.16% Mismatches: 68
Query Match: 64.76% Indels: 2
DB: 15 Gaps: 2

US-10-670-454-2 (1-331) x AB125232 (1-1292)

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QY 21 ThrProLeuPheThrGlyLeProValValAspLeuThrHisProAspAlaLysAsnLeu 40
Db 135 TCCTATCTTCAATGCTGTTCCATGATAGACCTCTCTAAACCTAACTCTAAGAACCTT 194

QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
Db 195 ATTGTTAAGGCCCTGTGAAGAAATTGGATTCTCTAAAGTCAATTAACCATGCGTCCCTACG 254

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VERSION AY588978.1 GI:50293060
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SOURCE ORGANISM
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Wrighteae; Nerium.
1 (bases 1 to 1406)
REFERENCE
AUTHORS Ubida-Tomas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I.
TITLE Isolation, characterization and multi-site polyadenylation of genes
GA 20-oxidases and GA 2-oxidases in Nerium oleander

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Unpublished
2 (bases 1 to 1406)
Ubada-Tomas,S., Garcia-Martinez,J.L. and Lopez-Diaz,I.
Direct Submission
Submitted (02-APR-2004) Instituto de Biologia Molecular de Plantas,
CSIC/Universidad Politecnica de Valencia, Avda de los Naranjos sn,
Valencia 46022, Spain

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AUTHORS Gaskin,P., Lange,T. and Hedden,P.
TITLE Gibberellin biosynthesis from gibberellin A12-aldehyde in endosperm
and embryos of Marah macrocarpus
JOURNAL Plant Physiol. 113 (4), 1369-1377 (1997)
PUBMED 9112781
REFERENCE 2 (bases 1 to 1479)
AUTHORS Hedden,P.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-1996) P. Hedden, University of Bristol,
Department of Agricultural Sciences, IACR-Long Ashton Research
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QY	101	GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro	120						
DB	448	GGCGAGCTCGGCTGGGTGGAATATCTCTCTCCATCCAAC-----TCCCAT	495						
QY	121	LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr	140						
DB	496	GCCTTCTCTCCATTTTCGCCCAAGACCCCAAAAGCTCCGCTCTGCTTTAAACGATTAC	555						
QY	141	IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly	160						
DB	556	ATCTGGGCTGTAGGAACATGGCGTGTGAATCGTAGATTATGTCGCGAAGGTTGAAG	615						
QY	161	IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe	180						
DB	616	ATTACGACAGAGGAATCGCTTGGACCAAGCTGTTGATGGCGAAGACGACGACTCTGTTTC	675						
QY	181	ArgLeuAsnHisTyrProProCysPro---GluValGlnAlaLeu---AsnArgAsnLeu	198						
DB	676	AGGCTGAACCATTTATCCGCCATGTCGGAGGAGCTTCAAGCTTTGGAAGGACAAACATG	735						
QY	199	ValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThr	218						
DB	736	ATTGGATTGGAGAACACACAGACCCACAGATCATTTTCGGTTTGTAGATCTAATAACACT	795						
QY	219	SerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThr	238						
DB	796	TCGTGACTTCAAAATTTCTCTCCCTGATGCCAATTTGGATTCTGTCTCTCTGATCAAACT	855						
QY	239	SerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSer	258						
DB	856	TCCTTCTTCAATGTTGGTGACTCTTTTACAGGTGATGACTAATGGAAGTTCAAAAGT	915						
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Alignment Scores:									
Pred. No.:	6.16e-95	Length:	1479						
Score:	1110.00	Matches:	216						
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Query Match:	63.50%	Indels:	14						
DB:	15	Gaps:	5						
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QY	1	MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer	20						
DB	169	ATGGTGGTTTTATCCAAACAGAAAATCCAACAGTTG-----TCT	207						
QY	21	ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu	40						
DB	208	TCCTTCTCTCTCTGGGTTCCATTTGATAGATCTCTCGCCACAGATGCCAAGCATTTG	267						
QY	41	IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu	60						
DB	268	ATCGTAAGGCGGTGTAAGAGCTGGATTCTTCAAGTCCATCAACCATGCGCGTCCCATG	327						
QY	61	GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu	80						
DB	328	GAATTCATTTCCACTCTCGAATCAGAAATCCACAAATTTCTTCCCTTCCCTCTCTGAA	387						
QY	81	LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn	100						
DB	388	AAACAGAGAGCGCGCCCTTCCCTTTCGGGTATGGCAACAGCAAAATCGCGCGCAAT	447						
QY	101	GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro	120						
DB	448	GGCGAGCTCGGCTGGGTGGAATATCTCTCTCCATCCAAC-----TCCCAT	495						
QY	121	LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr	140						
DB	496	GCCTTCTCTCCATTTTCGCCCAAGACCCCAAAAGCTCCGCTCTGCTTTAAACGATTAC	555						
QY	141	IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly	160						
DB	556	ATCTGGGCTGTAGGAACATGGCGTGTGAATCGTAGATTATGTCGCGAAGGTTGAAG	615						
QY	161	IleArgG							

Db	916	GTGAAGCAGTAGAGTATTGACCAACAGTTTAAAGTCAAGAATTTCAATGATATATTTGGT	975
Qy	279	GlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGlu	298
Db	976	GGGCCACCTTTTGAGTGAAGAAGATAGCCCTTTACCTTCCCTAATG---AAAGGAGAAGAA	1032
Qy	299	CysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeu	318
Db	1033	AGTTTGTACAAAGAGTTCACTTGGTTTGAGTACAAGAGATGAGCTTACAACCTAGGTTG	1092
Qy	319	AlaAspAsnArgLeuAlaProPheGlnLysSerAlaAla	331
Db	1093	GCAGATAACAGACTTGTACATTTTGAAGAATTCGGGCC	1131
RESULT 12			
CMA315663			
LOCUS	Cucurbita maxima partial mRNA for Gibberellin 2-oxidase (ga2ox	1383 bp	mRNA linear PLN 19-JUN-2003
DEFINITION	gene).		
ACCESSION	AJ315663		
VERSION	AJ315663.1	GI:32127336	
KEYWORDS	ga2Ox gene; gibberellin 2-oxidase.		
SOURCE	Cucurbita maxima (winter squash)		
ORGANISM	Cucurbita maxima		
REFERENCE	1 Frisse, A. and Lange, T.		
AUTHORS	Gibberellin biosynthesis in young seedlings of Cucurbita maxima L		
TITLE	Unpublished		
JOURNAL	2 (bases 1 to 1383)		
REFERENCE	Lange, T.		
AUTHORS	Direct Submission		
TITLE	Submitted (19-JUN-2001) Lange T., Botanical Institute, TU		
JOURNAL	Braunschweig, Mendelssohnstr. 4, D-38106 Braunschweig, GERMANY		
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Alignment Scores:			
Pred. No.:	1.51e-94	Length:	1383
Score:	1105.50	Matches:	207
Percent Similarity:	81.15%	Conservative:	47
Best Local Similarity:	66.13%	Mismatches:	58
Query Match:	63.24%	Indels:	1
DB:	15	Gaps:	1
US-10-670-454-2 (1-331) x CMA315663 (1-1383)			

Qy	20	SerThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsn	39
Db	64	TCTGCAGCATTTCTACTCTCGGATTCATTTGATAGACCTCTCTGCACCGAGATGCTAAACAA	123
Qy	40	LeuIleValAenAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValPro	59
Db	124	CTCATTTGTCAAAGCTTGTGAAGAAGCTCGGATCTTTAAGGTTGTCAACATGGTGTGCCCC	183
Qy	60	LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSer	79
Db	184	ATGGAATTAATCTCTCTCTTGAATCAGAATCCACCAAAATCTTCTCCCTTCCCTCTCTCT	243
Qy	80	GluLysAspArgAlaGlyProProAspPheGlyTyrGlySerLysArgIleGlyPro	99
Db	244	GAATAAAGAGAGAGCTGGCCCTCTCTCCCTTTTGGCTATGAAACAAACAATTTGGCGC	303
Qy	100	AsnGlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSer	119
Db	304	AATGGCATGTCTGGTTGGTTGAATATCTCTCTTGAACACTCATCTCGAATCCCACTCC	363
Qy	120	ProLysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsn	139
Db	364	GATGGGTTCTCTCTCCATTTTCGGCCAAGACCCACAAAAATCTCGCTCTGCTGTGAACGAT	423
Qy	140	TyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeu	159
Db	424	TACATCTCGGCTGTGAGGAACATCGCGGTGAAATCTCTCGAGCTTAATTTGGCGAAGGTTG	483
Qy	160	GlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCys	179
Db	484	AAGATTCAACAAACGAACTGTTTCAGTAAGCTCTGTGATGATGAACAGAGCGCATCTGTT	543
Qy	180	PheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeu--AsnArgAsnLeu	198
Db	544	TTCAGATGAACCATTAATTCGCCATGTCAGACCTTCAAGCTTTAAAAAGGAACAAACATG	603
Qy	199	ValGlyPheGlyGluHisThrAspProGlnIleSerValIleuArgSerAsnSerThr	218
Db	604	ATTGGATTTGGAGAACACACAGACCCCTCAATCATTTTCAGTTTTCAGATCAAAACACT	663
Qy	219	SerGlyLeuGlnIleCysLeuThrAspGlyThrTyrValSerValProAspGlnThr	238
Db	664	TCTGGATTTCAAATCTCTCTCGCAGATGGGAATTTGGATATCTGTCTCTCCGATCACAGC	723
Qy	239	SerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSer	258
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Db	784	GTGAGCATAGGGTTTTTGACAAACAGCTCGAAGTCAAGGGTTTTCAATGATCTACTTCGGT	843
Qy	279	GlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGlu	298
Db	844	GGGCCACCGTTGAGTGAAGAAGATAGCTCTTTAGCTTCCCTTATGCAAGGAGAGAAGA	903
Qy	299	CysLeuTyrLysGluPheThrTyrCysGluTyrLysLysAlaIleTyrThrSerArgLeu	318
Db	904	AGTTTGTACAAAGAGTTTACATGTTTGTGAGTACAAAGATCAGCTTCAACTCCAGGTTG	963
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RESULT	13		
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LOCUS		1292 bp	mRNA
DEFINITION		Lactuca sativa Ls2ox1 mRNA for gibberellin 2-oxidase No1, complete cds.	linear PLN 28-JUL-2004
ACCESSION	AB031206		
VERSION	AB031206.1		GI:9971226
KEYWORDS			gibberellin 2-oxidase No1.

SOURCE
ORGANISM
 Lactuca sativa
 Lactuca sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
 Cichorieae; Lactuca.
 1

REFERENCE
AUTHORS
 Nakaminami, K., Sawada, Y., Suzuki, M., Kenmoku, H., Kawaide, H.,
 Mitsuhashi, W., Sassa, T., Inoue, Y., Kamiya, Y. and Toyomasu, T.
 Deactivation of gibberellin by 2-oxidation during germination of
 photoblastic lettuce seeds
JOURNAL
 Biosci. Biotechnol. Biochem. 67 (7), 1551-1558 (2003)
 12913300
PUBMED
 12913300
REFERENCE
AUTHORS
 Toyomasu, T., Mitsuhashi, W. and Kamiya, Y.
 Direct Submission
JOURNAL
 Submitted (17-AUG-1999) Tomonobu Toyomasu, Yamagata University,
 Faculty of Agriculture; Wakaba-cho 1-23, Tsuruoka, Yamagata
 997-8555, Japan (E-mail: toyomasu@tdsl1.tr.yamagata-u.ac.jp,
 Tel:81-235-28-2861, Fax:81-235-28-2812)
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ORIGIN
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 Pred. No.: 1.73e-94 Length: 1292
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 Best Local Similarity: 63.20% Mismatches: 66
 Query Match: 63.19% Indels: 7
 DB: 15 Gaps: 4

US-10-670-454-2 (1-331) x AB031206 (1-1292)
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 Qy 20 ---SerThrProLeu---PheThrGlyIleProValValAspLeuThrHisProAspAla 37
 Db 149 AACACAAACCCGTTGATCTTTTCCACGATTCTCTCTCATTCGACCTCTCGAAACCTGAATCA 208
 Qy 38 LysAsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGly 57
 Db 209 AAACAACATCTGTTTAAAGCTTCGCCAAGATTTCGGATTTCCTTAAGTCGCTTAACCAATGA 268
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 Db 269 GTTCCCAACCAAGTTCATATAAAAACTCGAGTCAGAAGCTCTCAAGTCTCTCTCTCTCTCT 328
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QY 118 IleSerProLysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValVal 137
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RESULT 14
CMA302041
LOCUS
DEFINITION Cucurbita maxima mRNA for gibberellin 2-oxidase (ga2ox gene).
ACCESSION AJ302041
VERSION AJ302041.1 GI:27123664
KEYWORDS ga2ox gene; gibberellin 2-oxidase.
SOURCE Cucurbita maxima (winter squash)
ORGANISM Cucurbita maxima
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
1
REFERENCE
AUTHORS Frisse, A. and Lange, T.
TITLE Expression studies on the major Gibberellin dioxygenases in
developing seeds of Cucurbita maxima L
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1308)
AUTHORS Lange, T.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-2000) Lange T., Botanical Institute, Dept. Plant
Physiology and Biochemistry, TU Braunschweig, Mendelssohnstr. 4,
Braunschweig, D-38106, GERMANY
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Pred. No.: 1102.50 Matches: 206
Score: 81.15% Conservative: 48
Percent Similarity: 65.81% Mismatches: 58
Best Local Similarity: 65.81% Indels: 1
Query Match: 15 Gaps: 1
DB: 15

US-10-670-454-2 (1-331) x CMA302041 (1-1308)

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QY 40 LeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValPro 59
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Qy      279  GlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGlu 298
Db      898  GGGCCACCGTTGAGTGAAAGATAGCTCTTTAGCTTCCCTTATCGAAGGAAAGAAGA 947
Qy      299  CysLeuThrLysGluPheThrTrpCysGluThrLysLysAlaAlaThrThrSerArgLeu 318
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Qy      319  AlaAspAsnArgLeuAlaProPheGlnLysSerAlaAla 331
Db      1008  GCTGACACAGCGTTGTGCCCTTTGAAGAATTGCAGCC 1046

RESULT 15
AX506655 LOCUS AX506655 1026 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 1350 from Patent WO0216655.
ACCESSION AX506655
VERSION AX506655.1 GI:23387892
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
REFERENCE Harper,J.F., Krens,J., Wang,X. and Zhu,T.
AUTHORS Stress-regulated genes of plants, transgenic plants containing
TITLE same, and methods of use
JOURNAL Patent: WO 0216655-A 1350 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match: 62.50% Indels: 5
DB: 6 Gaps: 3

US-10-670-454-2 (1-331) x AX506655 (1-1026)
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Qy 19 LysSerThrProLeuPheThr-----GlyIleProValValAspLeuThrHisProAsp 36
Db 61 AAACCGGTTCCGGTTCTCACTTCCCATTCATCCCGTCGTCAACCTAGCCGATCCGGAA 120
Qy 37 AlaLysAsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHis 56

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Db      181  GGAGTCCGACCCGAACCTCATGCTCGGTTAGACGACGAGGAGCTATTGGCTTCTTCGGCTTG 240
Qy      77  SerGlnSerGluLysAspAlaGlyProProAspPropheGlyThrGlySerLysArg 96
Db      241  CCTCAGTCTCTTAAAAACCGGGCCGCTCACCTGAACCGTACGGTTATGGTAAATAAACCG 300
Qy      97  IleGlyProAsnGlyAspValGlyTrpValGluThrLeuLeuAsnThrAsnProAsp 116
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Qy      177  AspSerCysPheArgLeuAsnHisThrProProCysProGluValGlnAlaLeuAsnArg 196
Db      541  GACTCGTCCTCGAGACTTAAACCATTTATCCGGCGGGGAGAGAA--GAGGCGGAGAGATG 597
Qy      197  AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn 216
Db      598  GTGAAGGTGGGGTTTGGGGAAACACACAGACCACAGATAATCTCAGTGTCTAAGATCTAAT 657
Qy      217  SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTpValSerValProProAsp 236
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Qy      237  GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
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Qy      297  GluGluCysLeuThrLysGluPheThrTrpCysGluThrLysLysAlaAlaThrThrSer 316
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Search completed: December 28, 2005, 03:25:09
Job time : 6080 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 27, 2005, 21:42:50 ; Search time 738 Seconds
(without alignments)
2989.178 Million cell updates/sec

Title: US-10-670-454-2

Perfect score: 1748

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1530.5	87.6	1359	3	Aaz55912 Runner be
4	1530.5	87.6	1359	6	Aaz299471 Soybean g
					Aad40261 Soybean G

5	1092.5	62.5	1026	6	ABZ113545
6	1092.5	62.5	1026	8	ADA67975
7	1092.5	62.5	1237	3	Aaz55916 Arabidops
8	1068.5	61.1	1352	12	ADM94213 Soybean D
9	1060.5	60.7	1365	12	ADM94205
10	1060	60.6	1403	3	Aaz299472 Soybean g
11	1060	60.6	1403	6	AAD40262 Soybean G
12	973	55.7	984	8	ADA70120 Rice gene
13	973	55.7	984	12	ADK00081
14	973	55.7	1271	14	AEB67784 Rice geno
15	973	55.7	1650	12	ADM94203 Rice Diox
16	973	55.7	1651	14	AEB67733 Rice geno
17	972	55.6	1473	12	ADM94207
18	957.5	54.8	1555	12	ADM94201
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20	950.5	54.4	927	12	ADI45210 Rice isop
21	936.5	53.6	1316	3	Aaz55915 Arabidops
22	925.5	52.9	1224	3	AAC39277 Arabidops
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24	835	47.8	1065	8	ADA69812 Rice gene
25	772	44.2	1322	13	ADX09682 Plant ful
26	746	42.7	783	3	Aaz299474 Cotton gi
27	746	42.7	783	6	AAD40264 Cotton GA
28	733.5	42.0	1179	12	ADK00079 Rice cDNA
29	706.5	40.4	831	13	ADX11608 Plant ful
30	676	38.7	860	13	ADX13286 Plant ful
31	661	37.8	966	3	Aaz299469 Arabidops
32	661	37.8	966	6	AAD40259 A. thalia
33	634.5	36.3	1562	4	AAH48175 Rice gibb
34	616.5	35.3	942	8	ADA69995 Rice gene
35	565	32.3	919	13	ADX63586 Plant ful
36	553	31.6	811	3	Aaz299478 Maize gib
37	553	31.6	811	6	AAD40268 Maize GA
38	540	30.9	504	12	ADI45683 Corn isop
39	481.5	27.5	894	8	ADA70601 Rice gene
40	442.5	25.3	406	3	Aaz299475 Cotton gi
41	442.5	25.3	406	6	AAD40265 Cotton GA
42	442	25.3	4170	3	Aaz299468 Arabidops
43	442	25.3	4170	6	AAD40258 A. thalia
44	430	24.6	403	3	Aaz299473 Soybean g
45	430	24.6	403	6	AAD40263 Soybean G

ALIGNMENTS

RESULT 1
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ID ADT62692 standard; DNA; 999 BP.
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AC ADT62692;
XX
DT 13-JAN-2005 (first entry)
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DE DNA encoding Phaseolus coccineus gibberellin 2-oxidase.

XX DNA plasmid; transfer DNA; T-DNA; Agrobacterium Ti plasmid; transgene;
XX expression cassette; transgenic plant; transgenic; plant;
XX gibberellin 2-oxidase; ds.
XX Phaseolus coccineus.
XX
XX WO2004092390-A2.
XX
XX 28-OCT-2004.
XX
XX 09-APR-2004; 2004WO-US011000.
XX
XX 09-APR-2003; 2003US-0461459P.
XX
XX (MONS) MONSANTO TECHNOLOGY LLC.
XX
XX Gilbertson L, Krieger E, Zhang W, Ye X;

DR WPI; 2004-758349/74.
 XX New DNA plasmid comprising a T-DNA comprising an Agrobacterium Ti plasmid
 PT first border region linked to a transgene linked to an Agrobacterium Ti
 PT plasmid second border region, useful for enhancing production of
 PT transgenic plants.
 XX

PS Example 1; SEQ ID NO 3; 77pp; English.

XX The present invention relates to a DNA plasmid comprising a transfer DNA
 CC (T-DNA) comprising an Agrobacterium Ti plasmid first border region linked
 CC to at least one transgene linked to an Agrobacterium Ti plasmid second
 CC border region, and located in the DNA plasmid outside of the T-DNA is a
 CC plant expression cassette comprising a plant cell non-lethal negative
 CC selectable marker gene linked to a vector backbone DNA. Also disclosed
 CC are a method for enhancing the selection of transgenic plants that do not
 CC contain vector backbone DNA, a method for reducing the copy number of a
 CC transgene in a plant cell, and a transgenic plant produced by the method.
 CC The DNA plasmid comprises the expression cassette comprising a promoter
 CC that functions in plant cells operably linked to a plant cell non-lethal
 CC negative selection marker gene. The promoter is a constitutive promoter.
 CC The promoter expresses the linked non-lethal negative selection marker.
 CC Gene product in tissue culture during plant regeneration. The plant cell
 CC non-lethal negative selectable marker gene comprises a plant hormone
 CC biosynthetic pathway gene, degradative gene, biosynthetic pathway
 CC substrate-diverting gene or signalling gene, or metabolic interference
 CC gene. The transgene is a plant positive selectable marker gene selected
 CC from antibiotic resistance and herbicide resistance. The transgene
 CC comprises a transgene of agronomic interest. The plant hormone
 CC biosynthetic pathway gene is selected from gibberellin acid pathway
 CC genes, cytokinin pathway genes, auxin pathway gene, ethylene pathway
 CC genes, and abscisic acid pathway genes. The plasmid is useful for
 CC enhancing the production of commercially viable transgenic plants. The
 CC present sequence represents DNA encoding Phaseolus coccineus gibberellin
 CC 2-oxidase. The sequence is used as a non-lethal negative selectable
 CC marker gene.
 XX

SQ Sequence 999 BP; 263 A; 221 C; 249 G; 266 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,61e-180 Length: 999
 Score: 1748.00 Matches: 331
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-670-454-2 (1-331) x ADT62692 (1-999)

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QY 121 LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr 140
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 QY 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
 DB 481 ATAAAGCAGAGAAATACGTTAAGCAGGTTCCTGAAGGATGAGAAAGTGAATTCGTCTTC 540
 QY 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
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 QY 201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGly 220
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 QY 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
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 QY 301 TyrLysGluPheThrTyrCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaSer 320
 DB 901 TACAAAGAGTTCACATGGTGTGAATACAAGAGGCTGGGTACACTTCAAGGCTAGCTGAT 960
 QY 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
 DB 961 AATAGGCTTGCCCTTTTCAGAAATCTGCTGCT 993
 RESULT 2
 AAZ55912
 ID AAZ55912 standard; cDNA; 1318 BP.
 XX
 AC AAZ55912;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Runner bean gibberellin 2-oxidase PgGA2ox1 cDNA.
 XX
 KW Gibberellin 2-oxidase; PgGA2ox1; runner bean; 2-beta-hydroxylation;
 KM inactivation; growth inhibition; ss.
 XX
 OS Phaseolus coccineus.
 XX
 FH Key Location/Qualifiers
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 FT /*tag= a
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 PN WO9966029-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 11-JUN-1999; 99WO-GB001857.
 XX
 PR 12-JUN-1998; 98GB-00012821.
 PR 15-JUL-1998; 98GB-00015404.

XX (UYBR-) UNIV BRISTOL.
 XX Thomas SG, Hedden P, Phillips AL;
 XX WPI; 2000-097742/08.
 DR P-PSDB; AAY58597.
 XX
 PT New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used
 PT to produce transgenic plants with improved or altered growth
 PT characteristics.
 XX
 PS Claim 1; Fig 1; 42pp; English.
 XX
 CC This sequence represents cDNA encoding a runner bean gibberellin (GA) 2-
 CC oxidase, PGCA2ox1. This enzyme is a GA 2-beta-hydroxylase that acts on
 CC C19-GAs and for which 2-beta-hydroxylation is its only activity
 CC Hydroxylation at the 2-beta position of a GA results in a biologically
 CC inactive product, and is the most important route for GA metabolism in
 CC plants, ensuring that the active hormones do not accumulate in plant
 CC tissues. The nucleic acids can be used to transform plants so that
 CC gibberellin 2-oxidase can be constitutively over-expressed or otherwise
 CC enhanced to reduce the concentration of bioactive GAs in the plants and
 CC therefore to inhibit plant growth. Growth inhibition is useful in many
 CC agricultural and horticultural applications such as enhancing lodging-
 CC resistance and grain yield in cereals, improving seedling quality,
 CC reducing the growth of amenity grasses, reducing shoot growth in orchard
 CC and ornamental trees, improving tolerance to cold, drought and infection,
 CC and increasing yields (by the diversion of assimilates from vegetative to
 CC reproductive organs). The nucleic acids may also be used to induce male
 CC and/or female sterility (by expression in floral organs), prevent pre-
 CC harvest sprouting, reduce shoot growth in hedging plants, inhibit
 CC reversibility in the development or germination of seeds and reduce shoot
 CC growth in commercial wood species. Antisense constructs of the nucleic
 CC acids can also be used to transform plants to reduce the expression of GA
 CC 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set
 CC and growth in seedless grapes, citrus fruits and pears), improve skin
 CC texture and fruit shape in apples, increase stem length and therefore
 CC yield in sugar cane, increase yield and earliness in celery and rhubarb,
 CC improve malting yields and quality in cereals (particularly barley), and
 CC increase growth in woody species
 XX
 SQ Sequence 1318 BP; 358 A; 296 C; 282 G; 382 T; 0 U; 0 Other;

Alignment Scores:
 Score: 3,89e-180 Length: 1318
 Std. No.: 1748.00 Matches: 331
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-670-454-2 (1-331) x AA255912 (1-1318)

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 QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
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QY 101 GlyAspValGlyTrpValGlyTrpLeuLeuAenThrAenProAspValIleSerPro 120
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 QY 121 LysSerLeuCysIlePheArgGluAenProHisHisPheArgAlaValValGluAenTyr 140
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 QY 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
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 QY 161 IleArgGlnArgAenThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
 DB 548 ATAAGCAGAGAGAAATACGTTAAGCAGGTGCTGAAGGATGAGAAAGTGAATTCGTGCTTC 607
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 AC AA299471;
 DT 03-JUL-2000 (first entry)
 DE Soybean gibberellin acid 2-oxidase 1 cDNA sequence.
 KW Gibberellin acid; copalyl diphosphate synthase; 3beta-hydroxylase;
 KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
 KW seed germination; seedling growth; gibberellin biosynthetic pathway;
 KW transgenic plant; hypocotyl; epicotyl; ss.
 OS Glycine max.
 XX
 FH Key Location/Qualifiers
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 FT /product= "gibberellin acid 2-oxidase 1"
 FT /trans_except= (pos: 633..635, aa: Xaa)
 FT /note= "Xaa is an unspecified amino acid"
 XX

RESULT 3

AAZ99471

ID AAZ99471 standard; cDNA; 1359 BP.

XX

AC AA299471;

DT

DE 03-JUL-2000 (first entry)

XX

DE Soybean gibberellin acid 2-oxidase 1 cDNA sequence.

KW

KW Gibberellin acid; copalyl diphosphate synthase; 3beta-hydroxylase;
 KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
 KW seed germination; seedling growth; gibberellin biosynthetic pathway;
 KW transgenic plant; hypocotyl; epicotyl; ss.

XX

OS Glycine max.

XX

FH Key Location/Qualifiers

FT

FT 102..1103

FT

FT /tag= a

FT /product= "gibberellin acid 2-oxidase 1"

FT /trans_except= (pos: 633..635, aa: Xaa)

FT /note= "Xaa is an unspecified amino acid"

XX

PN W0200009722-A2.
 XX 24-FEB-2000.
 XX 10-AUG-1999; 99WO-US018066.
 XX 10-AUG-1998; 98US-0096111P.
 PR 07-JUN-1999; 99US-013797P.
 XX (MONS) MONSANTO CO.
 XX Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
 PI Filler KJ, Rao S, Ream JE;
 XX P-PSDB; AAY84039.
 DR WPI: 2000-224351/19.
 XX P-PSDB; AAY84039.
 XX Obtaining transgenic plant useful for controlling seed germination and
 PT seedling growth comprises transgene comprising a sequence expressing
 PT altered levels of an essential hormone.
 XX Claim 45; Page 248; 267pp; English.
 XX The present sequence encodes a gibberellic acid 2-oxidase 1 protein
 CC sequence, which is used in the method of the invention. The specification
 CC describes methods for the inhibition and control of gibberellic acid
 CC levels. Gibberellic acid levels may be inhibited or controlled by use of
 CC a chimeric expression construct expressing a RNA or protein which
 CC suppresses the gibberellin biosynthetic pathway sequence, diverts
 CC substrate from the pathway, or degrades pathway substrates or products.
 CC The methods uses copalyl diphosphate synthase, 3beta-hydroxylase, 2-
 CC oxidase, phytoene synthase, C-20 oxidase, and a 2beta,3beta-hydroxylase
 CC polynucleotides to achieve this. The method is used to control seed
 CC germination and seedling growth especially to regulate gene products of
 CC gibberellin biosynthetic pathway and restoration of normal seed
 CC germination, in transgenic plants. The plants produced are gibberellin
 CC deficient, and have shortened hypocotyl and/or epicotyl phenotypes
 CC compared to normal plants
 XX SQ Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;

Alignment Scores:
 Pred. No.: 2,05e-156 Length: 1359
 Score: 1530.50 Matches: 296
 Percent Similarity: 90.36% Conservative: 4
 Best Local Similarity: 89.16% Mismatches: 31
 Query Match: 87.56% Indels: 1
 DB: 3 Gaps: 1

US-10-670-454-2 (1-331) x AA299471 (1-1359)

QY 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
 Db 102 ATGGTTGTTCTGCTCAGCCAGCAATTAACACAGTTTTTCTCTGAAAAACATGACGCC 161
 QY 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
 Db 162 ACGCCCTTGTTCCGGGGATTCTGTGGTGCAGCTCAGGACCCCGATGCCAAGACCCAC 221
 QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
 Db 222 ATAGTCAATGCTGCAGGGACTTCGGCTTCTTCAAGCTCGTGAACACCGGTGTTCCGTTA 281
 QY 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuAArgPhePheLysLysSerGlnSerGlu 80
 Db 282 CAGTTTCATGGCCCAATTTGGAAAAACGAAACCCCTCGGGTTCTTCAAAAAACCTCAATCCGAG 341
 QY 81 LysAsnArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
 Db 342 AAAGACAGGGCTGGTCCCCCTGACCCCTTGGGTACGGCAGCAAGAGGATGGCCCTAAC 401
 QY 101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120

Db 402 GCGCATGTCGGTGGGTGGAATACCTCTTCTCAACACCAACCTGATGTCATCTCCCC 461
 QY 121 LysSerLeuCysIlePhePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr 140
 Db 462 AAGTCACAGTTTCATTTTCAGAGAGGTCTCTCAGAAATTTTCAGGGCGGTGGAGGATAC 521
 QY 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
 Db 522 ATTAGAGCGGTGAAGAACAATGTCTATGAGGTGTTGGAATTTGGAATTCAGGATGGGG 581
 QY 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
 Db 582 ATAACGACAGGAATGTGTTGAGTAGGTTCCTGAAGGATGAGAAGAGTCAATCTCTCTTC 641
 QY 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsn--ArgAsnLeuVal 199
 Db 642 AGACTTAAACCACTACCCGCCATGCCCGAGGTGCAAGCAATTAACGAAGGAATTTGGTT 701
 QY 200 GlyPheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSer 219
 Db 702 GGATTTGGAGAGACACACAGACCCACAGATAATTTCTGTCTTGAGATCTAACAGCACCTCA 761
 QY 220 GlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSer 239
 Db 762 GGCCTGCAAAATCTGTCTCAGATGGCACTTGGGTTTCTGTCCACCTGATCAAACTTCC 821
 QY 240 PhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerVal 259
 Db 822 TTTTTCATCAATGTTGGTGACACTCTTCAGGTAATGACTAATGAGGAGTTTAAAGTGTA 881
 QY 260 LysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGly 279
 Db 882 AAGCATAGAGTTTGGCTGACCCCAACCAAGTCAAGTTGTCATGATCTACTTTGGAGCA 941
 QY 280 ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCys 299
 Db 942 CCACCCCTTGTGTGAAAAAGATAGCACCTTTACCTTCACTCATGTAAAGAGAGAGAGT 1001
 QY 300 LeuTyrLysGluPheThrTrpCysGluTyrLysAlaAlaTyrThrSerArgLeuAla 319
 Db 1002 TTCTCAAAAGAGTTCACATGGTGGGAATACAAGAGCTGCGTACCGTCAAGGCTAGCG 1061

RESULT 4
 AAD40261
 ID AAD40261 standard; cdNA; 1359 BP.
 XX AAD40261;
 AC AAD40261;
 XX 22-OCT-2002 (first entry)
 DT 1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCT 1097
 DE Soybean GA 2-oxidase 1 cDNA.
 XX Gibberellin; transgenic plant; seed germination; seedling growth;
 KW transgenic; 2-oxidase 1; enzyme; GA; soybean; gene; ss.
 XX Glycine max.
 OS
 FH Key Location/Qualifiers
 FT CDS 102..1103
 FT /*tag= a
 FT /product= "GA 2-oxidase 1 protein"
 FT /transl_except= (pos:633..635, aa:xaa)
 FT /note= "xaa = any amino acid"
 XX US2002053095-A1.
 PN
 XX 02-MAY-2002.
 XX 10-AUG-1999; 99US-00371307.
 PF

XX 10-AUG-1999; 99US-00371307.
 XX (BROW/) BROWN S M.
 XX Brown SM, Ellich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
 XX Pillier KJ, Rao S, Ream JE;
 XX WPI; 2002-489107/52.
 DR P-PSDB; AAE24921.
 XX Control of gibberellin levels in plants useful to avoid unfavorable
 PT conditions in crops to increase yields, using transgenic plants having
 PT reduced seed germination and early seedling growth then treatment to
 PT restore these properties.
 XX Claim 45; Page 92-93; 155pp; English.
 XX The invention relates to control of gibberellin (GA) levels in plants.
 CC The method involves producing transgenic plants having a phenotype of
 CC reduced seed germination and reduced early seedling growth, then
 CC restoring seed germination and early seedling growth by treating plants
 CC with an appropriate compound when conditions are favourable. The method
 CC is useful to control seed germination and/or early seedling growth in
 CC agricultural production so that unfavorable environmental conditions
 CC normally reducing agronomic output can be avoided and yields increased.
 CC Plants also demonstrate increased uniformity of germination, emergence
 CC and seedling vigor, so increasing yields at harvest. The method is
 CC especially useful in crop plants such as e.g. canola, soybean, cotton,
 CC etc., and is also useful in storage and transport of seeds to reduce
 CC premature germination which may affect agronomic or food quality of the
 CC seeds. The present sequence is soybean GA 2-oxidase 1 cDNA
 XX Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;
 SQ

Alignment Scores:

Pred. No.: 2,05e-156 Length: 1359
 Score: 1530.50 Matches: 296
 Percent Similarity: 90.36% Conservative: 4
 Best Local Similarity: 89.16% Mismatches: 31
 Query Match: 87.56% Indels: 1
 DB: 6 Gaps: 1

US-10-670-454-2 (1-331) x AAD40261 (1-1359)

QY 1 MetValValLeuSerGlnProAlaLeuAenGlnPhePheLeuLeuLysProPheLysSer 20
 DB 102 ATGGTTGTCTGTCTCAGCCGACATTAAACCAAGTTTCTCTTCTGAAACATGCAAGCCC 161
 QY 21 ThrProLeuPheThrGlyLeuProValValAspLeuThrHisProAspAlaLysAsnLeu 40
 DB 162 AGCCCTTGTTCGGGGGATTCCTGTGTGACCTCAGGACCCGATGCCAAGCCAC 221
 QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
 DB 222 ATAGTCAATGCTCGACGGACCTCGGCTTCTTCAAGCTCGTGAACCAACGCTGTTCGTTA 281
 QY 61 GluLeuMetAlaAsnLeuGluAenGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
 DB 282 CAGTTTCATGGCCAAATTTGGAAACGAAACCCCTCGGGTCTTCAAAACCACTCAATCCGAG 341
 QY 81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
 DB 342 AAAGACGGCTGTGTCCTCCCTGACCTTTGGCTACGGCAGCAAGAGGATTCGCCCTAAC 401
 QY 101 GlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
 DB 402 GCGATGTCGGTGGTTCGATACCTCTTCTCAACCAACCAACCTGATGTATCTCCCC 461
 QY 121 LysSerLeuCysIlePheArgGluAenProHisPheArgAlaValValGluAenTyr 140
 DB 462 AAGTCACAGTTCATTTTCAGAGAAGGTCCTCAGAAATTCAGGCGGTGGTGGAGGAATAC 521

QY 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGlyLeuGly 160
 DB 522 ATTAGAGCGGTGAAGAACATGTCTATGAGGTGTGGAAATGATGGCTGAGGATTTGGG 581
 QY 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
 DB 582 ATAACGCGAGAGGATGTGTTCGATAGTGTTCGTAAGGATGAGAAGAGTGATCTTGTCTTC 641
 QY 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAen---ArgAsnLeuVal 199
 DB 642 AGACTTAACCACTACCCGCCATGCCCGAGGTGCAAGCATTGAACGGAAGGAATTTGGTT 701
 QY 200 GlyPheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSer 219
 DB 702 GGATTTGGAGAGCACACAGACCCACAGATAATTTCTGTCTTGAGATCTTAACAGCACCTCA 761
 QY 220 GlyLeuGlnIleCysLeuThrAspGlyThrTyrValSerValProProAspGlnThrSer 239
 DB 762 GGCCTGCAAACTGTCTCAGATGGCACTTGGGTTTCTGCTCCACCTGATCAAACTTCC 821
 QY 240 PhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerVal 259
 DB 822 TTTTTCATCAATGTTGGTGACACTCTTCAGGTATGACTAATGGGAGGTTTAAAGTGTA 881
 QY 260 LysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGly 279
 DB 882 AAGCATAGAGTTTGGCTGACCCCAACCAAGTCAAGTTGTCAATGATCTACTTTGGAGGA 941
 QY 280 ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluCys 299
 DB 942 CCACCTTGTGTGAAGATAGCACCTTTACCTTCATCATGTTAAAGGAGGAAGAGAGT 1001
 QY 300 LeuTyrLysGluPheThrTyrCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAla 319
 DB 1002 TTCTACAAAGAGTTCACATGGTGGGAATACAAGAGGCTCGCTACGCTCAAGCTAGCG 1061
 QY 320 AspAsnArgLeuAlaProPheGlnLysSerAlaAla 331
 DB 1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCT 1097
 RESULT 5
 ABZ13545
 ID ABZ13545 standard; DNA; 1026 BP.
 XX AC ABZ13545;
 XX DT 21-JAN-2003 (first entry)
 XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1350.
 XX KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX OS Arabidopsis thaliana.
 XX PN WO200216655-A2.
 XX PD 28-FEB-2002.
 XX PF 24-AUG-2001; 2001WO-US026685.
 XX PR 24-AUG-2000; 2000US-0227866P.
 XX PR 26-JAN-2001; 2001US-0264647P.
 XX PR 22-JUN-2001; 2001US-0300111P.
 XX PA (SCRI) SCRIPPS RES INST.
 XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX PI Harper JF, Kreps J, Wang X, Zhu T;
 XX WPI; 2002-304127/34.
 PT Identifying a stress condition to which a plant cell has been exposed and
 PT producing plants with increased tolerance to these abiotic stresses.

XX Claim 144; SEQ ID NO 1350; 577pp + Sequence Listing; English.
 PS The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising: (a) contacting nucleic acid
 CC representative of expressed polynucleotides in the plant cell with an
 CC array or probes representative of the plant cell genome; and (b)
 CC detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
 CC in methods of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office

XX Sequence 1026 BP; 274 A; 242 C; 251 G; 259 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7.39e-109 Length: 1026
 Score: 1092.50 Matches: 210
 Percent Similarity: 76.81% Conservatives: 45
 Best Local Similarity: 63.25% Mismatches: 72
 Query Match: 62.50% Indels: 5
 DB: 6 Gaps: 3

US-10-670-454-2 (1-331) x ABZ13545 (1-1026)

QY 1 MetValValLeuSerGlnProAlaLeu-----AsnGlnPheLeuLeuLysProPhe 18
 DB 1 ATGGTGGTTTGGCCACAGCCAGTCACCTTTAGATAAACACATCTCCCTAATCCCCACATAC 60
 QY 19 LysSerThrProLeuPheThr-----GlyIleProValValAspLeuThrHisProAsp 36
 DB 61 AAACGGTTCGGGTTCTCCTCCCAATCAATCCCGTCGTCACCTAGCCGATCCGGAA 120
 QY 37 AlaLysAsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHis 56
 DB 121 GCGAAACCCGATCGTAAAGCTCGGAGAGTTCTGGGTTCTTCAAGGTGCTAAACAC 180
 QY 57 GlyValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLys 76
 DB 181 GGAGTCGCGACCCGATCATGACTCGGTTAGAGCAGGAGCTATTGGCTTCTTCGGCTTG 240
 QY 77 SerGlnSerLysLeuValAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArg 96
 DB 241 CCTCAGTCCTTAAACCCGGGCGGTCACCTGACCGTACGTTATGGTAAATAACCG 300
 QY 97 IleGlyProAsnGlyAspValGlyTyrValGluTyrLeuLeuAsnThrAsnProAsp 116
 DB 301 ATTGGACCAACCGTGCAGTTGGTTGGATTGAGTATCTCTCTCAATGCTAATCTCAG 360
 QY 117 ValIleSerProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaVal 136
 DB 361 CTCTCCTCTCTAAACCTCCGCGGTTCTCCGTCACCAACCCCTCAAAATTTCCGTCAGTCG 420
 QY 137 ValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAla 156
 DB 421 GTGGAGGAGTACATGAGGAGATTAAAGGAGTCTGTCACAAAGTGTGGAGATGGTTGCC 480
 QY 157 GluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSer 176
 DB 481 GAAGAATAGGATAGACCCAGGACACTCTGAGTAAATGCTGAGATGAGATGAGAGAT 540
 QY 177 AspSerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArg 196
 DB 541 GACTCGTCTGAGACTAAACCATTTATCCGCGCGGAGGAA--GAGCGCGGAGAGATG 597
 QY 197 AsnLeuValGlyPheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsn 216
 DB 598 GTGAAGTGGGGTTGGGGAACACACAGACCCACAGATAATCTCAGTGTCAAGATCTAAT 657
 QY 217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTyrValSerValProAsp 236

DB 658 AACACGGCGGCTCTTCAAAATCTGTGTGAAAGATGGAAGTGGGTCCCTGCTCCCTCGAT 717
 QY 237 GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
 DB 718 CACTCTCTCTTCTTCAATTAATGTTGGAGATGCTCTTCAGGTTATGACTAACGGGAGGTT 777
 QY 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyr 276
 DB 778 AAGAGTGTAAACACAGGCTCTTAGCCGATACACAGGAGATCCAGGATTTCAATGATAT 837
 QY 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296
 DB 838 TTCCGCGGACCGCATTTAGCCAGAAGATCGCACCATTCGCTTGTCCCTGAGCAA 897
 QY 297 GluGluCysLeuTyrLysGluPheThrTyrCysGluTyrLysLysAlaAlaTyrThrSer 316
 DB 898 GATGATTGGCTTTTACAAAGAAATTCATCTGGTCTCAATACAAATCTTCTGCTTACAAGTCT 957
 QY 317 ArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
 DB 958 AAGCTTGGTATATAGACTTGGTCTCTTTGAGAAA 993
 AC ADA67975
 ID ADA67975 standard; DNA; 1026 BP.
 AC ADA67975;
 DT 20-NOV-2003 (first entry)
 XX Arabidopsis thaliana gene, SEQ ID 223.
 DE Plant; bacterial infection; fungal infection; viral infection; ds.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 PN WO2003000898-A1.
 XX 03-JAN-2003.
 PD 22-JUN-2001; 2001WO-IB001105.
 PF 22-JUN-2001; 2001WO-IB001105.
 PR 22-JUN-2001; 2001WO-IB001105.
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX WPI; 2003-175290/17.
 DR Identifying at least one gene involved in plant resistance or response to
 XX pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.
 XX Claim 6; SEQ ID NO 223; 899pp; English.
 PS The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.
 XX Sequence 1026 BP; 274 A; 242 C; 251 G; 259 T; 0 U; 0 Other;
 SQ Alignment Scores:

Pred. No.:	7.39e-109	Length:	1026
Score:	1092.50	Matches:	210
Percent Similarity:	76.81%	Conservative:	45
Best Local Similarity:	63.25%	Mismatches:	72
Query Match:	62.50%	Indels:	5
DB:	8	Gaps:	3

US-10-670-454-2 (1-331) x ADA67975 (1-1026)	
Qy	1 MetValValLeuSerGlnProAlaLeu-----AsnGlnPhePheLeuLeuLysProPhe 18
Db	1 ATGGTGGTTTTGCCACGCCAGTCACCTTTAGATAACCAACATCTCCCTTAATCCCCACATAC 60
Qy	19 LysSerThrProLeuPheThr-----GlyIleProValValAspLeuThrHisProAsp 36
Db	61 AAACCGGTTCCGGTCTCACCTTCCCATTTCAATCCCGCTCGTCAACCTACCGCATCCGGAA 120
Qy	37 AlaLysAsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHis 56
Db	121 CGGAAACCCGAAATCGTAAAGCCTCGCAGGAGTTCGGGTCTTCAAGGTCGTAAACCA 180
Qy	57 GlyValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLys 76
Db	181 GGAGTCCGACCCGAACCTCATGACTCGGTAGACGAGGAGGCTATTGGCTTCTTCGGCTTG 240
Qy	77 SerGlnSerGluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArg 96
Db	241 CCTCAGTCTCTTTAAACACCGGCGCGGTCCACCTGAACCGGTACGGTATGGTAAATAAACGG 300
Qy	97 IleGlyProAsnGlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAsp 116
Db	301 ATTGGACCAACCGGTGAGTGGTGGATTGATGTATCTCTCTCAATGCTTAATCCTCAG 360
Qy	117 ValIleSerProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaVal 136
Db	361 CTCCTCTCTCTCTAAACCTCGCGCGGTTTTCCGTCAAAACCCCTCAAAATTTCCGTGAGTCG 420
Qy	137 ValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAla 156
Db	421 GTGAGGAGTACATGAAGGAGATTAAGGAAGTTCGTACAGGTGTGGAGATGGTTGCC 480
Qy	157 GluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLysAspGluLysSer 176
Db	481 GAAGAACTAGGGATAGACCAAGGGACACTCTGAGTAAAAATGCTGAGAGATCAGAAGAGT 540
Qy	177 AspSerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArg 196
Db	541 GACTCGTGCCTTGAGACTAAACCATTTATCCGGCGCGCGAGGAA--GAGCGGAGAGAGATG 597
Qy	197 AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn 216
Db	598 GTGAAGGTGGGTTTTGGGGAACACACAGACCCACAGATAATCTCAGTGTCTAAGATCTAAT 657
Qy	217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTyrValSerValProProAsp 236
Db	658 AACACGGCGGGTCTTCAAAATCTGTGTGAAGATGGAAGTTGGGTTCGTCTCTCTCTCTGAT 717
Qy	237 GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
Db	718 CACTCTCTCTTCTTCATTAATGTTGGAGATGCTCTTTCAGGTTTATGACTAACCGGAGGTTTC 777
Qy	257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyr 276
Db	778 AAGAGTGTTTAAACACAGGGTCTTTACCCGATACAGGAGATCGAGGATTTCAATGATATAT 837
Qy	277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296
Db	838 TTCGCGGACCGCATTCAGCCAGAAGATCGCACCATTCGCATTCCTGTCTCTCTGAGCAA 897
Qy	297 GluGluCysLeuTyrLysGluPheThrTyrCysGluTyrLysGlyAlaAlaTyrThrSer 316
Db	898 GATGATTGGCTTTACAAAGAAATTCACTGGTCTCAATCAAAATCTTCTGCTTACAGTCT 957

Qy	317	ArgLeuAlaAspAsnArgLeuAlaProPheGlnIlys	328
Db	958	AAAGCTTGGTGATTATAGACTTGGTCTCTTTGGAAA	993
RESULT 7			
AAZ55916			
ID	AAZ55916	standard; cDNA; 1237 BP.	
XX	AAZ55916;		
AC			
XX	10-APR-2000	(first entry)	
DT			
XX	Arabidopsis thaliana	gibberellin 2-oxidase AtGA2ox2	CDNA.
DE			
XX	Gibberellin 2-oxidase; AtGA2ox2; 2-beta-hydroxylation; inactivation; growth inhibition; ss.		
KW			
XX	Arabidopsis thaliana.		
OS			
XX	Key	Location/Qualifiers	
FH	CDS	109..1134	
FT	FT	/*tag= a	
FT	FT	/product= "Gibberellin 2-oxidase AtGA2ox2"	
XX	W09966029-A2.		
XX	23-DEC-1999.		
XX	11-JUN-1999;	99WO-GB001857.	
XX	12-JUN-1998;	98GB-00012821.	
PR	15-JUL-1998;	98GB-00015404.	
XX	(UYBR-) UNIV BRISTOL.		
XX	Thomas SG, Hedden P, Phillips AL;		
XX	WPI; 2000-097742/08.		
DR	P-PSDB; AAY58599.		
XX	New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, to produce transgenic plants with improved or altered growth characteristics.		
PT			
FT			
PT			
XX			
PS	Example 3; Fig 7; 42pp; English.		
XX			
CC	This sequence represents cDNA encoding an Arabidopsis thaliana gibberellin (GA) 2-oxidase, PGCAox2. This enzyme is a GA 2-beta-hydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is its only activity. Hydroxylation at the 2-beta position of a GA results in a biologically inactive product, and is the most important route in GA metabolism in plants, ensuring that the active hormones do not accumulate in plant tissues. The nucleic acids can be used to transform plants so that gibberellin 2-oxidase can be constitutively over-expressed or otherwise enhanced to reduce the concentration of bioactive GA in plants and therefore to inhibit plant growth. Growth inhibition is used in many agricultural and horticultural applications such as enhancing lodging-resistance and grain yield in cereals, improving seedling quality, reducing the growth of amenity grasses, reducing shoot growth of orchard and ornamental trees, improving tolerance to cold, drought or infection, and increasing yields (by the diversion of assimilates for vegetative to reproductive organs). The nucleic acids may also be used to induce male and/or female sterility (by expression in floral organs) to prevent pre-harvest sprouting, reduce shoot growth in hedging plants, inhibit reversibility in the development or germination of seeds and reduce shoot growth in commercial wood species. Antisense construction of the nucleic acids can also be used to transform plants to reduce the expression of GA 2-oxidase (claimed) to promote plant growth, (e.g. improve fruit set and growth in seedless grapes, citrus fruits and pears), improve skin texture and fruit shape in apples, increase starch length and therefore yield in sugar cane, increase yield and earliness of celery and rhubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species		

XX	SQ	Sequence 1237 BP; 356 A; 277 C; 280 G; 324 T; 0 U; 0 Other;
Alignment Scores:		
Pred. No.:	9 66e-109	Length: 1237
Score:	1092.50	Matches: 210
Percent Similarity:	76.81%	Conservative: 45
Best Local Similarity:	63.25%	Mismatches: 72
Query Match:	62.50%	Indels: 5
DB:	3	Gaps: 3
US-10-670-454-2 (1-331) x AAZ55916 (1-1237)		
Qy	1	MetValValLeuSerGlnProAlaLeu-----AsnGlnPhePheLeuLeuLysProPhe 18
Db	109	ATGGTGGTTTGGCCACAGCCAGTCACTTTAGATAACCATCTCCCTAATCCCCACATAC 168
Qy	19	LysSerThrProLeuPheThr-----GlyIleProValValAspLeuThrHisProAsp 36
Db	169	AAACCGGTTCCGGTCTCTCACTCCCATTCATATCCCGTCGTCACACTAGCCGATCCGAA 228
Qy	37	AlaLysAsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHis 56
Db	229	GCAGAAACCCGATCGTAAAGCGTCGAGAGTTCGGGTCTTCAAGAGTCGTAACCCAC 288
Qy	57	GlyValProLeuLeuMetAlaAsnLeuGluAsnGluAlaLeuAlaPhePheLysLys 76
Db	289	GGAGTCGACCCGAACTCATGACTCGTTAGAGCAGGAGGCTATTTGGCTCTTCGCGTTG 348
Qy	77	SerGlnSerGluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArg 96
Db	349	CCTCAGTCTCTTAAAAACCGGCGCGTCCACCTGAACCGTACCGGTTATGGTAAATAACGG 408
Qy	97	IleGlyProAsnGlyAspValGlyTyrValGlyTyrLeuLeuLeuAsnThrAsnProAsp 116
Db	409	ATTGGACCAACAGCGTACGCTGGTGGATTTAGATATCTCCTCCTCAATGCTTAATCCCTCAG 468
Qy	117	ValIleSerProLysSerLeuCysIlePheArgGluAsnProHisPheArgAlaVal 136
Db	469	CTCTCTCTCTTAAAAACCTCCGCGGTTTCGTCGTAACCCCTCAAAATTTTCGTCAGTCG 528
Qy	137	ValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAla 156
Db	529	GTGGAGGAGTACATGAAGAGAGATTAAGGAAGTGTCTGTAACAGGTGTTGGAGATGTTGCC 588
Qy	157	GluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSer 176
Db	589	GAAGAACTAGGGATAGACCAAGGGACACTCTGAGTAAATGCTGAGAGATGAGAAGAGT 648
Qy	177	AspSerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArg 196
Db	649	GACTCGTGCCTGAGACTAAACCAATATCCGGCGGGAGGAA---GAGCGGAGAGATG 705
Qy	197	AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn 216
Db	706	GTCAAGGTGGGGTTTGGGGAACACACAGACCCACAGATAATCTCAGTCTTAAGATCTAAT 765
Qy	217	SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTyrValSerValProProAsp 236
Db	766	AACACGGCGGGTCTTCAAAATCTGTGTGAAGATGGAAGTTGGGTGCGCTGCTCCCTCGAT 825
Qy	237	GlnThrSerPheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
Db	826	CATCTCTCTTCTTCATTATGTGTGAGAGTCTTTCAGTTATGACTTAACGGGAGGTTTC 885
Qy	257	LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLysSerMetIleTyr 276
Db	886	AAGAGTGTAAACACAGGGTCTTAGCCGATACAGAGAGATCGAGATTTCAATGATATAT 945
Qy	277	PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLysGly 296
Db	946	TTGCGGGGACCGGCATTGAGCCAGAGATCGCACCATTTGCCATTGCGCTTGTCCCTGAGCAA 1005

3-beta hydroxylase, Riboflavin specific deaminase, Ethylene response factor, Acyl-CoA thioesterase II, ABC transporter GCN20-like, P-glycoprotein I, P-glycoprotein 3, P-glycoprotein ATPGP, P-glycoprotein HVMR2, ABC transporter, PMP70 ABC transporter and MRP4 ABC transporter. The nucleic acid fragments may be used to create transgenic plants where the polypeptides are present at higher or lower levels than normal or in cell types or in developmental stages in which they are not normally found. The polynucleotides can be used as probes for genetically and physically mapping genes and as markers for traits linked to those genes. The nucleic acid fragments may be used as restriction fragment length polymorphism (RFLP). It can also be used to probe Southern blots containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. The nucleic acid fragments may also be used as hybridisation probes against PCR amplification products generated from the mutation population using the mutation tag sequence primer in conjunction with an arbitrary genomic site primer. The peptides can also be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides or proteins comprising the amino acid sequences. Antibodies are useful for detecting the polypeptides in situ in cells or in vitro in cell extracts. The present sequence encodes a plant metabolism protein (or fragment).

XX Sequence 1352 BP; 439 A; 255 C; 243 G; 415 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.53e-106 Length: 1352
Score: 1068.50 Matches: 201
Percent Similarity: 77.95% Conservative: 57
Best Local Similarity: 60.73% Mismatches: 68
Query Match: 61.13% Indels: 5
DB: 12 Gaps: 2

US-10-670-454-2 (1-331) x ADM94213 (1-1352)

Qy 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
Db 159 ATGGTGTGGTGGTCCAAAGCAACACAGAACAAATCTCTCATTAAGAACTGCATGCCA 218
Qy 21 ThrProLeuPheThrGlyLeuProValValAlaPheLeuThrHisProAspAlaLysAsnLeu 40
Db 219 ACCAAATTTCTCAACAAATTCCTCAATAGTGGACCTCTCAACCTGATGCAAGACCTT 278
Qy 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
Db 279 ATAGTGAAGCTTGTGAGGAGTTGGATTCTTCAAGTCATCAATCATGGTGTCTCCATG 338
Qy 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
Db 339 GAAGCTATATCCGAATTGGAAATATGAAGCCTTCAAAATCTCTCTATGCTCAATGAA 398
Qy 81 LysAspArgAlaGlyProProAspPheGlyTyrGlySerLysArgIleGlyProAsn 100
Db 399 AAGGAAATAGTAGACCTCCCAATCCATTTGGTATGGTAGCAAGAAATTTGACACAA 458
Qy 101 GlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
Db 459 GGGGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 506
Qy 121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
Db 507 CACAACCTCTCTGTTTATGGGAAAAACCCCTGAGAAATTCAGGTGTCTGTGTAACAGTTAC 566
Qy 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
Db 567 ATGCTCTCTGTGGAAGATGTCATGTGAGATTTCTGAGTTGATGTCAGAGAGGTGAAG 626
Qy 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
Db 627 ATTCAGCAAAAGGATGTGTTAGCAAGCTCTTAATGGATATAACAAAGTGACTCTATTTC 686
Qy 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200

Db 587 AGGTGAATCATTTACCTGCTTGTCTCGAATGACTCTGATGATCAGAACTTGATTGGG 746
Qy 201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGly 220
Db 747 TTTGGAGAACACACAGAGCCCAAAATCATCTCTCTGTTAAGATCCACACACTTCAGGC 806
Qy 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhe 240
Db 807 CTTTCAAGATTATCTTAGAGATGGAAATTTGGATTTCAGTCCCAACAGATGACAAATCCTTT 866
Qy 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
Db 867 TTTATTAACGTGGTGGTATCTCTTCAGGTTATGACAAATGGAAGTCCGAAGTGTGAGA 926
Qy 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
Db 927 CACAGAGTGTGGCAAAATGGGTTTCAAGTCCAGGCTTTCAATGATTTACTTTGGAGGTCCA 986
Qy 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
Db 987 CTTTGTGATGAGAAATAGACCACTTATCTCTCTCATG---AAAGGAAAGAAAGTCTTA 1043
Qy 301 TyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp 320
Db 1044 TATAAAGAGTTTACTCTGTTGAGTACAAATAATCAATCTACGGTTCAGATTATCTATA 1103
Qy 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
Db 1104 AATAGACTTGAACATTTTGAAGAAGATTCAGCT 1136
RESULT 9
ADM94205
ID ADM94205 standard; cDNA; 1365 BP.
AC ADM94205;
XX 17-JUN-2004 (first entry)
XX Soybean Dioxygenase cDNA #1.
Soybean; ss; plant; plant metabolism;
GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase;
Dioxygenase; Ent-Kaurene Synthase A; GA-20 oxidase;
Gibberellin 3-beta hydroxylase; Riboflavin specific deaminase;
Ethylene response factor; Acyl-CoA thioesterase II;
ABC transporter GCN20-like; P-glycoprotein I; P-glycoprotein 3;
P-glycoprotein ATPGP; P-glycoprotein HVMR2; ABC transporter;
PMP70 ABC transporter; MRP4 ABC transporter; transgenic.
Glycine max.
OS US6677502-B1.
XX 13-JAN-2004.
XX 12-JUL-2000; 2000US-00614912.
XX 12-JUL-1999; 99US-0143401P.
PR 12-JUL-1999; 99US-0143412P.
PR 30-JUL-1999; 99US-0146650P.
PR 15-DEC-1999; 99US-0170906P.
PR 21-DEC-1999; 99US-0172946P.
PR 21-DEC-1999; 99US-0172959P.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX Allen SM, Kinney AJ, Rafalski JA, Orozco EM, Miao G, Famodu OO;
PI Lee J, Lohman KN, Rendina AR, Sakai H, Weng Z, Caimi PG, Fang Y;
PI Shen JB, Zoughi IL, Anderson SL, Shi J, Lu G, Helentjaris TG;
PI Li CP;
XX WPI; 2004-088430/09.

DR P-PSDB; ADM94206.
XX New isolated GTP cyclohydrolase II/3, 4-dihydroxy-2-butanone-4-phosphate
PT synthase nucleic acid and proteins, useful for creating transgenic plants
PT where polypeptides are present at higher or lower levels.
XX
PS Example 3; SEQ ID NO 5; 186pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a
CC nucleotide sequence encoding a polypeptide having GTP cyclohydrolase
CC II/3, 4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing as
CC ADM94266. Also included are a vector comprising the polynucleotide, a
CC recombinant DNA construct comprising the polynucleotide operably linked
CC to at least one regulatory sequence, transforming a cell with the
CC polynucleotide, a cell comprising the recombinant DNA construct,
CC producing a plant (comprising transforming a plant cell with the
CC polynucleotide and regenerating a plant from the transformed plant cell),
CC a plant comprising the recombinant DNA construct and a seed comprising
CC the recombinant DNA construct. Also disclosed as new are nucleic acid
CC (cDNA) fragments and assembled contigs encoding plant metabolism proteins
CC chosen from GTP cyclohydrolase II/3, 4-dihydroxy-2-butanone-4-phosphate
CC synthase, dioxynase, Ent-kaurene Synthase A, GA-20 oxidase, Gibberellin
CC 3-beta hydroxylase, riboflavin specific deaminase, Ethylene response
CC factor, Acyl-CoA thioesterase II, ABC transporter GCN20-like, P-
CC glycoprotein 1, P-glycoprotein 3, P-glycoprotein ATPGP, P-glycoprotein
CC HvMDR2, ABC transporter, PMP70 ABC transporter and MRP4 ABC transporter.
CC The nucleic acid fragments may be used to create transgenic plants where
CC the polypeptides are present at higher or lower levels than normal or in
CC cell types or in developmental stages in which they are not normally
CC found. The polynucleotides can be used as probes for genetically and
CC physically mapping genes and as markers for traits linked to those genes.
CC The nucleic acid fragments may be used as restriction fragment length
CC polymorphism (RFLP). It can also be used to probe Southern blots
CC containing restriction endonuclease-treated genomic DNAs of a set of
CC individuals representing parent and progeny of a defined genetic cross.
CC The nucleic acid fragments may also be used as hybridisation probes
CC against PCR amplification products generated from the mutation population
CC using the mutation tag sequence primer in conjunction with an arbitrary
CC genomic site primer. The peptides can also be used to immunise animals to
CC produce polyclonal or monoclonal antibodies with specificity for peptides
CC or proteins comprising the amino acid sequences. Antibodies are useful
CC for detecting the polypeptides in situ in cells or in vitro in cell
CC extracts. The present sequence encodes a plant metabolism protein (or
CC fragment).
XX
SQ Sequence 1365 BP; 448 A; 258 C; 244 G; 415 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3, 42e-105 Length: 1365
Score: 1060.50 Matches: 200
Percent Similarity: 77.64% Conservative: 57
Best Local Similarity: 60.42% Mismatches: 69
Query Match: 60.67% Indels: 5
DB: 12 Gaps: 2

US-10-670-454-2 (1-331) x ADM94205 (1-1365)

QY 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLeuSerProPheLeuSer 20
Db 166 ATGGTGTGTTGTCCTCAAGCAACCAACAGAACATATCTCTTACATTAAGAACCTGCATGCCA 225

QY 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLeuAsnLeu 40
Db 226 ACCAAATTTTCTCAACATTCCTAGTGGACCTCTCCAAACCTGATGCNAGACCTT 285

QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHisGlyValProLeu 60
Db 286 ATAGTGAAGGCTGTGAGGAGTTGATCTCTTCAAAGTCATCAATCATGTGTCTCCATG 345

QY 61 GluLeuMetAlaAsnLeuGluAsnGlnAlaLeuArgPhePheLeuSerGlnSerGlu 80
Db 346 GAAGCTATATCCGAATTGGAATATGAAGCCCTCAAAATTTCTTCTATGTCACCTCAATGAA 405

QY 81 LysAspArgAlaGlyProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
Db 406 AAGGAAAAAGTAGGACCTCCCAATCCATTTGGTATGGTAGCAGAAAAATTCGACACAT 465

QY 101 GlyAspValGlyTyrValGluTyrIleLeuLeuAsnThrAsnProAspValIleSerPro 120
Db 466 AGGACGTTGGTGGATTGATGATCTTCTTCAACACCAATCAAGAA----- 513

QY 121 LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr 140
Db 514 CACAACCTCTCTGTTTATGGCAAAACCTCGAATAATTCAGGTGTCTGTTGACAGTTAC 573

QY 141 IleThrAlaValLeuAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
Db 574 ATGCTCTCTGTCGAGCAAGATGTCATGTGAGATTCTTGTAGTTGATGCGACAGGGTTGAAG 633

QY 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLeuAspGluLysSerAspSerCysPhe 180
Db 634 ATTACGCAAAAGGATGTGTTTAGCAAGCTTCTTAATGGATATAAAGTAGTACTCTATTTC 693

QY 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
Db 694 AGGGTGAATCATTCCTGCTGTCTGAAATGACTCTCAATGATCAGAACTTGATGGG 753

QY 201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGly 220
Db 754 TTTGAGAAACACACAGACCCACAAATCATCTCTGTTAAGATCCAAACACACTTCAGGC 813

QY 221 LeuGlnIleCysLeuThrAspGlyThrTyrValSerValProAspGlnThrSerPhe 240
Db 814 CTTCAAGTTTATCTTAGAGATGCAATTTGGATTTCAGTCCCAACAGATCAAAATCCTTT 873

QY 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
Db 874 TTTATTACGTTGGTGATCTCTTCAGTTATGACAAATGAAGGTTCGAAAGTGTGAGA 933

QY 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
Db 934 CACAGAGTTTGGCAAAATGGGTTCAAGTCCAGCTTTCATCAATGATTTACTTTGGAGGTCCA 993

QY 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
Db 994 CTTTGTAGTGAATAATAGCACCATTTATCTCTCTCATG---AAAGGAAAGAAAGTCTA 1050

QY 301 TyrLysGluPheThrTyrCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp 320
Db 1051 TATAAAGAGTTTACTCTGTTTGATGACAAAAAATCAATCTACGTTCAAGATTATCTAA 1110

QY 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
Db 1111 AATAGACTTGAACATTTTGAAGAATTGCGACT 1143

RESULT 10
AAZ99472
ID AAZ99472 standard; cDNA; 1403 BP.
XX
AC AAZ99472;
XX
DT 03-JUL-2000 (first entry)
XX
DE Soybean gibberellic acid 2-oxidase 2 cDNA sequence.
XX
KW Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
KW seed germination; seedling growth; gibberellin biosynthetic pathway;
KW transgenic plant; hypocotyl; epicotyl; ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 149..1129
FT /tag= a
FT /product= "gibberellic acid 2-oxidase 2"

XX WO200009722-A2.
 PN 24-FEB-2000.
 XX 10-AUG-1999; 99WO-US018066.
 XX 10-AUG-1998; 98US-0096111P.
 PR 07-JUN-1999; 99US-0137977P.
 XX (MONS) MONSANTO CO.
 XX Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
 PI Piller KJ, Rao S, Ream JE;
 XX WPI; 2000-224351/19.
 DR P-PSDB; AAY84100.
 XX
 PT Obtaining transgenic plant useful for controlling seed germination and
 PT seedling growth comprises transgene comprising a sequence expressing
 PT altered levels of an essential hormone.
 XX
 PS Claim 45; Page 250; 267pp; English.
 XX The present sequence encodes a gibberellic acid 2-oxidase 2 protein
 CC sequence, which is used in the method of the invention. The specification
 CC describes methods for the inhibition and control of gibberellic acid
 CC levels. Gibberellic acid levels may be inhibited or controlled by use of
 CC a chimeric expression construct expressing a RNA or protein which
 CC suppresses the gibberellin biosynthetic pathway sequence, diverts
 CC substrate from the pathway, or degrades pathway substrates or products.
 CC The methods uses copoly diphosphate synthase, 3beta-hydroxylase, 2-
 CC oxidase, phytoene synthase, C-20 oxidase, and a 2beta,3beta-hydroxylase
 CC polynucleotides to achieve this. The method is used to control seed
 CC germination and seedling growth especially to regulate gene products of
 CC gibberellin biosynthetic pathway and restoration of normal seed
 CC germination, in transgenic plants. The plants produced are gibberellin
 CC deficient, and have shortened hypocotyl and/or epicotyl phenotypes
 CC compared to normal plants
 XX
 SQ Sequence 1403 BP; 440 A; 269 C; 261 G; 433 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4,03e-105 Length: 1403
 Score: 1060.00 Matches: 200
 Percent Similarity: 76.44% Conservatives: 53
 Best Local Similarity: 60.42% Mismatches: 72
 Query Match: 60.64% Indels: 6
 DB: 3 Gaps: 3

US-10-670-454-2 (1-331) x AA299472 (1-1403)

QY 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
 DB 149 ATGGTGTTCCTCCAAAGGCAACACAGAACCAATCTCTCATCAAGCAATCATGCGCA 208
 QY 21 ThrProLeuPheThrGlyLeuProValValAspLeuThrHisProAspAlaLysAsnLeu 40
 DB 209 ACGGCAATTCCTCAACAATTCCTGAGTGACCTCTCCAAACAGATGCAAGACCTTC 268
 QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
 DB 269 ATAGTGAAGCTTTGTGAGGAATTTGGATTTCTTCAAAGTCATCAACCATGTTCCCATG 328
 QY 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
 DB 329 GAAACTATATCCCAATTCGAATCTGAAGCCTTCAAGCTTCTCTATGCACTCAATGAG 388
 QY 81 LysAspArgAlaGlyProProAspProPheGlyTyTrpGlySerLysArgTleGlyProAsn 100
 DB 389 AAGGAAAGATAGTGGCCCTCCCAACCATATGTTGGTATGGTAGCAAGAAATTTGACACAT 448
 QY 101 GlyAspValGlyTrpValGluTyTrpValGluLeuLeuAsnThrAsnProAspValIleSerPro 120

DB 449 GGGGATGTTGGTGGTTGAGTACCTTCTTCTCAACACCAATCAAGAA----- 496
 QY 121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
 DB 497 CACAACCTTCTCTGTTTATGGCAAAAACGCTGAGAAATTTAGGTGTTGTGTGACAGTTAC 556
 QY 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
 DB 557 ATGCTCTCTGTGAGGAAATGGCATGTGAGATTCTTGTAGTAAAGAGAGAGTACTCTGTTTT 616
 QY 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
 DB 617 ATACAACAAAAAATGTGTTTAGCAAGCTTCTTATGGATAAAGAGAGAGTACTCTGTTTT 676
 QY 181 ArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
 DB 677 AGGTGATCATCACTACCTCTGCTTCCCTGACTT---GTGAATGGTCAAAACATGATAGG 733
 QY 201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGly 220
 DB 734 TTTGGAGAACACACGACCCACAAATCATTTCTTACTTAGGTCCCAACAATACTTTCAGGC 793
 QY 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSerPhe 240
 DB 794 CTTTCAGATTTTCTTAGAGATGGAAACTGGATTTTCAGTCCCACTGATCACAATCTTTC 853
 QY 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyValGlyPheLysSerValLys 260
 DB 854 TTCATAATGTTGGTGATTTCTTTCAGGTATGACCAATGGAGGTTTCCAAAGTGTGAAA 913
 QY 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
 DB 914 CACAGAGTTTGGACAAATGGATTTTAAAGTCTAGACTCTCAATGATTTACTTTGGAGTCCA 973
 QY 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
 DB 974 CCATTGAGTGAGAAATATGATACCATTTATCTTCTTATG---AAAGGAAAGAAAGCTTA 1030
 QY 301 TyrLysGluPheThrTyTrpCysGluTyLysLysAlaAlaTyrThrSerArgLeuAlaAsp 320
 DB 1031 TACAAGAGATTACGTGGTTCGAGTATAAAATTTAACTATGCTTCAAGATTGGCTGAT 1090
 QY 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
 DB 1091 AATAGGCTTGGACATTTTGAGAGAAATTTGTTGCT 1123
 RESULT 11
 AAD40262
 ID AAD40262 standard; cDNA; 1403 BP.
 XX AAD40262;
 AC AAD40262;
 XX 22-OCT-2002 (first entry)
 DT 22-OCT-2002 (first entry)
 DE Soybean GA 2-oxidase 2 cDNA.
 KW Gibberellin; transgenic plant; seed germination; seedling growth;
 KW transgenic; 2-oxidase 2; enzyme; GA; soybean; gene; ss.
 XX Glycine max.
 OS
 FH Key Location/Qualifiers
 FT CDS 149..1129
 FT /*tag= a
 FT /product= "GA 2-oxidase 2 protein"
 XX US2002053095-A1.
 XX 02-MAY-2002.
 XX 10-AUG-1999; 99US-00371307.
 XX

PR 10-AUG-1999; 99US-00371307.
 XX (BROW/) BROWN S M.
 XX Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
 PI Piller KJ, Rao S, Ream JE;
 XX WPI; 2002-489107/52.
 DR P-PSDB; AAE24922.
 XX Control of gibberellin levels in plants useful to avoid unfavorable
 PT conditions in crops to increase yields, using transgenic plants having
 PT reduced seed germination and early seedling growth then treatment to
 PT restore these properties.
 XX Claim 45; Page 94-95; 155pp; English.
 XX The invention relates to control of gibberellin (GA) levels in plants.
 CC The method involves producing transgenic plants having a phenotype of
 CC reduced seed germination and reduced early seedling growth, then
 CC restoring seed germination and early seedling growth by treating plants
 CC with an appropriate compound under conditions are favourable. The method
 CC is useful to control seed germination and/or early seedling growth in
 CC agricultural production so that unfavorable environmental conditions
 CC normally reducing agronomic output can be avoided and yields increased.
 CC plants also demonstrate increased uniformity of germination, emergence
 CC and seedling vigor, so increasing yields at harvest. The method is
 CC especially useful in crop plants such as e.g. canola, soybean, cotton,
 CC etc., and is also useful in storage and transport of seeds to reduce
 CC premature germination which may affect agronomic or food quality of the
 CC seeds. The present sequence is soybean GA 2-oxidase 2 cDNA
 XX
 SQ Sequence 1403 BP; 440 A; 269 C; 261 G; 433 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4.03e-105 Length: 1403
 Score: 1060.00 Matches: 200
 Percent Similarity: 76.44% Conservative: 53
 Best Local Similarity: 60.42% Mismatches: 72
 Query Match: 60.64% Indels: 6
 DB: 6 Gaps: 3
 US-10-670-454-2 (1-331) x AAD40262 (1-1403)
 QY 1 MetValValLeuSerGlnProAlaLeuAenGlnPhePheLeuLeuLysProPheLysSer 20
 DB 149 ATGGTGTGCTGCTCCAGGCAACACAGAACATATCTCTACATCAAGAACTACATGCCA 208
 QY 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
 DB 209 ACGGCATTCTCTCAACAAATCCCGTAGTGACCTCTCCAAACCAAGATGCAAGACCTC 268
 QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHisGlyValProLeu 60
 DB 269 ATAGTGAAGCTGTGTGAGGAATTTGGATTCTTCAAGTCAATCAACCATGTTTCCCATG 328
 QY 61 GluLeuMetAlaAsnLeuGluAenGluAlaLeuAargPhePheLysSerGlnSerGlu 80
 DB 329 GAAACATATATCCCAATTTGGAATCTGAAGCCTTCAAGTCTCTATGCCACTCAATGATG 388
 QY 81 LysAspArgAlaGlyProProAspProPheGlyTyTrGlySerLysArgIleGlyProAsn 100
 DB 389 AAGGAAAAGTAGCCCTCCCAACCAATATGGTATGGTAGCAAGAAATTTGACACAAAT 448
 QY 101 GlyAspValGlyTrpValGluTyTrLeuLeuLeuAenThrAsnProAspValIleSerPro 120
 DB 449 GGGGATGTTGGTGGGTGAGTACCTCTCTCAACACCAATCAAGAA----- 496
 QY 121 LysSerLeuCysIlePheAargGluAenProHisPheAargAlaValValGluAenTyTr 140
 DB 497 CACAACATCTCTGTTTATGCAAAACGCTGAGAAATTTAGGTGGTGTGTTGAAACAGTTAC 556
 QY 141 IleThrAlaValLysAsnMetCysTyTrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160

Db 557 ATGTCCTCTGTGAGAAATGCGATGTGAGATTTCTTGTAGCTGATGCGACAGAGATTGAAG 616
 QY 161 IleAargGlnAargAsnThrLeuSerArgLeuLeuLysAspGlyLysSerAspSerCysPhe 180
 DB 617 ATACAAACAAAAAATGTTTGTAGCAAGCTTCTTATGGAATAAGAGAGTACACTCTGTTTTT 676
 QY 181 ArgLeuAsnHisTyTrProProCysProGluValGlnAlaLeuAenAargAsnLeuValGly 200
 DB 677 AGGTGATCACTACCTCTGCTGCTGAACIT--GTGAATGGTCAAAACATGATAGGG 733
 QY 201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuAargSerAsnSerThrSerGly 220
 DB 734 TTTGGAGAACACACGACCCACAAATCAATTTCTTACTTAGGTCCCAACAATACTTCAGGC 793
 QY 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSerPhe 240
 DB 794 CTTAGATTTTCTTAGAGATGGAACCTGGATTTCAGTCCCACCTGATCACAATCTTTC 853
 QY 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyAargPheLysSerValLys 260
 DB 854 TTCATAAATGTTGGTGAATCTCTTCAGGTATGACCAATGGAAGTTTCGAAGTGTGAAA 913
 QY 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyTrPheGlyGlyPro 280
 DB 914 CACAGAGTTTTCACAAATGGATTTAAGTCTAGACTCTCAATGATTACTTTGGAGGTCCA 973
 QY 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
 DB 974 CCATTGAGTGAAGAAATAGTACCATTTCTTCACTTATG---AAAGGAAAGAAAGACTTA 1030
 QY 301 TyTrLysGluPheThrTrpCysGluTyTrLysLysAlaAlaTyTrThrSerArgLeuAlaAsp 320
 DB 1031 TACAAAGATTTTACGTGGTTCGAGTATAAAATTTAACCTATGCTTCAAGATTGGCTGAT 1090
 QY 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
 DB 1091 AATAGCTTGGACATTTTGAGAGAAATTTGTGCT 1123
 RESULT 12
 ID ADA70120 standard; DNA; 984 BP.
 XX ADA70120;
 AC ADA70120;
 DT 20-NOV-2003 (first entry)
 DE Rice gene, SEQ ID 3443.
 KW plant; bacterial infection; fungal infection; viral infection; rice;
 XX gene; ds.
 OS Oryza sativa.
 XX WO2003000898-A1.
 PN 03-JAN-2003.
 PD 22-JUN-2001; 2001WO-IB001105.
 XX 22-JUN-2001; 2001WO-IB001105.
 PR (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX WPI; 2003-175290/17.
 DR Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.

XX PS Claim 6; SEQ ID NO 3443; 899pp; English.

XX CC The present invention relates to a method (M1) for identifying genes

CC involved in plant resistance or response to pathogenic infection. M1

CC comprises identifying a gene whose expression is significantly altered in

CC the incompatible interaction of plant gene expression relative to

CC the incompatible interaction of plant gene expression relative to

CC expression of the gene in an uninfected plant, in a mutant plant that

CC does not express a gene associated with response to pathogenic infection,

CC or in a corresponding incompatible or compatible interaction. (M1) is

CC useful for conferring resistance to resistance or tolerance to a plant to

CC bacterial, fungal or viral infection. The present sequence was used to

CC illustrate the invention.

XX SQ Sequence 984 BP; 165 A; 311 C; 341 G; 167 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7,33e-96	Length:	984
Score:	973.00	Matches:	190
Percent Similarity:	72.67%	Conservative:	52
Best Local Similarity:	57.06%	Mismatches:	79
Query Match:	55.66%	Indels:	12
DB:	8	Gaps:	3

US-10-670-454-2 (1-331) x ADA70120 (1-984)

QY 1 MetValValLeuSer---GlnProAlaLeuAenGlnPhePheLeuLeuLysProPheLys 19

DB 1 ATGGTGGTCTCTGCTGGCGCGCGCGCGTGCATCATCCCGCTGCTGAGGTCCGCGAC 60

QY 20 SerThrProLeuPheThrGlyLeuProValValAspLeuThrHisProAspAlaLysAsn 39

DB 61 CCGCGGCGACGCTCTCTCCGGCGTCCGGTCTGACCTCGGACCGCGCGCGCGCGG 120

QY 40 LeuLeuValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValPro 59

DB 121 GCGGTGGTGGCGCGCGCGCGTTCCTCAAGGTCTGTCACACCGCGCGTGGCC 180

QY 60 LeuGluLeuMetAlaAsnLeuGluAenGluAlaLeuArgPhePheLysLysSerGlnSer 79

DB 181 ACGACACATGACACAGCGCGCGTCCGAGCGCGTCTGAGTTCTTCCACAGCGCGCGC 240

QY 80 GluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgLysGlyPro 99

DB 241 GACAAGGACCGCTCCGCGCGCGCGCTACCGTTCGGGTACGCGACGAGCGGATCGGGTC 300

QY 100 AsnGlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsn-----Pro 115

DB 301 AATGGCGACATGGGTGGTTCGAGTACCTCTCTCCGCGCGCGCGCGCGCGCGCGC 360

QY 116 AspValIleSerProLysSerLeuCysIlePheArgGluAsnProHisPheArgAla 135

DB 361 GACGCTGCACCGTCCGCTCTCGCGCGGTC-----TTCGCGCGC 399

QY 136 ValValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMet 155

DB 400 GCTCTCAACAGTACATCTCCGGGGTCCGAGAGTGGCGGTGGCGGTGATGAGCGCATG 459

QY 156 AlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLys 175

DB 460 TCGGAGGGGTGGGCAATTCGCGAGCGCGCGCGTTCGAGCGCGTGTGACGCGGAGGG 519

QY 176 SerAspSerCysPheArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsn 195

DB 520 AGCGACAGGTGTTCGCGGTGAACCACTACCGCGCGTCCGCGCGTCCGCGCGTCCGCG 579

QY 196 ArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleLysSerValLeuArgSer 215

DB 580 TGCAGGCTCACCGGCTTCGCGGAGCACACCGACCGCGCGCTCGCTCTCGCTCGCTCA 639

QY 216 AsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProPro 235

DB 640 AACGGCACGCTCGCGCTCGAGATCGCGCTCCGCGCGCGCGTGGGTGTCGCGCTCC 699

QY 236 AspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArg 255

DB 700 GACCGCGACTCTCTCTGTCACAGCTCGCGACTCGTTGCAGTTCTGACCAATGGGAG 759

QY 256 PheLysSerValLysHisArgValLeuAlaAspThrLysSerArgLeuSerMetIle 275

DB 760 TTCAGAGCGGTGAACACAGCGGTGGTGGCCACAGCCTAAAGCTTAGGGTTTCTTCATC 819

QY 276 TyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLys 295

DB 820 TACTTTGGAGGCGCCACCGTTAGCACAGAGATTGCACCATGCCACAGCTGTGGGGAG 879

QY 296 GlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaLysThr 315

DB 880 GGAGAGCAGAGCCTGTACAGGAGTTTCATCGGATGAGTACAGAGGCTGCCTACAAA 939

QY 316 SerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328

DB 940 TCAAGGCTTGGAGACACAGCGCTGGCCCGCAGTTTGAGNAG 978

RESULT 13

ADK00081

ID ADK00081 standard; cDNA; 984 BP.

XX AC ADK00081;

XX DT 17-JUN-2004 (first entry)

XX DE Rice cDNA encoding gibberellin 2-oxidase, OsGA2ox3.

XX KW Rice; ss; gene; plant; gibberellin 2-oxidase; OsGA2ox3; plant growth; gibberellin A20; gibberellin A29; gibberellin A29-catabolite.

XX OS Oryza sativa.

XX FH Key

FT CDS 1..984

FT Location/Qualifiers

FT /*tag= a

FT /product= "OsGA2ox3"

XX US2004060080-A1.

XX PD 25-MAR-2004.

XX PF 18-MAR-2003; 2003US-003932325.

XX PR 20-SEP-2002; 2002JP-00276051.

XX PA (NAG-) NAT INST AGROBIOLOGICAL SCI.

XX PI (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.

XX PI Tanaka H, Kayano T, Matsuoka M, Kobayashi M, Saito T, Sakamoto T; Sakai M;

XX WPI; 2004-268919/25.

XX P-PSDB; ADK00082.

XX New DNA encoding plant-derived proteins having gibberellin 2-oxidation activity, useful for the inactivation of plant gibberellins and plants whose gibberellin activity has been modified by regulating the expression of these DNAs.

XX Claim 1; SEQ ID NO 3; 23pp; English.

XX The invention relates to a DNA encoding a plant protein having gibberellin 2-oxidation activity, comprising ADK00079 or ADK00081 or a DNA encoding a protein comprising ADK00080 or ADK00082, where one or more amino acid residues are substituted, deleted, added, and/or inserted or a DNA hybridising to ADK00079 or ADK00081 under stringent conditions. The DNA is also selected from an antisense RNA, a DNA encoding an RNA having the ribozyme activity that specifically cleaves the transcript of the DNA above, a DNA encoding an RNA that suppresses the expression of the DNA

CC polynucleotide, a cell comprising the recombinant DNA construct,
 CC producing a plant (comprising transforming a plant cell with the
 CC polynucleotide and regenerating a plant from the transformed plant cell),
 CC a plant comprising the recombinant DNA construct and a seed comprising
 CC the recombinant DNA construct. Also disclosed as new are nucleic acid
 CC (cDNA) fragments and assembled configs encoding plant metabolism proteins
 CC chosen from GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate
 CC synthase, Dioxynase, Ent-Kaurine Synthase A, GA-20 oxidase, Gibberellin
 CC 3-beta hydroxylase, Riboflavin specific deaminase, Ethylene response
 CC factor, Acyl-CoA thioesterase II, ABC transporter GGN20-like, P-
 CC glycoprotein I, P-glycoprotein 3, P-glycoprotein ATPase, P-glycoprotein
 CC HMDR2, ABC transporter, PMP70 ABC transporter and MRP4 ABC transporter.
 CC The nucleic acid fragments may be used to create transgenic plants where
 CC the polypeptides are present at higher or lower levels than normal or in
 CC cell types or in developmental stages in which they are not normally
 CC found. The polynucleotides can be used as probes for genetically and
 CC physically mapping genes and as markers for traits linked to those genes.
 CC The nucleic acid fragments may be used as restriction fragment length
 CC polymorphism (RFLP). It can also be used to probe Southern blots
 CC containing restriction endonuclease-treated genomic DNAs of a set of
 CC individuals representing parent and progeny of a defined genetic cross.
 CC The nucleic acid fragments may also be used as hybridisation probes
 CC against PCR amplification products generated from the mutation population
 CC using the mutation tag sequence primer in conjunction with an arbitrary
 CC genomic site primer. The peptides can also be used to immunise animals to
 CC produce polyclonal or monoclonal antibodies with specificity for peptides
 CC or proteins comprising the amino acid sequences. Antibodies are useful
 CC for detecting the polypeptides in situ in cells or in vitro in cell
 CC extracts. The present sequence encodes a plant metabolism protein (or
 CC fragment).

XX

SQ Sequence 1650 BP; 353 A; 463 C; 476 G; 358 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,54e-95 Length: 1650
 Score: 973.00 Matches: 190
 Percent Similarity: 72.67% Conservative: 52
 Best Local Similarity: 57.06% Mismatches: 79
 Query Match: 55.66% Indels: 12
 DB: 12 Gaps: 3

US-10-670-454-2 (1-331) x ADM94203 (1-1650)

QY 1 MetValValLeuSer---GlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLys 19
 DB 128 ATGTTGTTCTCTGCGCGCGCGCGCGTGCATCATCCGCTGCTGAGTCCGCGGAC 187
 QY 20 SerThrProLeuPheThrGlylleProValValAspLeuThrHisProAspAlaLysAsn 39
 DB 188 CCGGGCGACGCTCTCTCCGCGGTGCGCGTCTGCTGACCTCGGCAGCCCGCGCGGAGG 247
 QY 40 LeuIleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHisGlyValPro 59
 DB 248 GCGTGTGGAGCCCTGCGAGCGGTACGGGTCTTCAAGTGTCAACACACGCGGTGGCC 307
 QY 60 LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSer 79
 DB 308 ACGACACGATGACAAAGCCGAGTCGAGGCGCTCAGGTTCTTCCACGACGACGCC 367
 QY 80 GluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArglleGlyPro 99
 DB 368 GACACAGGACCGCTCCGCGCGCGCTACCGGTTCGCGTACGCGACGAAGCGGATCGGGTTC 427
 QY 100 AsnGlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsn-----Pro 115
 DB 428 AATGGCGACATGGGGTGGGTGAGTACCTCTCTCGCCCTCGACGCGCTCGCTCGCC 487
 QY 116 AspValIleSerProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAla 135
 DB 488 GAGCGCTGCACCGCTCCGCTCTCGCGGTC-----TTCCGGGCC 526
 QY 136 ValValGluAsnTyrIleThrAlaLysAsnMetCysTyrAlaValLeuGluLeuMet 155
 DB 155

DB 527 GCTCTGAACAGTACATCTCGGGGGTGCAGAAAGTGGCGGTGATGGAGGCGATG 586
 QY 156 AlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLys 175
 DB 587 TCGAGGGGCTGGGCATTCGCGAGCGGCGCTGAGCGCTGGTGTGACGGCGGAAGG 646
 QY 176 SerAspSerCysPheArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsn 195
 DB 647 AGCGACCAAGTGTTCGCGGTGAACCACTACCCGCGGTGCGCGGCTGCAGGGGCTCGGC 706
 QY 196 ArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSer 215
 DB 707 TGCAGGCTCATCGGCTTCGCGGAGCACACCGACCGCAGCTGCTCTCGTCCGCTCA 766
 QY 216 AsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTyrValSerValProPro 235
 DB 767 AACGGCACGTCGCGCTTCAGATCGCGCTCCGCGACGCGCAGTGGGTGTCCGTGCCCTCC 826
 QY 236 AspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArg 255
 DB 827 GACCGCGACTCTCTTCTTCTGCAACGTCGCGGACTCGTTGACGTTCTGACCAATGGAGG 886
 QY 256 PheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIle 275
 DB 887 TTCAGAGCGTGAAGCACAGGCTGGTGGCCACAGCCTAAAGTCTAGGGTTTCTCTTCATC 946
 QY 276 TyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLys 295
 DB 947 TACTTTGGAGGGCCACCGTTAGCACAGAGATTGACCAATTGCCACAGCTGTGGGGGAG 1006
 QY 296 GlyGluGluCysLeuTyrLysGluPheThrTyrCysGluTyrLysLysAlaIleTyrThr 315
 DB 1007 GGAGAGCAGAGCTGTACAAAGGAGTTTCATCGGATGAGTACAAAGAGGCTGCCTACAAA 1066
 QY 316 SerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
 DB 1067 TCAAGGCTTGGAGACAAACAGGCTGGGCCAGTTTGAGAAG 1105

Search completed: December 28, 2005, 01:42:39
 Job time : 747 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 28, 2005, 00:46:50 ; Search time 4749 Seconds
(without alignments)
3261.007 Million cell updates/sec

Title: US-10-670-454-2

Perfect score: 1748

Sequence: 1 MVVLSQPALNOFFLLKPKFS.....AAYTSRLADNRLAPFKSAA 331

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -ENDS=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_est2:*
3: gb_est3:*
4: gb_hc1:*
5: gb_est4:*
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7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1092.5	62.5	1362	4	CNSOABSJ BX816963 Arabidops
2	1092.5	62.5	1365	4	CNSOACGN BX814544 Arabidops
3	1088.5	62.3	1141	4	CNSO9Y5Q BX841768 Arabidops
4	1065.5	61.0	1363	4	CNSOABKL BX815974 Arabidops
5	1041	59.6	1339	4	CNSOAC3R BX814383 Arabidops
6	957.5	54.8	1554	4	AY104425 Zea mays
7	917.5	52.5	1128	4	CNSOADM1 BX814091 Arabidops

8	902.5	51.6	785	1	AJ803092
9	868.5	49.7	893	8	DN589159
10	837	47.9	792	3	BI935635
11	825	47.2	566	3	BM085298
12	817	46.7	653	1	AW184969
13	812	46.5	694	2	BI208568
14	798	45.7	755	5	BM690134
15	798	45.7	776	5	BM692820
16	785	45.1	622	5	BU549366
17	781	44.7	789	5	BM685035
18	781	44.7	847	8	DN982067
19	772.5	44.2	789	7	CV470333
20	769.5	44.0	698	8	DR399076
21	763.5	43.7	853	7	CV469374
22	730.5	41.8	738	8	DN501878
23	729.5	41.7	625	7	CV292693
24	729.5	41.7	642	7	CV292668
25	728	41.6	1332	4	CNSOAA33
26	722.5	41.3	711	1	AW222239
27	715.5	40.9	743	2	BG646259
28	715.5	40.9	854	8	DN980660
29	714.5	40.9	663	7	CV292717
30	708	40.5	800	3	BI970132
31	705.5	40.4	478	1	AL382874
32	704.5	40.3	753	3	BI968577
33	698	39.9	646	6	CF088691
34	697.5	39.9	737	2	BG886490
35	694.5	39.7	808	3	BJ575888
36	690.5	39.5	779	3	BJ571134
37	682	39.0	611	1	AW309039
38	680.5	38.9	639	5	BM691193
39	680.5	38.9	685	2	BG523146
40	679	38.8	612	2	BE802903
41	676.5	38.7	659	2	BE434782
42	674	38.6	655	5	B0404995
43	670.5	38.4	579	6	CA844444
44	670.5	38.4	724	6	CA844443
45	665.5	38.1	787	8	DN982887

ALIGNMENTS

RESULT 1
CNSOABSJ 1362 bp mRNA linear HTC 06-FEB-2004
LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
DEFINITION GSLTPGH78ZH09 of Hormone Treated Callus of strain col-0 of
Arabidopsis thaliana (thale cress).

ACCESSION BX816963
VERSION BX816963.1 GI:42471779
KEYWORDS HTC; GSLT cDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 1362)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, P., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.,
Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation

JOURNAL Unpublished
AUTHORS 2 (bases 1 to 1362)
TITLE Genoscope.
JOURNAL Direct Submission
COMMENT Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M., URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full_length

<http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis>.

FEATURES

source

Location/Qualifiers
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/mol_type="mRNA"
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1. .1362
/gene="Atlg30040"

ORIGIN

Alignment Scores:
Pred. No.: 5.18e-118 Length: 1362
Score: 1092.50 Matches: 210
Percent Similarity: 76.81% Conservative: 45
Best Local Similarity: 63.25% Mismatches: 72
Query Match: 62.50% Indels: 5
DB: 4 Gaps: 3

US-10-670-454-2 (1-331) x CNSOBSJ (1-1362)

QY 1 MetValValLeuSerGlnProAlaLeu-----AsnGlnPhePheLeuLeuLysProPhe 18
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QY 97 IleGlyProAsnGlyAspValGlyTrpValGluTyTrLeuLeuLeuAsnThrAsnProAsp 116
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QY 117 ValIleSerProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaVal 136
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QY 137 ValGluAsnTyTrIleThrAlaValLysAsnMetCysTyTrAlaValLeuGluLeuMetAla 156
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QY 217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAsp 236
DB 759 AACACGGCGGTCTTCAAAATCTGTGTAAGAGATGGAAGTGGTCTCGCTCCCTCTCGAT 818
QY 237 GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
DB 819 CACTCTCTCTTCTTCAATTAATGTGGAGATGCTCTCAGGTTATGACTAACGGAGGTTTC 878
QY 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyTr 276
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QY 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296
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QY 297 GluGluCysLeuTyTrLysGluPheThrTrpCysGluTyTrLysLysAlaLysThrSer 316
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RESULT 2
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LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
DEFINITION GSLTGH78Z01 of Flowers and buds of strain col-0 of Arabidopsis
thaliana (Chale cress).
ACCESSION BX814544
VERSION BX814544.1 GI:42472102
KEYWORDS HTC; GSLT cDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 1365)
AUTHORS Castelli V., Aury J.M., Jaillon O., Wincker P., Clepet C., Menard M., Cruaud C., Quetier F., Scarpelli C., Schachter V., Temple G., Caboche M., Weissenbach J. and Salanoubat M.
TITLE Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1365)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full_length
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Qy	297	GluGluCysLeuTyrLysGluPheThrTyrCysGluTyrLysLysAlaAlaTyrThrSer	316
Db	1002	GATGATTGGCTTTTACAAAGAAATTCACCTTGGTCTCAATACAAATCTTCTGCTTCAAGTCT	1061
Qy	317	ArgLeuAlaAspAenArgLeuAlaProPheGlnLys	328
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RESULT 3			
LOCUS	CNS09Y5Q	1141 bp mRNA linear HTC 06-FEB-2004	
DEFINITION	Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSUFB202E08 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).		
ACCESSION	BX8411768	GI:42454442	
VERSION	BX8411768.1	GI:42454442	
KEYWORDS	HTC; GSLT cDNA.		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE	1 (bases 1 to 1141)		
AUTHORS	Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.		
TITLE	Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1141)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (18-NOV-2003) Genoscope - Centre National de Sequences : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)		
COMMENT	- Web : www.genoscope.cns.fr The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URUG INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.		
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ORIGIN			
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Percent Similarity:	76,81%	Conservative:	45
Best Local Similarity:	63,25%	Mismatches:	72
Query Match:	62,50%	Indels:	5
DB:	4	Gaps:	3
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Qy	19	LysSerThrProLeuPheThr-----GlyIleProValValAspLeuThrHisProAsp	36
Db	165	AAACCGGTTTCGGTTCTCACTTCCCATTCATCCCGTCGTCACCTAGCCGATCCGGAA	224
Qy	37	AlaLysAenLeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAenHis	56
Db	225	GCMAAACCCGNAATCGTAAGACCTGCGAGAGTTCGGGTTCTTCAAGTTCGTAAACCCAC	284
Qy	57	GlyValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLys	76
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Qy	77	SerGlnSerGluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArg	96
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Qy	157	GluGlyLeuGlyLysArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSer	176
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Qy	177	AspSerCysPheArgLeuAenHisTyrProProCysProGluValGlnAlaLeuAenArg	196
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Qy	197	AenLeuValGlyPheGlyGluHisThrAspProGlnIlelleSerValLeuArgSerAsn	216
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Qy	217	SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTyrValSerValProAsp	236
Db	762	AAACCGCGGGTCTTCAATCTGTGTGAAGATGGAAGTGGGCTGCTGCTCCCTCTGAT	821
Qy	237	GlnThrSerPheIleAenValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe	256
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Query Match:	62.27%	Indels:	5
DB:	4	Gaps:	3
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QY	37	AlaLysAsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHis	56
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QY	157	GluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLysAspGluLysSer	176
DB	555	GAAGACTAGGATAGACCGCAAGGACACTCTGAGTAAATGCTGAGAGTAGAAGAGT	614
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DB	615	GACTCGTCCCTGAGACTAAACCATTAATCCGCGCGCGAGGAA--GAGGCGGAGAGATG	671
QY	197	AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn	216
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QY	217	SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAsp	236
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QY	237	GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe	256
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QY	257	LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyr	276
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QY	277	PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly	296
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CNSOABKL1363 bp mRNA linear HTC 06-FEB-2004

Arabidopsis thaliana Full-length cDNA Complete sequence from clone

GSJLTPGH20C07 of Hormone Treated Callus of strain col-0 of

Arabidopsis thaliana (thale cress).

BX815974

HTC; GSJL cDNA.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons; rosids; eucotids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1363)

Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.

Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation

Unpublished

2 (bases 1 to 1363)

Genoscope.

Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis Genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length

http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

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Best Local Similarity: 62.05% Mismatches: 73

Query Match: 60.96% Indels: 5

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DB 163 AAACCGGTTCGGTTCCTCACTTCCCAATTCATCCCGTCTGCTCAACCTAGCCGATCCGGAA 222

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CNSOAC3R 1339 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTFFB70ZF11 of flowers and buds of strain col-0 of Arabidopsis
thaliana (thale cress).
BX814383
BX814383.1 GI:42472054
HTC; GSLT cDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

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REFERENCE
AUTHORS
1 (bases 1 to 1339)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
JOURNAL
REFERENCE
AUTHORS
2 (bases 1 to 1339)
Direct Submission
JOURNAL
TITLE
COMMENT
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
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Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Percent Similarity: 62.77% Mismatches: 65
Best Local Similarity: 59.55% Indels: 18
Query Match: 4 Gaps: 5
DB:
US-10-670-454-2 (1-331) x CNSOAC3R (1-1339)
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Db 283 GGAGTCCGACCGAACTATGACTCGGTAGAGCAGGAGGCTATTGGCTTCTTCGGCTTG 342
Qy 77 SerGlnSerGluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArg 96
Db 343 CCTCAGTCTCTTAAACACCGGGCCGCTCCACCTGAACCGTACGGTTATGGTAATAAAC 402
Qy 97 IleGlyProAsnGlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAsp 116
Db 403 ATTGGACCAACCGGTGCGTGGATTAGTATCTCTCTCAATGCTAATCCTCAG 462

```

QY 117 ValLysSerProLysSerLeuCysIlePheArgGluAsnProHisPheArgAlaVal 136
 Db 463 CTCCTCTCTCTTAAACCTCCGCGCTTTCGGTCAAAACCCCTCAATTTTCGTGAGTCG 522

QY 137 ValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAla 156
 Db 523 GTGGAGGAGTACATGAAGGAGATTAAGGAAGTGTCTACAGGTGTGGAGATGGTGC 582

QY 157 GluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSer 176
 Db 583 GAAGAACTAGGGATAGACGCAAGGGACACTCTGAGTAAATCTGAGAGATGAGAAGCT 642

QY 177 AspSerCysPheArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsnArg 196
 Db 643 GACTCGTGCTGAGACTAAACCACTATTCGGCGCGAGAA---GAGCGGAGAGATG 699

QY 197 AsnLeuValGlyPheGlyGluHisThrAspProGlnIleSerValLeuArgSerAsn 216
 Db 700 GTGAAGGTGGGTTTGGGGAACACACAGACCACAGATAATCTCAGTCAAGATCTAAT 759

QY 217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAsp 236
 Db 760 AACACGGCGGCTTCAATCTGTGTGAAGATGGAAGTTGGGTGCTGCTCTCTCTGAT 819

QY 237 GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
 Db 820 CACTCTCTCTTCTTCAATTAATGTGGAGATGCTTTCAGGTTATGACTAACGGAGGTT 879

QY 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyr 276
 Db 880 AAGAGTGTAAACACAGGGTCTTAGCCGATACAGAGGAGATCGAGGATTTCAATGATAT 939

QY 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296
 Db 940 TTCGGCGGACCGCATTTGAGCCAGAGATCGCACCATTCGCATG----- 984

QY 297 GluGluCys-----LeuTyrLysGluPheThrTrpCysGluTyr 309
 Db 985 ---CCCTGTCCCTGACCAAGATGATTTGCTTTACAAAGATTCACCTTGGTCTCAATAC 1041

QY 310 LysLysAlaAlaTyr 314
 Db 1042 AAATCTCTGCTTAC 1056

RESULT 6
 AY104425 1554 bp mRNA linear HTC 18-FEB-2005
 LOCUS Zea mays P00148306 mRNA sequence.
 DEFINITION
 ACCESSION AY104425
 VERSION AY104425.1 GI:21207503
 KEYWORDS HTC.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 1554)
 Gardiner, J., Schroeder, S., Polacco, M.L., Sanchez-Villeda, H.,
 Fang, Z., Morgante, M., Landewe, T., Fengler, K., Uebeche, F.,
 Hanafey, M., Tingey, S., Chou, H., Wing, R., Soderlund, C. and Coe, E.H.
 Jr.
 Anchoring 9,371 maize expressed sequence tagged unigenes to the
 bacterial artificial chromosome contig map by two-dimensional
 overgo hybridization
 Plant Physiol. 134 (4), 1317-1326 (2004)
 15020742
 2 (bases 1 to 1554)
 Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S.,
 Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
 Maize Mapping Project/DuPont Consensus Sequences for Design of
 Overgo Probes
 Unpublished (2002)

REFERENCE 3 (bases 1 to 1554)
 AUTHORS Coe, E.H.
 TITLE Direct Submission
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

COMMENT
 If you are interested in getting corresponding physical clones, these are publicly available from ZmDB, and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES
 Location/Qualifiers
 source
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 /organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="MaizeGDB:638751"
 /db_xref="taxon:4577"
 /clone_lib="Maize Mapping Project/DuPont Consensus Library"
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN
 Alignment Scores:
 Pred. No.: 6,61e-102 Length: 1554
 Score: 957.50 Matches: 191
 Percent Similarity: 70.75% Conservative: 46
 Best Local Similarity: 57.01% Mismatches: 83
 Query Match: 54.78% Indels: 15
 DB: 4 Gaps: 4

US-10-670-454-2 (1-331) x AY104425 (1-1554)

QY 1 MetValValLeuSerGln---ProAlaLeuAsnGlnPhePheLeuLysProPheLys 19
 Db 118 ATGGTGTGCTCGCAAAACCGCTGTCTGACACAGATCCCGCTCTCGGTCCCGCGGC 177

QY 20 SerThrProLeuPheThrGlyIleProValValAlaAspLeuThrHisProAspAlaLysAsn 39
 Db 178 CCCAGGACAGCTTCTCGGAGTGCGGTGCTGACCTGTCCAGCCACCGCGCGCGCG 237

QY 40 LeuIleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHisGlyValPro 59
 Db 238 GCGATGTCGACGCGCTTCGAGCGCTTCGAGGTCTTCAAGGTCTCAACACACGCGGTGCC 297

QY 60 LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSer 79
 Db 298 GCGGCCACCATGGACAGGCGCGAGTCCGAGGCGCTCAGGTCTTCCGCGAGGCGCAGCG 357

QY 80 GluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyPro 99
 Db 358 GACAGGACCGCGCGGCGCGGTACCGTTCGGGTACGCGCAGCAAGCGGATCGGGCTC 417

QY 100 AsnGlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSer 119
 Db 418 AATGGCGACATGGGTGGTTCGAGTACCTCTCTCTCGCGCTCGACCGCGCTCTCC 477

QY 120 -----ProLysSerLeuCysIlePheArgGluAsnProHisPheArg 134
 Db 478 GAGCGCTGCCCGTGCCTCCAGCGCGCG-----TTCCGG 513

QY 135 AlaValValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeu 154
 Db 514 AGCGCGCTGAACGAGTACGTTCGCGCGCGTGGAGAGTGGCGCGGTGTGCTGGAGCG 573

QY 155 MetAlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLysAspGlu 174
 Db 574 ATGGCGAGGCGCTGGGCATTCGGACGCGGCGCGCTGAGCTCCATGTGTGAGCGCGCC 633


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728 CCCGATCACACTTCCTCTCTCTTCAACGTTGGTGAAGTCTCTCCAGGTGATGACAAATGGG 787
Db

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255 ArgPheLysSerVallyshisargValleyAlaAaspThrThrLysSerArgLeuSerMet 274
Qy

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788 AGGTTCAAGAGCGTGAGGATAGGTTTGTAGCTCACTGTAAATAATCTAGGGTTTCTATC 847
Db

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
275 IleTyPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeu 294
Qy

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
848 ATTACTTCGCTGGACCTTCATGTACTCAGAAATCGCTCCGTTCCATGTTGTATAGAC 907
Db

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
295 LysGlyGluGluCysLeuTyPheThrThrCysGluTyPheLysLysAlaAlaTy 314
Qy

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
908 AATGAGGACGAGGTTGTACGAGGAGTTTACTTGGTCTGTAATACAAAACTCTACCTAC 967
Db

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
315 ThrSerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
Qy

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968 AACTCTAGATTGCTGATAATAGGCTTCAACAATTCGAAAG 1009
Db

RESULT 8
AJ803092
LOCUS
DEFINITION
AJ803092 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
018_5_05_018, mRNA sequence.
ACCESSION
AJ803092
VERSION
AJ803092.1 GI:51118420
KEYWORDS
EST.
SOURCE
Antirrhinum majus (snapdragon)
ORGANISM
Antirrhinum majus
REFERENCE
1 (bases 1 to 785)
Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
Saedler,H. and Zachgo,S.
TITLE
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
DEFICIENS
JOURNAL
Plant Cell 16 (12), 3197-3215 (2004)
PUBMED
15539471
COMMENT
Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES
Location/Qualifiers
1..785
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_5_05_018"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
ORIGIN
Alignment Scores:
Pred. No.: 7,72e-96 Length: 785
Score: 902.50 Matches: 169
Percent Similarity: 81.30% Conservative: 31
Best Local Similarity: 68.70% Mismatches: 45
Query Match: 51.63% Indels: 1
DB: 1 Gaps: 1

US-10-670-454-2 (1-331) x AJ803092 (1-785)
Qy 77 SerGlnSerGluLysAspArgAlaGlyProProAspPheGlyTyTyGlySerLysArg 96
Db
14 GCCTCTTCTGAAAGGAGAAACAGGGACCCCTTGACCCCTTTGGCTATGGAAGTAAGAA 73
Qy 97 IleGlyProAsnGlyAspValGlyTyTrpValGluTyTrpLeuLeuAsnThrAsnProAsp 116
Db
74 ATTGGACGAATGCGATGGGATGGTGGATCTGTAATCTGCTCCTAAACACTAAATCTGAT 133

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Qy 117 ValIleSerProLysSerLeuCysIlePheArgGluAsnProHisPheArgAlaVal 136
Db
134 TCTGATTACAGAAAATTTGCATTCGGTTTTTGTGTAAGCTGCAGAAAAAATTCAGGTGTATA 193
Qy 137 ValGluAsnTyIleThrAlaValLysAsnMetCysTyTrpAlaValLeuGluLeuMetAla 156
Db
194 GTGAATGATTATGTTTTCGACGTAAAGAGATGGCGTGTGAGATTCTTGAATGTTGGCT 253
Qy 157 GluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSer 176
Db
254 GATGAACCTTAAGATTCAACAAGAACGCTTTTACCAAACTTTTAATGGATGAACAGAGT 313
Qy 177 AspSerCysPheArgLeuAsnHisTyProProCysProGluValGlnAlaLeuAsnArg 196
Db
314 GACTCTGTTTTTCAGGCTAAATCCTATCCACATGCCCGCAATTTCAAGAAATCCAAC--- 370
Qy 197 AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn 216
Db
371 AACTTAATCGGGTTTTGGTGAACATACTACCCGCAATAATAATCCGTTTGTAGATCCCAAC 430
Qy 217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAsp 236
Db
431 AACACTTCGGGTCTTCAAAATTCGTTGAAGATGGGAATTCGATTCTTATCCCACTGAT 490
Qy 237 GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
Db
491 CAAAGTCTCTTCTTCATTAATGTTGCTGACTCCTATGCAGGTTATGACTAATGCCAGGTTT 550
Qy 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTy 276
Db
551 AAGAGTGTAAAGACACAGAGGTTGTGGCCAACAGCTCAAAACCCAGACTTTTCAATGATATAT 610
Qy 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296
Db
611 TTGGAGGACCAACCAATTAAGTGAAGAAGTAGCTCCATTCGCTTCACTACTAATGAAGA 670
Qy 297 GluGluCysLeuTyLysGluPheThrTrpCysGluTyTrpLysLeuAlaAlaTyThrSer 316
Db
671 GAAGACAGCTTGTACACAGGAATTTACTTGGTTTGAGTACAAAAAATCTGCTTATAATCAA 730
Qy 317 ArgLeuAlaAspAsnArg 322
Db
731 GGCTGGCGTGATAATAGG 748

RESULT 9
DN589159 893 bp mRNA linear EST 15-MAR-2005
LOCUS
DEFINITION
50141.1 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
50141_5', mRNA sequence.
ACCESSION
DN589159
VERSION
DN589159.1 GI:61239615
KEYWORDS
EST.
SOURCE
Solanum tuberosum (potato)
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 893)
Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Lague,M., De
Koeyer,D., Audy,P., Goyer,C., Li,X.-Q., Wang-Pruski,G. and Regan,S.
Generation of ESTs from late blight-challenged potato tubers
Unpublished (2005)
CONTACT: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.
FEATURES
Location/Qualifiers
1..893
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"

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/clone="50141"
 /tissue_type="Tubers"
 /lab_host="XL10-Gold"
 /clone_lib="Late Blight-Challenged Tubers"
 /note="Vector: pBluescript II SK(+); XE: Site 1: EcoRI;
 Site_2: XhoI; supplier: Pathogen-challenge series. Tubers
 from pathogen-free Solanum tuberosum var. Shepody, clone
 1756, were inoculated with 5 ul of Phytophthora infestans
 (A2-mating type), through 2 puncture wounds 3 cm apart.
 The tubers were incubated 1 minute to allow inoculum
 absorption. The infection area was outlined for future
 collection reference. Surface slices were sampled from the
 tubers at 1 day, 5 days, 7 days, 11 days and 14 days
 post-infection. All samples were pooled and used for RNA
 isolation and library construction. A normalized library
 was constructed following a modified protocol of Bonaldo
 et al. (1996. Genome Research 6: 791-806)."

ORIGIN

Alignment Scores:

Pred. No.: 1.02e-91 Length: 893
 Score: 868.50 Matches: 168
 Percent Similarity: 79.92% Conservativeness: 27
 Best Local Similarity: 68.85% Mismatches: 46
 Query Match: 49.69% Indels: 3
 DB: 8 Gaps: 3

US-10-670-454-2 (1-331) x DN589159 (1-893)

QY 88 AspProPheGlyTyrGlySerIysArgIleGlyProAsnGlyAspValGlyTyrValGlu 107
 DB 3 GACCCCTTTGGCTATGGAATAAGAAATTTGACCTAATGATGTTGGTGGTGA 62
 QY 108 TyrLeuLeuAsnThrAsnProAspValIleSerProLysSerLeuCysIlePheArg 127
 DB 63 TACATCTTTTGTCACAAATTTCTGAGTCAATTAACAAAATTTGTCATCTATTGGGT 122
 QY 128 GluAsnProHisPheArgAlaValValGluAsnTyrIleThrAlaValIysAsnMet 147
 DB 123 GTCAATCCAAAAGATATAAGAGATGCTGTGAATGATTATGATTAGCAATGAAGAAATG 182
 QY 148 CysTyrAlaValLeuLeuLeuMetAlaGluGlyLeuGlyIleArgGlnArgAsnThrLeu 167
 DB 183 GCTTGTGAGATTCTTGAATTTTAGCAGAGGAGATTAAATAATTCATCCAAAGATGTATT 242
 QY 168 SerArgLeuLeuAspGlySerAspSerCysPheArgLeuAsnHisTyrProPro 187
 DB 243 AGTAAGCTTTTATGGATGAAAAGATGATTCACTTTTATAGGCTAAATCATTTACCTCCA 302
 QY 188 CysPro---GluValGlnAlaLeuAsn---ArgAsnLeuValGlyPheGlyGluHisThr 205
 DB 303 TGTCTGTGATGAATTTCAAGAAATATAATGAAGAAATTTAATTTGGATTGTCGAACATCT 362
 QY 206 AspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGlyLeuGlnIleCysLeu 225
 DB 363 GATCCACAAATATTCTTTTATAGATCAATTAACACTTCTGGACTTCAAAATTTCACTT 422
 QY 226 ThrAspGlyThrTyrValSerValProAspGlnThrSerPhePheIleAsnValGly 245
 DB 423 GTTGATGGCCATGGATTCTGTCCCACTGATCAAAATTCATCTTCATCAATGTGTGT 482
 QY 246 AspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValIysHisArgValLeuAla 265
 DB 483 GATTCAATCCAGGTGATGACAAATGGAGGTTTAAAGATGTAACATAGATTTTGGCC 542
 QY 266 AspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyProAlaLeuSerGluAsn 285
 DB 543 AATAGTGTAAATCAAGACTCTCAATGATTTATTTTGGAGGGGCCACCATTAGTGAAAAG 602
 QY 286 IleAlaProLeuProSerValMetLeuLysGly---GluGluCysLeuTyrLysGluPhe 304
 DB 603 ATAGCACCATTTGTCATCACTATTAATAAAGGGGATCAAGACGCTTGTCAAGAAATTT 662

QY 305 ThrTrpCysGluTyrLysLeuAlaAlaTyrThrSerArgLeuAlaAspAsnArgLeuAla 324
 DB 663 ACATGGTTTGGATCAAAAATTCAGCATATAAATCTAGATTGGCTGATAATAGGTGGTC 722
 QY 325 PropheGlnLys 328
 DB 723 CTATTTGAGAA 734

RESULT 10

BI935635

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Seq primer: T3.

Location/Qualifiers

1..792

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="CTOD23D23"

/tissue_type="flower"

/dev_stage="anthesis"

/clone_lib="tomato flower, anthesis"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:

XhoI; supplier: Cornell University; sequencing: The

Institute for Genomic Research; Flower buds and flowers

were taken from greenhouse plants (4-8 wks old, TA496).

They were immediately frozen in liquid nitrogen and then

size-separated while remaining frozen."

ORIGIN

Alignment Scores:

Pred. No.: 4.62e-88 Length: 792

Score: 837.00 Matches: 158

Percent Similarity: 73.53% Conservativeness: 42

Best Local Similarity: 58.09% Mismatches: 56

Query Match: 47.88% Indels: 16

DB: 3 Gaps: 2

US-10-670-454-2 (1-331) x BI935635 (1-792)

QY 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLysProPheLysSer 20

DB 12 ATGGTGAATCTGTCC-----AAACAA 32

QY 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40

DB 33 ACCTCATCTTTTAATGGTGTTCATTGATTGACCTCTCTAAACCCGACTCCCAAGAACCTC 92

QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60

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Db      93  ATCGTTAATGCTCCGCAAGAATTCGGATTCTTCAAAATCATAAACACCATGACGTTCCTATG 152
QY      61  GluLeuMetAlaAenLeuGluAenGluAlaLeuArgPhePheLysSerGlnSerGlu 80
Db      153  GAATTCATAGTAATCGAATCCGAAGCCATCAGTTCCTCTCCCTCCCTCTCTGAG 212
QY      81  LysAspArgAlaGlyProProAspPropheGlyTyrGlySerLysArgIleGlyProAsn 100
Db      213  AAGCTAAAGCAGGCGCTGCTGATCCTTTGGCTATGGCAATAAACAATTCGAACAAT 272
QY      101  GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
Db      273  GCGGATTGTGTCGGTTCGAACACATCTCGTATTCGACAAATTCGAATTAATCCAG 332
QY      121  LysSerLeuCysIlePheArgGluAenProHisPheArgAlaValAluGluAenTyr 140
Db      333  AATTGTGATCTATATAGTGTCATCTCCGAAACATTCGGGCTCGGCTTAATGATTAT 392
QY      141  IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
Db      393  GTTTCAGCAGTGAAGAAATGCTCTGTGATATTTCTTGAATGTTGGCGGAGGATTAAAG 452
QY      161  IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
Db      453  ATTATATCCGACGAATGTTTTCAGTAAGCTTTTGATGACGAAATAGCGACTCCGTTTC 512
QY      181  ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsn----- 197
Db      513  AGCTGATCATCTATCCGCTATCTCAGAGATTTGAACGATTGAACGATTAATATATGAT 572
QY      198  LeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSer 217
Db      573  TTGATTGGATTGGAGAACATCTGACCCACCAATCATATCGATATTAAGATCCATATAC 632
QY      218  ThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGln 237
Db      633  ACTTCGGGGCTCCAAATATTACTGAAGATGGACACTGGATCTCTGTCCACCTCATGAA 692
QY      238  ThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLys 257
Db      693  AATTCCTTCTCTGCAATGTGTGACTCATTCAGGTTATGACTAACGGAAGGGTTAAG 752
QY      258  SerValLysHisArgValLeuAlaAspThrThrLys 269
Db      753  AGTGTGAAGCATAGGTATTGGSCAATAGTGTGAAA 788

RESULT 11
BM085298          566 bp  mRNA  linear  EST 23-JUL-2004
LOCUS            saj34h07.y1 Gm-c1066 Glycine max cDNA clone SOYBEAN CLONE ID:
DEFINITION      Gm-c1066-4957 5' similar to TR:Q9XG83 Q9XG83 GA 2-OXIDASE. ;, mRNA
sequence.
BM085298          1  GI:16995926
VERSION          BM085298.1
KEYWORDS         EST.
SOURCE           Glycine max (soybean)
ORGANISM         Glycine max
REFERENCE        1 (bases 1 to 566)
AUTHORS          Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Corvett, V.,
                Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
                Beck, C., Wylie, T., Underwood, K., Sceptoe, M., Theising, B., Allen, M.,
                Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
                Schurr, R., Ritter, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
                McCann, R., Waterston, R. and Wilson, R.
                Public Soybean EST Project
                Unpublished (1999)
                Contact: Shoemaker R/Public Soybean EST Project
                Washington University School of Medicine
```

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 426.
Location/Qualifiers
1. 566
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1066-4957"
/tissue_type="Leaf and shoot tip, salt stressed, 2 week old seedling"
/lab_host="DH10B"
/clone_lib="Gm-c1066"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from unexpanded leaves and the shoot tips of 2 week old seedling from the cultivar Williams. The 2 week old seedlings were salt stressed in a solution of 500mM NaCl for 3 days prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN

Alignment Scores:
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Best Local Similarity: 86.89% Mismatches: 19
Query Match: 47.20% Indels: 0
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101	Gly	Asp	Val	Gly	Tyr	Trp	Val	Glu	Tyr	Leu	Leu	Leu	Leu	Asn	Thr	Asn	Pro	Asp	Val	120
278	GCG	GAT	TGT	TGT	CGGG	CGAA	CAC	ATC	CTC	GAT	CGT	GAT	CGA	CAC	AAT	TCT	GCA	AAT	TCT	337
121	Lys	Ser	Leu	Cys	Ile	Phe	Arg	Glu	Asn	Pro	His	His	Phe	Arg	Ala	Val	Val	Glu	Asn	140
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181	Arg	Leu	Asn	His	Tyr	Pro	Cys	Pro	Glu	Val	Gln	Ala	Leu	Asn	Arg	Asn	-----	----	----	197
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218	Thr	Ser	Gly	Leu																

RESULT 15					
BW692820					
LOCUS	BW692820	776 bp	mRNA	linear	EST 27-APR-2005
DEFINITION	Lycopersicon esculentum cv. Micro-Tom fruit Lycopersicon esculentum cDNA clone FC26CC12 5', mRNA sequence.				

ACCESSION
BW692820
VERSION
BW692820.1
KEYWORDS
EST.
GI:62935234

RECORDS	SOURCE	ORGANISM
251.		<i>Lycopersicon esculentum</i> (<i>Solanum lycopersicum</i>)
		<i>Lycopersicon esculentum</i>
		Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
		asterids; lamids; Solanales; Solanaceae; <i>Solanum</i> ; <i>Lycopersicon</i> .
	1	(bases 1 to 776)
REFERENCE		

REFERENCE
AUTHORS
I. (bases 1 to 776)
Tsugane, T., Watanabe, M., Yano, K., Suzuki, H., Sakurai, N. and
Shibata, D.
TITLE
Expressed sequence tags of full-length cDNA clones prepared from
the laboratory-grown miniature tomato (*Lycopersicon esculentum*)
cultivar Micro-Tom
Unpublished (2005)
JOURNAL

CONTACT: Daisuke Shibata
Kazusa DNA Research Institute;
2-6-7 Kazusa-Kamatari, Kisarazu,
Chiba, 292-0818, Japan
Tel: 81-438-52-3947
Fax: 81-438-52-3948
Email: shibata@kazusa.or.jp.

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FEATURES
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/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Micro-Tom"
/db_xref="taxon:4081"
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Email: snibata@kazuo.ri.jp
Location/Qualifiers

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ORIGIN

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Best Local Similarity:	57.92%	Mismatches: 53
Query Match:	45.65%	Indels: 16
DB:	5	Gaps: 2
US-10-670-454-2 (1-331)	x	BW692820 (1-776)

US-10-670-454-2 (1-331) x BW692820 (1-776)

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Db	59	ACCTCATCTTTAATGGTGTTCATGATGACCTCTCTAAACCCGACTCCGAAGACCTC	118
Qy	41	IleValAsnAlaCyAsArgAspGlyPhePhePheLeuValAsnHisGlyValProLeu	60
Db	119	ATCGTTAATGCCTCGAAGAAATTCGGATCTCTCAAAATCATATAACCATGACGTTCTCTATG	178
Qy	61	GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLeuLySerGlnSerGlu	80
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Qy	81	LyAspArgAlaGlyProProAspProPheGlyTyrGlySerLyAsArgIleGlyProAsn	100
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Qy	101	GlyAspValGlyTyrValGlyTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro	120
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Qy	141	IleThrAlaValLyAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly	160
Db	419	GTTTTCAGCAGTGAAGAAATCTCCTGTGATATCTCTGAAATGTGTGCGGAGGGATTAAG	478
Qy	161	IleArgGlnArgAsnThrLeuSerArgLeuLeuLyAspGluLySerAspSerCysPhe	180
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Qy	181	ArgLeuAsnHisTyrProProCyProGluValGlnAlaLeuAsnArgAsn-----	197
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Qy	218	ThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTyrValSerValProProAspGln	237
Db	659	ACTTCGGGGCTCCAAATATTACTGAAGATGACACTGGATCTCTGTGCCACTGATGAA	718
Qy	238	ThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe	256
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 28, 2005, 01:23:14 ; Search time 249 Seconds
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2362.943 Million cell updates/sec

Title: US-10-670-454-2

Perfect score: 1748

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Searched: 1303057 seqs, 888780828 residues

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Maximum Match 100%

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Database : Issued Patents NA:

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- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
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- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1060.5	60.7	1365	3	US-09-614-912-5
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7	973	55.7	1650	3	US-09-614-912-3
8	972	55.6	1473	3	US-09-614-912-7
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11	936.5	53.6	1318	3	US-09-719-108-5	Sequence 5, Appli
12	746	42.7	783	3	US-09-371-307-57	Sequence 67, Appl
13	661	37.8	966	3	US-09-371-307-58	Sequence 58, Appl
14	553	31.6	811	3	US-09-371-307-71	Sequence 71, Appl
15	442.5	25.3	406	3	US-09-371-307-68	Sequence 68, Appl
16	442	25.3	4170	3	US-09-371-307-56	Sequence 57, Appl
17	430	24.6	403	3	US-09-371-307-66	Sequence 66, Appl
18	428	24.5	1228	2	US-08-823-986A-1	Sequence 1, Appli
19	428	24.5	1228	2	US-08-784-385-1	Sequence 1, Appli
20	414	23.7	1270	6	PCT-US95-10403-1	Sequence 1, Appli
21	402.5	23.0	1250	2	US-08-379-556A-9	Sequence 9, Appli
22	384	22.0	1030	3	US-09-371-307-5	Sequence 5, Appli
23	373.5	21.4	1293	3	US-09-454-034-7	Sequence 7, Appli
24	365	20.9	426	3	US-09-371-307-70	Sequence 70, Appl
25	365	20.9	1663	2	US-08-823-986A-3	Sequence 3, Appli
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ALIGNMENTS

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; Sequence 1, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/09/719,108
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
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; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: Phaseolus coccineus
US-09-719-108-1

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Percent Similarity: 100.00%
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Conservative: 0
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; Sequence 62, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Glycine max
; US-09-371-307-62
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Score: 1530.50 Matches: 236
Percent Similarity: 90.38% Conservative: 4
Best Local Similarity: 89.16% Mismatches: 31
Query Match: 87.1% Indels: 1
DB: 3 Gaps: 1
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Qy 220 GlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSer 239
Db 762 GGCCTGCACAAATCTGCTCACAGATGGCACTTGGGTTTCTGTCCCACTGATCAAACTTCC 821
Qy 240 PhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLeuSerVal 259
Db 822 TTTTTCATCAATGTTGGTGACACTCTTCAGGTAATGACTAATGGAGGTTTAAAGTGTA 881
Qy 260 LysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyPheGlyGly 279
Db 882 AAGCATAGAGTTTGGCTGACCCCAACCAAGTCAAGGTTGTCAATGATCTACTTTGGAGGA 941
Qy 280 ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluClyCys 299
Db 942 CCACCTTGTGTGAAAGATAGCACCTTTTACCTTCACTCATGTTTAAAGGAGAGAGAGT 1001
Qy 300 LeuTyLysGluPheThrTrpCysGluTyLysAlaAlaTyThrSerArgLeuAla 319
Db 1002 TTCTACAAAGAGTTTCACTGTTGGGAAATACAAAGAGGCTGCTACGCTCAAGGCTAGG 1061
Qy 320 AspAsnArgLeuAlaProPheGlnLysSerAlaAla 331
Db 1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCT 1097

RESULT 3

US-09-719-108-7
; Sequence 7, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/09/719, 108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 7
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-719-108-7

Alignment Scores:
Pred. No.: 7 38e-124 Length: 1237
Score: 1092.50 Matches: 210
Percent Similarity: 76.81% Conservative: 45
Best Local Similarity: 63.25% Mismatches: 72
Query Match: 62.50% Indels: 5
DB: 3 Gaps: 3

US-10-670-454-2 (1-331) x US-09-719-108-7 (1-1237)

Qy 1 MetValValLeuSerGlnProAlaLeu-----AsnGlnPhePheLeuLysProPhe 18
Db 109 ATGGTGGTTTTCACAGAGCAGTCACTTTAGATAACCAATCTCCCTAATCCCAATAC 168
Qy 19 LysSerThrProLeuPheThr-----GlyIleProValValAspLeuThrHisProAsp 36
Db 169 AAACCGGTTTCGGTTCCTCACTTCCCAATTCATTCCTGCTCAACCTGAGGAGTCCGGA 228

Qy 37 AlalysAsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHis 56
Db 229 CGCAAAACCGCAATTCGTAAGAGCTCGAGAGTTCGGGTTCTTCAAGGTCGTAAACAC 288
Qy 57 GlyValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLys 76
Db 289 GGAGTCGACCCGAACTCATCTGCTTAGAGCAGGAGGCTATTGGCTTCTTCGGCTTG 348
Qy 77 SerGlnSerGluLysAspArgAlaGlyProProAspPropheGlyTyArgSerLysArg 96
Db 349 CCTCAGTCTCTTAAACACCGGCGGTCACCTGAACCGTACGGTTATGGTATATTAACCG 408
Qy 97 IleGlyProAsnGlyAspValGlyTrpValGluTyLeuLeuLeuAsnThrAsnProAsp 116
Db 409 ATTGGACCAACCGGTGACGTTGGTTGATTCAGTATCTCCTCCTCAATGCTAATCCTCAG 468
Qy 117 ValIleSerProLysSerLeuCysIlePheArgGluAsnProHisPheArgAlaVal 136
Db 469 CTCCTCTCTCTAAACCTCCGCGGTTTCGTCAAACCCCTCAATTTTCGCTGAGTCG 528
Qy 137 ValGluAsnTyIleThrAlaValLysAsnMetCysTyAlaValLeuGluLeuMetAla 156
Db 529 GTGAGGAGGATACATGAAGGAGATTAAAGGAGTGTCTACAAGGTTGTGAGATGCTGCC 588
Qy 157 GluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSer 176
Db 589 GAAGAACTTAGGATAGAGCCCAAGGACACTCTCGATGATAAATGCTGAGAGTGAAGAGT 648
Qy 177 AspSerCysPheArgLeuAsnHisTyProProCysProGluValGlnAlaLeuAsnArg 196
Db 649 GACTCGTCCCTGAGACTAAACCATATCCGGCGGCGGAGGAA---GAGCGGAGAGATG 705
Qy 197 AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn 216
Db 706 GTGAAGTGGGTTTGGGGACACACACACACACAGATAATCTCAGTGTCTAAGATCTAAT 765
Qy 217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAsp 236
Db 766 AACACGGCGGCTCTTCAAACTCTGTGAAAGATGGAAGTGGGTCGCTGTCTCCTCTGAT 825
Qy 237 GlnThrSerPheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
Db 826 CACTCTCTTCTTCAATTAATGTTGGAGATGCTCTTCAGGTTATGACTAACGGAGGTTTC 885
Qy 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTy 276
Db 886 AAGAGTGTAAACACAGAGGCTCTTAGCCGATACAGAGGATCGAGGATTTCAATGATAT 945
Qy 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296
Db 946 TTCGGCGGACCGCAATTCAGCCAGAGATCGCACCATTTGCCATTCGCTTGTCTCCCTGAGCAA 1005
Qy 297 GluGluCysLeuTyLysGluPheThrTrpCysGluTyLysLeuLysAlaAlaTyThrSer 316
Db 1006 GATGATTGGCTTTTACAAAGAAATTCATTTGGTCTCAATACAAATCTTCTGCTTACAGTCT 1065
Qy 317 ArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
Db 1066 AAGCTTGGTGAATTATAGACTTGGTCTCTTTGAGAAA 1101

RESULT 4

US-09-614-912-13
; Sequence 13, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude

```

; APPLICANT: Caimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 1352
; TYPE: DNA
; ORGANISM: Glycine max
US-09-614-912-13

Alignment Scores:
Pred. No.: 7,49e-121 Length: 1352
Score: 1068.50 Matches: 201
Percent Similarity: 77.95% Conservative: 57
Best Local Similarity: 60.73% Mismatches: 68
Query Match: 61.13% Indels: 5
DB: 3 Gaps: 2

US-10-670-454-2 (1-331) x US-09-614-912-13 (1-1352)

QY 1 MetValValSerGlnProAlaLeuAenGlnPhePheLeuLeuLysProPheLysSer 20
DB 159 ATGGTGTTCCTCCAAAGCAACACAGAACTACTCTACATTAAGAACTGCATGCCA 218
QY 21 ThrProLeuPheThrGlyLeuProValValAspLeuThrHisProAspAlaLysLeu 40
DB 219 ACCAAATTTCTCCAAATTCCTCCATAGTGGACCTCTCCAAACCTGATCCAAAGACCCCTT 278
QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHisGlyValProLeu 60
DB 279 ATAGTGAAGCTGTGAGAGTTGGATTCTTCAAGTCAATCATCATGTTCTCTCCATG 338
QY 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
DB 339 GAAGCTATATCCGAATTGGAATATGAAGCTTCAAAATCTCTCTATGTCACCTCAATGAA 398
QY 81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
DB 399 AAGGAAAAAGTAGGACCTCCCAATCCATTTGGTATGGTAGCAAGAAAATGGACACAA 458
QY 101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
DB 459 GGGGAGTTGGTGGATTGAGTACCTCTCTCAACACCAATCAAGAA----- 506
QY 121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
DB 507 CACAACCTCTCTGTTATGGGAAAAACCTGAGAAATTCAGGTGTCGTGTGAACAGTTAC 566
QY 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
DB 567 ATGCTCTCTGTGAGGAAGATGGCATGTGAGATTCTTGAGTTGATGCGACAGGGTTGAAG 626
QY 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
DB 627 ATTCAGCAAAAGATGTGTTTACAGAGCTCTTAATGGATAAAACAAAGTGACTCTATTTC 686
QY 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200

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Db 687 AGGGTGAATCATTTACCTCTGTCTGCTGAATGACTCTGAATGATCAGAACTTGATTGGG 746
QY 201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGly 220
DB 747 TTTGGAGAACACACAGACCCACAAATCATCTCTCTGTTAAGATCCCAACACACTTCAGGC 806
QY 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSerPhe 240
DB 807 CTTTCAGATTATCTTAGAGATGGAATTTGGAATTCAGTCCCACAGATGACAAATCCTTT 866
QY 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
DB 867 TTTATTAACTGTTGGTGAATCTCTTCAGGTATTGACAAATGGAAGGTTCGAAAGTGTGAGA 926
QY 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
DB 927 CACAGAGTGTGGCAATGGGTTCAAGTCCAGCTTCAATGATTACTTTGGAGGTCCA 986
QY 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
DB 987 CCTTTGAGTGAGAAATAGCACCATTTATCTCTCTCATG---AAGGAAAAGAAAGTCTTA 1043
QY 301 TyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp 320
DB 1044 TATAAAGAGTTTACCTGTTGAGTACAAAAAATCAATCTACGGTTCAAGATTATCTAAA 1103

RESULT 5
US-09-614-912-5
; Sequence 5, Application US/09614912
; Patent No. 6677502
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Orozco, Buddy
; APPLICANT: Miao, Gou-Hau
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Lee, Jian Ming
; APPLICANT: Sakai, Hajime
; APPLICANT: Weng, Zude
; APPLICANT: Caimi, Perry G
; APPLICANT: Anderson, Shawn
; TITLE OF INVENTION: Plant Metabolism Genes
; FILE REFERENCE: BB1378 US NA
; CURRENT APPLICATION NUMBER: US/09/614,912
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,401
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,412
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/146,650
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Glycine max
US-09-614-912-5

Alignment Scores:
Pred. No.: 7,29e-120 Length: 1365
Score: 1060.50 Matches: 200

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[illegible]

QY 316 SerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
 Db 1067 TCAAGGCTTGGAGACAACAGGTCGCCCAAGTTTGAGAAG 1105

RESULT 8

US-09-614-912-7
 ; Sequence 7, Application US/09614912
 ; Patent No. 6677502
 ; GENERAL INFORMATION:
 ; APPLICANT: Allen, Steve
 ; APPLICANT: Rafalski, Antoni
 ; APPLICANT: Orozco, Buddy
 ; APPLICANT: Miao, Gou-Hau
 ; APPLICANT: Famodu, Omolayo O.
 ; APPLICANT: Lee, Jian Ming
 ; APPLICANT: Sakai, Hajime
 ; APPLICANT: Weng, Zude
 ; APPLICANT: Caimi, Perry G
 ; APPLICANT: Anderson, Shawn
 ; TITLE OF INVENTION: Plant Metabolism Genes
 ; FILE REFERENCE: BB1378 US NA
 ; CURRENT APPLICATION NUMBER: US/09/614,912
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: 60/143,401
 ; PRIOR FILING DATE: 1999-07-12
 ; PRIOR APPLICATION NUMBER: 60/143,412
 ; PRIOR FILING DATE: 1999-07-12
 ; PRIOR APPLICATION NUMBER: 60/146,650
 ; PRIOR FILING DATE: 1999-07-30
 ; PRIOR APPLICATION NUMBER: 60/170,906
 ; PRIOR FILING DATE: 1999-12-15
 ; PRIOR APPLICATION NUMBER: 60/172,959
 ; PRIOR FILING DATE: 1999-12-21
 ; PRIOR APPLICATION NUMBER: 60/172,946
 ; PRIOR FILING DATE: 1999-12-21
 ; NUMBER OF SEQ ID NOS: 204
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 7
 ; LENGTH: 1473
 ; TYPE: DNA
 ; ORGANISM: Triticum aestivum
 US-09-614-912-7

Alignment Scores:

Pred. No.: 5,97e-109 Length: 1473
 Score: 972.00 Matches: 194
 Percent Similarity: 72.64% Conservative: 45
 Best Local Similarity: 58.97% Mismatches: 86
 Query Match: 55.61% Indels: 4
 DB: 3 Gaps: 3

US-10-670-454-2 (1-331) x US-09-614-912-7 (1-1473)

QY 1 MetValValLeu---SerGlnProAlaLeuAenGlnPhePheLeuLeuLysProPheLys 19
 Db 124 ATGTGGTGTCTCGCAGCAGCGCGCGTGCATCATCCCGCTCTCCGCTCGCCCGC 183
 QY 20 SerThrProLeuPheThrGlyLeProValValLeuLeuThrHisProAspAlaLysAen 39
 Db 184 CCGGGGACTACTTCTCGGCGATCGGCGTGGTGCACCTCTCCAGCCCTGGCGCGCGCGG 243
 QY 40 LeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValPro 59
 Db 244 GCCATCGCGCAGCGTGCAGCGCTTCGGGTTCTTCAAGCTGTCACACCGGGTGCC 303
 QY 60 LeuGluLeuMetAlaAsnLeuGluAenGluAlaLeuArgPhePheLysLysSerGlnSer 79
 Db 304 GCGACACCGTACAGGCTCGAGTCGAGCGCGTCAGGTTCTTCTCGCTCGCGCGCGCC 363
 QY 80 GluLysAspArgAlaGlyProProAspProPheGlyThrGlySerLysArgIleGlyPro 99
 Db 364 GACAAGGACCGCTCGCGCGCGCGCTACCGGTTTCGCTACGCGCAGCAGCGCATCGGCTC 423

QY 100 AsnGlyAspValGlyTrrpValGlyLysLeuLeuAenThrAsnProAspValLys 119
 Db 424 AATGGCAGCATGGGTGGCTCGAGTACTGCTCTCTCCGCGCTC-----GACTCCCGCTCG 477
 QY 120 ProLysSerLeuCysIlePheArgGluAenProHisPheArgAlaValValGluAen 139
 Db 478 CTCCTCCGCGCTGGCGCTC---CCGTCTCGCGCTCTTCCGCGCGCTGCGCGCGAG 534
 QY 140 TyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeu 159
 Db 535 TACATCGCGCGCTGGCGAGTGGCGGTGATGAGCGGATGCGAGCGATGCGCGAGCGCTG 594
 QY 160 GlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCys 179
 Db 595 GGCATTCGCGCGCTGGACGCTGAGCGGATGGTGGCGCGCGAGCGCGAGCGAGCGAG 654
 QY 180 PheArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAenArgAenLeuVal 199
 Db 655 TTCGGGTGAACCACTACCGCGCTGCCCGCTGCGAGGGCTGGGCTGCGAGCGCCACC 714
 QY 200 GlyPheGlyGluHisThrAspProGlnIleSerValLeuArgSerAsnSerThrSer 219
 Db 715 GCTTCGCGCGAGCACACGACCGCGCTCATCTCGGTCTGCGCTCCCAACGCGCAGCTCC 774
 QY 220 GlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSer 239
 Db 775 GGCCTGCAGATCGCGCTCCAGAACGGCGAGTGGGTGCTCGCTCGGACCGCGACGCC 834
 QY 240 PhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerVal 259
 Db 835 TTCCTGTCACAGCTCGCGCTCTGTTGCGAGTGTGTCACACGCGAGGTTCAAGAGCGTG 894
 QY 260 LysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGly 279
 Db 895 AAGCACAGGCTGGTGGCCACACAGCCTAAAGTCTAGGTTTCCATGATCTTCTTGGAGG 954
 QY 280 ProAlaLeuSerGluAenIleAlaProLeuProSerValMetLeuLysGlyGluGluCys 299
 Db 955 CCAGCGATGACACAGAGATTGTCACATTGCGCGAGCTGCTGGCGCGCGAGAGAGAGC 1014
 QY 300 LeuTyrLysGluPheThrTrrpCysGlyTyrLysLysAlaAlaTrrpSerArgLeuAla 319
 Db 1015 CTGTACAAGGACTTCACATGGGCGAGTACAAGAAGGCTGCCTACACTCCAGGCTCGGG 1074
 QY 320 AspAsnArgLeuAlaProPheGlnLys 328
 Db 1075 GACAACAGGCTGGCTCAGTTCACAGG 1101
 RESULT 9
 US-09-614-912-1
 ; Sequence 1, Application US/09614912
 ; Patent No. 6677502
 ; GENERAL INFORMATION:
 ; APPLICANT: Allen, Steve
 ; APPLICANT: Rafalski, Antoni
 ; APPLICANT: Orozco, Buddy
 ; APPLICANT: Miao, Gou-Hau
 ; APPLICANT: Famodu, Omolayo O.
 ; APPLICANT: Lee, Jian Ming
 ; APPLICANT: Sakai, Hajime
 ; APPLICANT: Weng, Zude
 ; APPLICANT: Caimi, Perry G
 ; APPLICANT: Anderson, Shawn
 ; TITLE OF INVENTION: Plant Metabolism Genes
 ; FILE REFERENCE: BB1378 US NA
 ; CURRENT APPLICATION NUMBER: US/09/614,912
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: 60/143,401
 ; PRIOR FILING DATE: 1999-07-12
 ; PRIOR APPLICATION NUMBER: 60/143,412
 ; PRIOR FILING DATE: 1999-07-12
 ; PRIOR APPLICATION NUMBER: 60/146,650
 ; PRIOR FILING DATE: 1999-07-30


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; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1555
; TYPE: DNA
; ORGANISM: Zea mays
US-09-614-912-1

Alignment Scores:
Pred. No.: 3,92e-107 Length: 1555
Score: 957.50 Matches: 191
Percent Similarity: 70.75% Conservative: 46
Best Local Similarity: 57.01% Mismatches: 83
Query Match: 54.78% Indels: 15
DB: 3 Gaps: 4

US-10-670-454-2 (1-331) x US-09-614-912-1 (1-1555)

QY 1 MetValValLeuSerGln---ProAlaLeuAsnGlnPhePheLeuLeuLeuSerProPheLeu 19
DB 118 ATGGTGGTCTCGCAACCGCTGTCGTCGACGATCCCGCTCTCGGGTCCCGGGC 177
QY 20 SerThrProLeuPheThrGlyLeProValValAspLeuThrHisProAspAlaLeu 39
DB 178 CCAGGAGCAGCTTCTCGGGAGTGGCGGTGCTCGACTGTCACGCGCACCGCGCGCGG 237
QY 40 LeuIleValAsnAlaCysArgAspPheGlyPheLeuValAsnHisGlyValPro 59
DB 238 GCGAGTGTGCGGCTCGAGCGCTTCGGGTCTTCAAGGTGCTCAACACCGCGGTGGCC 297
QY 60 LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLeuLeuSerGlnSer 79
DB 298 GGGCCACCATGGACAGGCCGAGTCCGAGGCGGTCTTTCGCGAGCGGCGAGGG 357
QY 80 GluLeuAspArgAlaGlyProProAspPheGlyTyrGlySerIysArgIleGlyPro 99
DB 358 GACAAGGACCGCGCGGGCGCGGTACCGGTTCGGGTACGCGAGCAAGCGGATCGGGCTC 417
QY 100 AsnGlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSer 119
DB 418 AATGGCGACATGGGGTGGCTCGAGTACCTCTCTCGCGCGCGCGCTGCTCTCC 477
QY 120 -----ProLysSerLeuCysIlePheArgGluAsnProHisPheArg 134
DB 478 GAGCGCTGCGCGCTGCTCCAGCGCGCG-----TTCCGG 513
QY 135 AlaValValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeu 154
DB 514 AGCGCGCTGAACGAGTACGTGCGGCGCGTGGCGAGGTGGCGGCGGTGCTGGAGGGC 573
QY 155 MetAlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGlu 174
DB 574 ATGGCGAGGCGCGTGGGCATTCGGACGCGGAGCGCGCTGAGCTCCATGCTGAGCGCGCG 633
QY 175 LysSerAspSerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeu 194
DB 634 GGGAGCGACACAGGTGTTCGCGTGAACCACTACCCGCCCTGCCCCCGCTGAGGGCCGTG 693
QY 195 AsnArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleSerValLeuArg 214
DB 694 GGCTGCAGCACACCGGCTTCGSCGAGCACACCGACCCGACAGATCATCTCGGTGCTCCGC 753
QY 215 SerAsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThr----TrpValSerVal 233
DB 754 TCCAACGGACCTTCGCGCTCGAGATCGCGCTCCGCGACGCGCGCGAGTGGGTCTCCGTG 813
QY 234 ProProAspGlnThrSerPheIleAsnValGlyAspAlaLeuGlnValMetThrAsn 253

; PRIOR APPLICATION NUMBER: 60/170,906
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 60/172,959
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/172,946
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1555
; TYPE: DNA
; ORGANISM: Zea mays
US-09-614-912-1

Alignment Scores:
Pred. No.: 3,92e-107 Length: 1555
Score: 957.50 Matches: 191
Percent Similarity: 70.75% Conservative: 46
Best Local Similarity: 57.01% Mismatches: 83
Query Match: 54.78% Indels: 15
DB: 3 Gaps: 4

US-10-670-454-2 (1-331) x US-09-614-912-1 (1-1555)

QY 1 MetValValLeuSerGln---ProAlaLeuAsnGlnPhePheLeuLeuLeuSerProPheLeu 19
DB 118 ATGGTGGTCTCGCAACCGCTGTCGTCGACGATCCCGCTCTCGGGTCCCGGGC 177
QY 20 SerThrProLeuPheThrGlyLeProValValAspLeuThrHisProAspAlaLeu 39
DB 178 CCAGGAGCAGCTTCTCGGGAGTGGCGGTGCTCGACTGTCACGCGCACCGCGCGCGG 237
QY 40 LeuIleValAsnAlaCysArgAspPheGlyPheLeuValAsnHisGlyValPro 59
DB 238 GCGAGTGTGCGGCTCGAGCGCTTCGGGTCTTCAAGGTGCTCAACACCGCGGTGGCC 297
QY 60 LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLeuLeuSerGlnSer 79
DB 298 GGGCCACCATGGACAGGCCGAGTCCGAGGCGGTCTTTCGCGAGCGGCGAGGG 357
QY 80 GluLeuAspArgAlaGlyProProAspPheGlyTyrGlySerIysArgIleGlyPro 99
DB 358 GACAAGGACCGCGCGGGCGCGGTACCGGTTCGGGTACGCGAGCAAGCGGATCGGGCTC 417
QY 100 AsnGlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSer 119
DB 418 AATGGCGACATGGGGTGGCTCGAGTACCTCTCTCGCGCGCGCGCTGCTCTCC 477
QY 120 -----ProLysSerLeuCysIlePheArgGluAsnProHisPheArg 134
DB 478 GAGCGCTGCGCGCTGCTCCAGCGCGCG-----TTCCGG 513
QY 135 AlaValValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeu 154
DB 514 AGCGCGCTGAACGAGTACGTGCGGCGCGTGGCGAGGTGGCGGCGGTGCTGGAGGGC 573
QY 155 MetAlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGlu 174
DB 574 ATGGCGAGGCGCGTGGGCATTCGGACGCGGAGCGCGCTGAGCTCCATGCTGAGCGCGCG 633
QY 175 LysSerAspSerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeu 194
DB 634 GGGAGCGACACAGGTGTTCGCGTGAACCACTACCCGCCCTGCCCCCGCTGAGGGCCGTG 693
QY 195 AsnArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleSerValLeuArg 214
DB 694 GGCTGCAGCACACCGGCTTCGSCGAGCACACCGACCCGACAGATCATCTCGGTGCTCCGC 753
QY 215 SerAsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThr----TrpValSerVal 233
DB 754 TCCAACGGACCTTCGCGCTCGAGATCGCGCTCCGCGACGCGCGCGAGTGGGTCTCCGTG 813
QY 234 ProProAspGlnThrSerPheIleAsnValGlyAspAlaLeuGlnValMetThrAsn 253

; Sequence 9, Application US/09719108
; Patent No. 6670527
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-719-108-9

Alignment Scores:
Pred. No.: 7,04e-107 Length: 1008
Score: 953.00 Matches: 186
Percent Similarity: 70.12% Conservative: 44
Best Local Similarity: 56.71% Mismatches: 96
Query Match: 54.52% Indels: 2
DB: 3 Gaps: 1

US-10-670-454-2 (1-331) x US-09-719-108-9 (1-1008)

QY 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
DB 1 ATGGTAATTTGTTTACAGCCAGCCAGTTTGTATAGCAACCTCTATGTTTAAATCCAAATGC 60
QY 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
DB 61 AAACCGCGTCCGGTTTAAATCCCTGTTATAGACTTAACCGACTCAGATGCCAAACCCAA 120
QY 41 IleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHisGlyValProLeu 60
DB 121 ATCGTCAAGGCATGTGAGAGTTTGGGTCTTCAAAGTCAACCATCGGGTCCGACCC 180
QY 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
DB 181 GATCTTTGACTCAGTTGGAGCAAGGCATCAACTTCTTTCCTTGGCATCACTCTCTC 240
QY 81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerIysArgIleGlyProAsn 100
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Db 163 AGAATGGACAGAGCTATTAACCTCTTTGCTAAACCGCTCAGCAGAGAAATCTGTCT 222
Qy 85 GlyProProasp---ProPheGlyTyrGlySerLysArgIleGlyProAsnGlyAspVal 103
Db 223 CGACCATTTAACAGCCTTTCCGGTATGTTTATAGACATTTGGACTCAACGGTACTCT 282
Qy 104 GlyTTPValGluTyrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 123
Db 283 GGTGAGGTTCAGTATTTGCTTTTACACTAACGACCTTCGC----- 324
Qy 124 CysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyrIleThrAla 143
Db 325 -----TTTCGC---FCTCAGCTCTCTTCACTCGCAGTGAATTTTACATAGAACA 375
Qy 144 ValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGlyIleArgGln 163
Db 376 GTTAAGCAGTTGGCTCGTCGATCTTAGATCTGACGGCTGAGGACTTCATGTC---CCA 432
Qy 164 ArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPheArgLeuAsn 183
Db 433 CCTCAGATTTTCAGTAGGTTAATACAGCTCCGTCGATAGTACTCCGTTCTGAGAGTGAAT 492
Qy 184 HisTyrProProCysProGluVal-----GlnAlaLeuAsn 195
Db 493 CATTATCCACCGTCCGATCAATCTTTGTTGTAAGCCAAATCTTTGACCAATCTGTGTCA 552
Qy 196 ArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSer 215
Db 553 CTGACAAGAGTTGGCTTCGAGAACACACACCGACCTCAGATTTTAACAGTTCTTAGACT 612
Qy 216 AsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTTPValSerValProPro 235
Db 613 AACGGTGTAGGAGGGTCCCAAGTGTCCAAATTCAGATGGCATGTGGGTTTCTGTCTCCCT 672
Qy 236 AspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArg 255
Db 673 GACCTTCAGCTTTCTGCGTCAATGTAGGAGACTTTGTACAGGTGATGACGAACGGGAGA 732
Qy 256 PheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIle 275
Db 733 TTTATAAGTGTAAAGCATAGACATTTGACTACGGAGAGAAAGCCGGTATCCACGGCG 792
Qy 276 TyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSer---ValMetLeu 294
Db 793 TACTTTGCGGACCAACCGCTTCAGGCGAAGATTGGGCTCTTTTCGCGCATGTTATGACG 852
Qy 295 LysGlyGluGluCysLeuTyrLysGluPheThrTTPCysGluTyrLysIleAlaTyr 314
Db 853 ATGAATCAGCCACCGTGTGTACCAAAACATTTACTTGGGGCGGAGTACAAAGAAACTTGGGTAC 912
Qy 315 ThrSerArgLeuAlaAspAsnArgLeuAlaProPheGln 327
Db 913 TCTCTACGACTTGAGNTAGCGTTTAGACATGTTTCGT 951

RESULT 14
US-09-371-307-71
; Sequence 71, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 811
; TYPE: DNA
; ORGANISM: Zea mays
US-09-371-307-71
Alignment Scores:
Pred. No.: 6,14e-58 Length: 811
Score: 553.00 Matches: 108
Percent Similarity: 71.88% Conservative: 30
Best Local Similarity: 56.25% Mismatches: 48
Query Match: 31.64% Indels: 6
DB: 3 Gaps: 2
US-10-670-454-2 (1-331) x US-09-371-307-71 (1-811)
Qy 140 TyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeu 159
Db 2 TACACGGTGGCGGTTCGGCGGATGGCGTGGCGGTGGAGCTGATGGCGAGGGGCTG 61
Qy 160 GlyIle-----ArgGlnArgAsnThrLeuSerArgLeuLysAspGluLysSer 176
Db 62 GCATCGCGCGCGCGCGCGGACCGCGTGTGGCGCGGCTGGTGGCGCGGACAGC 121
Qy 177 AspSerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArg 196
Db 122 GACTGCATGCTCGCGGTGAACCACTTACCGCGCGCGCGCG-----GCGCTCAACCCC 172
Qy 197 AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn 216
Db 173 AGCTTCACGGGTTTCGGCGGACACACCGACCGCAGATCATCTCGGTGCTCCGCGCCAAC 232
Qy 217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTTPValSerValProProAsp 236
Db 233 GGCACCTCGCGCTGGAGATCGCGTGGCGGACCGCGCTGGGCTCGCTCCGCGCCGAC 292
Qy 237 GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
Db 293 GGGGACGCTTCTTCGTCAACGTCGCGACACCCCTGCGAGGTGTTGACGAACGGGAGTTC 352
Qy 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyr 276
Db 353 AGGAGCTGGAGCAGAGGTGGTGAACACGAGAAAGTCCCGGTTGTCATGTGCTTC 412
Qy 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296
Db 413 TTCGCGCGCGCGCGCGCGGAGGCTGGGCGCGCTTCGCGACGCTCTCGGCGACGGC 472
Qy 297 GluGluCysLeuTyrLysGluPheThrTTPCysGluTyrLysIleAlaTyrThrSer 316
Db 473 GCGCGGACCGGTACCGGACTTCACCTGGAGCGAGTTCAGACCCAGACCGGGTGCAGGACC 532
Qy 317 ArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
Db 533 AGGCTCGCGAAGACCGCTGTCCGCTTCGAGAG 568

RESULT 15
US-09-371-307-68
; Sequence 68, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216

; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (306)
; OTHER INFORMATION: n = a, c, g, or t
US-09-371-307-68

Alignment Scores:
Pred. No.: 7.5e-45 Length: 406
Score: 442.50 Matches: 87
Percent Similarity: 75.71% Conservative: 19
Best Local Similarity: 62.14% Mismatches: 25
Query Match: 25.31% Indels: 9
DB: 3 Gaps: 4

US-10-670-454-2 (1-331) x US-09-371-307-68 (1-406)

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QY 83 ArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsnGlyAsp 102
   :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2 AAAACAGGACAAACCCAGCCTTATGCTATGGTAATAAAGGATTGGACCAATGGTGAT 61

QY 103 ValGlyTrrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerProLysSer 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 GTTGGTTGGGTGGATATCTCTCTCCACAAACCAACCAAGAC-----CCGAATCTC 112

QY 123 LeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyrIleThr 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 CTT-----GGAACAGAAACCCAGAGAGTTTCAGGATTGCTTTGGATAATTATATGGCA 166

QY 143 AlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGlyIleArg 162
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 167 GCAGTCGAGAAATGGCATCTGAGATACCTTGAATCATAGCTGATGGGCTAAAGGTTTCA 226

QY 163 GlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPheArgLeu 182
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 227 CCAAGAAATGTTTAAAGTAAGCTGATGATGATGATGATGATGATGATGATGATGATG 286

QY 183 AsnHisTyrProProCysProGlu---ValGlnAlaLeuAsn-----ArgAsnLeu 198
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 287 AACCATACCCCTCCGTCNAGAGGTGGTTCAGTCTTGAATGGAAACGAGCAGTAATGTG 346

QY 199 ValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThr 218
   :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 347 ATTGGATTGGTGAAACACACTGACCCACCAATCATTTTCAGTCTTAAGATCCACACACT 406
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Search completed: December 28, 2005, 04:48:40
Job time : 256 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 28, 2005, 01:30:23 ; Search time 975 Seconds
(without alignments)
2807.348 Million cell updates/sec

Title: US-10-670-454-2

Perfect score: 1748

Sequence: 1 MVVLSQPALNQFLLKPKFS.....AAYTSRLADNLAPQKSA 331

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USFIO.spool/US10670454/runat_27122005_124842_29154/app_query.fasta_1.519

-DB=Published Applications NA Main -QFMT=fastap -SUFFIX=p2n.rnpbm

-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1

-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct

-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext

-HEA=SIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US10670454 @CGN 1.1 1026 @runat_27122005_124842_29154 -NCPU=6 -ICPU=3

-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main.*

1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq.*

2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq.*

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6: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq.*

7: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq.*

8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq.*

9: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq.*

10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1748	100.0	999	8	US-10-821-711-3
2	1748	100.0	1318	8	US-10-670-454-1
3	1530.5	87.6	1359	3	US-09-371-307-62
4	1530.5	87.6	1359	6	US-10-401-321-62
5	1092.5	62.5	1026	3	US-09-938-842A-1350
6	1092.5	62.5	1026	3	US-09-938-842A-1350
7	1092.5	62.5	1237	8	US-10-670-454-7

Alignment Scores:

Pred. No.:	2.28e-219	Length:	999
Score:	1748.00	Matches:	331
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

ALIGNMENTS

RESULT 1

US-10-821-711-3

; Sequence 3, Application US/10821711

; Publication No. US20040237142A1

; GENERAL INFORMATION:

; APPLICANT: Gilbertson, Larry A

; APPLICANT: Krieger, Elysia K

; APPLICANT: Ye, Xudong

; APPLICANT: Zhang, Wanggen

; TITLE OF INVENTION: DNA CONSTRUCTS AND METHODS TO ENHANCE THE PRODUCTION OF

; FILE REFERENCE: 38-21(52967)B

; CURRENT APPLICATION NUMBER: US/10/821,711

; PRIOR FILING DATE: 2004-04-08

; PRIOR APPLICATION NUMBER: 60/461,459

; NUMBER OF SEQ ID NOS: 16

; SEQ ID NO 3

; LENGTH: 999

; TYPE: DNA

; ORGANISM: Phaseolus coccineus

US-10-821-711-3

Sequence 64, Appl
Sequence 64, Appl
Sequence 21951, A
Sequence 3, Appl1
Sequence 78659, A
Sequence 69575, A
Sequence 9, Appl1
Sequence 141, Appl
Sequence 5, Appl1
Sequence 1288, Ap
Sequence 4257, Ap
Sequence 103352,
Sequence 67, Appl
Sequence 67, Appl
Sequence 1, Appl1
Sequence 16086, A
Sequence 6183, Ap
Sequence 129307,
Sequence 7861, Ap
Sequence 58, Appl
Sequence 58, Appl
Sequence 177171,
Sequence 159585,
Sequence 34429, A
Sequence 71, Appl
Sequence 71, Appl
Sequence 20123, A
Sequence 614, App
Sequence 9278, Ap
Sequence 82089, A
Sequence 68, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 136729,
Sequence 66, Appl
Sequence 66, Appl

US-10-670-454-2 (1-331) x US-10-821-711-3 (1-999)

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Qy 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
Db 1 ATGGTTGTTCTGTCTCAGGCAGCATTTGAACCACTTTTCTCTGAACCACTTCAAGTCC 60
Qy 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
Db 61 ACGCCCTTGTTCACGGGGATCTCTGTGTGCAGCTCAGCACCCCGATGCCAAGATCTC 120
Qy 41 IleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHisGlyValProLeu 60
Db 121 ATAGTGAACGCTGTAGGACTTCGGCTTCTCAAGCTTGTAACCACTGTGTCTCATTTG 180
Qy 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
Db 181 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240
Qy 81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
Db 241 AAAGACAGAGCTGGTCCCGCCGACCTTTCGGCTATGGTAGCAAGAGGATGGCCCCAAC 300
Qy 101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
Db 301 GGTGATGTGGTGGTTCGAATACCTCTCTCAACACCAACCCCTGATGTATCTCACCC 360
Qy 121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
Db 361 AATATCACTTTGGCATTTTCCGAGAAAATCCTCATCTTTCAGGGCGGTGGTGAGAACTAC 420
Qy 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
Db 421 ATTACAGCAGTGAAGAACTGCTATGCGTGTGGATTTGATGGCGAGGGGTGGGG 480
Qy 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
Db 481 ATAAGGCAGAGGAATACGTTAAGCAGGTTCCTGAAGGATGAGAAAAGTGATTCGTGCTTC 540
Qy 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
Db 541 AGGTTGAACCACTACCGGCTTCCCGTGAAGTGCACGACCTGAACCGGAATTTGGTGGG 600
Qy 201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGly 220
Db 601 TTTGGGGAGACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGC 660
Qy 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSerPhe 240
Db 661 TTGCAAAATCTGTCTCAGATGGCACTTGGGTTTTCAGTCCCACTGATCAGACTTCCTTT 720
Qy 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
Db 721 TTCATCAATGTGGTCAGCGCTACAGGTAATGACTAATGGGAGGTTTAAAGTGTAAAG 780
Qy 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
Db 781 CATAGGTTTGGCTGACACAGAGTCAAGGTATCAATGATCTACTTTGGAGGACCA 840
Qy 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
Db 841 GCGTTGAGTGAAATAATAGCACCTTTTACCTTCAGTGATGTTAAAGGAGAGGAGTGTGG 900
Qy 301 TyrLysGluPheThrTrpCysGluTyrLysLeuAlaAlaTyrThrSerArgLeuAlaAsp 320
Db 901 TACAAAAGAGTTTCATGGTGTGAATACAAAGAGGCTCGGTACACTTCAAGGCTAGCTGAT 960
Qy 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
Db 961 AATAGGCTTGGCCCTTTCCAGAAAATCTGCTGCT 993

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RESULT 2

US-10-670-454-1

, Sequence 1, Application US/10670454

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; Publication No. US20040229357A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/10/670,454
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Phaseolus coccineus
US-10-670-454-1

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Alignment Scores:

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Pred. No.: 3,55e-219 Length: 1318
Score: 1748.00 Matches: 331
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

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US-10-670-454-2 (1-331) x US-10-670-454-1 (1-1318)

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Db 68 ATGGTTGTTCTGTCTCAGGCAGCATTTGAACCACTTTTCTCTGAACCACTTCAAGTCC 127
Qy 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
Db 128 ACGCCCTTGTTCACGGGGATTCCTGTGGTGCAGCTCAGCACCCCGATGCCAAGATCTC 187
Qy 41 IleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHisGlyValProLeu 60
Db 188 ATAGTGAACGCTGTAGGAGCTTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCATTG 247
Qy 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
Db 248 GAGTTAATGGCCAAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 307
Qy 81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
Db 308 AAAGACAGAGCTGGTCCCGCCGACCTTTCGGCTATGGTAGCAAGAGGATGGCCCCAAC 367
Qy 101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
Db 368 GGTGATGTGGTGGTTCGAATACCTCTCTCAACCAACCCCTGATGTATCTCACCC 427
Qy 121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
Db 428 AATATCACTTTGCAATTTTCCGAGAAAATCCTCATCATTTTCAGGGCGGTGGTGAGAACTAC 487
Qy 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
Db 488 ATTACAGCAGTGAAGAACTATGCTATGCGGTGTGTGAAATGATGGCGAGGGGTGGGG 547
Qy 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
Db 548 ATNAGGCAGAGGAATACGTTAAGCAGGTTGCTGAGAGGATGAGAAAAGTGATTCGTGCTTC 607
Qy 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200

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Db 608 AGTTGAACCACTACCCGCTTGCCTGAGGTGCAAGCACTGAACCGGAATTTGTTGGG 667
 Qy 201 PheGlyGluHisThrAspProGlnIleSerValLeuArgSerAsnSerThrSerGly 220
 Db 668 TTTGGGAGGACACACAGACCCACAGATAATTTCTGCTTAAGATCTAAACAGCACATCTGGC 727
 Qy 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSerPhe 240
 Db 728 TTGCAAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCACACCTGATCAGACTTCCTTT 787
 Qy 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLeuSerVallys 260
 Db 788 TTCATCAATGTTGGTGAGCTCTACAGGTAAATGACTAATGGAGGTTTAAAGGTGAAG 847
 Qy 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyPro 280
 Db 848 CATAGGGTTTTGGCTGACACAAAGTCAAGTTATCAATGATCTACTTTGGAGGACCA 907
 Qy 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluCysLeu 300
 Db 908 GCGTTGAGTGAATAATAGCACCTTTACCTTCAGTGTATTTAAAGAGGAGAGGTTTGG 967
 Qy 301 TyrLysGluPheThrTrpCysGluTyrLysValAlaTyrThrSerArgLeuAlaAsp 320
 Db 968 TACAAGAGTTTACATGTTGTGAATACAAAGAGGCTGCGTACACTTCAAGGCTAGCTGAT 1027
 Qy 321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
 Db 1028 AATAGGCTTGCCCTTTCCAGAAATCTGCTGCT 1060

RESULT 3

US-09-371-307-62
 ; Sequence 62, Application US/09371307A
 ; Patent No. US20020053095A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Sherri M.
 ; APPLICANT: Heck, Gregory R.
 ; APPLICANT: Pillar, Kenneth J.
 ; APPLICANT: Kishore, Ganesh M.
 ; APPLICANT: Ellich, Tedd D.
 ; APPLICANT: Logusch, Eugene W.
 ; APPLICANT: Rao, Sudabathula
 ; APPLICANT: Ream, Joel E.
 ; APPLICANT: Logusch, Sherry J.
 ; TITLE OF INVENTION: Methods for controlling gibberellin levels
 ; FILE REFERENCE: MOST:216
 ; CURRENT APPLICATION NUMBER: US/09/371,307A
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 62
 ; LENGTH: 1359
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 US-09-371-307-62

Alignment Scores:
 Pred. No.: 1,78e-190 Length: 1359
 Score: 1530.50 Matches: 296
 Percent Similarity: 90.36% Conservative: 4
 Best Local Similarity: 89.16% Mismatches: 31
 Query Match: 87.56% Indels: 1
 DB: 3 Gaps: 1

US-10-670-454-2 (1-331) x US-09-371-307-62 (1-1359)

Qy 1 MetValValLeuSerGlnProAlaLeuAsnGlnPheLeuLeuLysProPheLysSer 20
 Db 102 ATGGTGTGTTCTCTCTCAGCCAGCATTAACCAAGTTTCTCTCTGAAACATGCAAGCC 161
 Qy 21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
 Db 162 ACGCCCTTGTTCGGGGGATTCCTGTGGTGCACCTTCAGGACCCCGATGCCAAGACCCAC 221

Qy 41 IleValIleAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
 Db 222 ATAGTCAATGCTCGAGGACTTCGGCTTCTTCAAGCTCGTGAACCAACGCGTTCCTCGGTTA 281
 Qy 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
 Db 282 CAGTTCATGGCCAAATTTGGAAACGAAACCTTCGGGTCTTCAAAAACCTCAATCCGAG 341
 Qy 81 LysAspArgAlaGlyProProAspPheGlyTyrGlySerLysArgIleGlyProAsn 100
 Db 342 AAAGACAGGGCTGTCTCCCTCGACCTTTGGCTACGGCAGCAGAGGATTTGGCCTTAAC 401
 Qy 101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
 Db 402 GCGCATGTGGTGGTTCGAATACCTCTCTCAACCAACCAACCTGTATCTATCTATCTCCCC 461
 Qy 121 LysSerLeuCysIlePheArgGluAsnProHisIlePheArgAlaValValGluAsnTyr 140
 Db 462 AAGTCACAGTTCAATTTTCAGAGAAGGCTCTCAGAAATTTTCAGGGCGGTGGTGGAGATAC 521
 Qy 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
 Db 522 ATTAGCGGGTGAAGACATGTGCTATCAGGTGTTCGAATTTGATGGCTGAGGGATTGGG 581
 Qy 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
 Db 582 ATAACGCGCAGAGGAATGTGTGAGTAGGTGTGTAAGGATGAGAAGAGTGATYCTTGTCTC 641
 Qy 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsn--ArgAsnLeuVal 199
 Db 642 AGACTTAACCACTACCCGCCATGCCGAGGTGCAAGCATTTGAACGGAAGGAATTTGGTT 701
 Qy 200 GlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSer 219
 Db 702 GGATTTGGAGAGCACACAGACCCACAGATAATTTCTGTCTTGAGATCTAACAGCACCTCA 761
 Qy 220 GlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSer 239
 Db 762 GGCCTTGCAAAATCTGTCTCACAGATGGCACTTGGGTTTCTGTCCACCTGTATCAAACTTCC 821
 Qy 240 PhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerVal 259
 Db 822 TTTTTCATCAATGTGTGGTGACACTTTCAGGTAAATGACTAATGGAGGTTTAAAAAGTGT 881
 Qy 260 LysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGly 279
 Db 882 AAGCATAGAGTTTGGCTGACCCCAACCAAGTCAAGTTGTCAATGATCTACTTTGGAGGA 941
 Qy 280 ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluCys 299
 Db 942 CCACCTTGTGTGAAAGATAGCACCTTTACCTTCACTCATGTTTAAAGAGGAGAGAGT 1001
 Qy 300 LeuTyrLysGluPheThrTrpCysGluTyrLysValAlaTyrThrSerArgLeuAla 319
 Db 1002 TTCTACAAAGAGTTTCATATGTTGGGAAATACAAAGGCTGCGTACGCGTCAAGGCTAGCG 1061
 Qy 320 AspAsnArgLeuAlaProPheGlnLysSerAlaAla 331
 Db 1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCT 1097

RESULT 4

US-10-401-321-62
 ; Sequence 62, Application US/10401321
 ; Publication No. US20030233679A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Sherri M.
 ; APPLICANT: Heck, Gregory R.
 ; APPLICANT: Pillar, Kenneth J.
 ; APPLICANT: Kishore, Ganesh M.
 ; APPLICANT: Ellich, Tedd D.
 ; APPLICANT: Logusch, Eugene W.
 ; APPLICANT: Rao, Sudabathula

APPLICANT: Ream, Joel E.
APPLICANT: Logusch, Sherry J.
APPLICANT: Baerson, Scott R.
TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
FILE REFERENCE: 11899.0216.DVUS01 (MOBT-216--1)
CURRENT APPLICATION NUMBER: US/10/401,321
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.2
SEQ ID NO 62
LENGTH: 1359
TYPE: DNA
ORGANISM: Glycine max
US-10-401-321-62

Alignment Scores:
Pred. No.: 1.78e-190 Length: 1359
Score: 1530.50 Matches: 296
Percent Similarity: 90.36% Conservative: 4
Best Local Similarity: 89.16% Mismatches: 31
Query Match: 87.56% Indels: 1
DB: 6 Gaps: 1

US-10-670-454-2 (1-331) x US-10-401-321-62 (1-1359)

QY 1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
DB 102 ATGGTTGTTCTCTCAGCAGCATTAACACGATTTTCTCTGAAACATGCAAGCCC 161
QY 21 ThrProLeuPheThrGlyLeuProValValAspLeuThrHisProAspAlaLysAsnLeu 40
DB 162 ACGCCCTTGTTCGGGGATTCGTGTGTCGACCTCAGGACCCCGATGCCAAGACCCAC 221
QY 41 IleValAsnAlaCysArgPheGlyPheLeuValAsnHisGlyValProLeu 60
DB 222 ATAGTCAATGCCCTGCGAGGACTTCGCGCTCTTCAAGCTCGTAACACCGATTCGGTGA 281
QY 61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
DB 282 CAGTTCATGCCAATTTGGAAACGAAACCTCGGGTCTTCAAAACCTCAATCCGAG 341
QY 81 LysAspArgAlaGlyProProAspProPheGlyTyrglyserlylsArgileGlyProAsn 100
DB 342 AAAGACAGGCTGGTCCCTCGACCTTTGGCTACGGCAGCAAGAGGATTGGCCCTAAC 401
QY 101 GlyAspValGlyTrpValGluTyrlleuLeuLeuAsnThrAsnProAspValIleSerPro 120
DB 402 GCGATGTCGGTGGGTGGAATACCTCTCAACACCAACCCCTGATGTCATCTCCCC 461
QY 121 LysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsnTyr 140
DB 462 AAGTCAAGTTCATTTTCAGAGAGGCTCTCAGAAATTCAGGCGGTGGTGAAGAAATAC 521
QY 141 IleThrAlaValLysAsnMetCysTyrlaValLeuGluLeuMetAlaGluGlyLeuGly 160
DB 522 ATTAGAGCGGTGAAGAACATGTGCTATGAGGTGTTGGAATTCATGCTCAGGGATTGGG 581
QY 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
DB 582 ATAAACACAGGGAATGTGTGATGATAGGTTCCTGAAGGATGAGAAGAGTATCTTGCCTTC 641
QY 181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsn--ArgAsnLeuVal 199
DB 642 AGACTTAACACTACCCGCCATGCCCGAGGTGCAAGCAATGAAACGAAGGAATTTGGTT 701
QY 200 GlyPheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSer 219
DB 702 GGATTTGGAGAGACACACAGCCACACAGATAATTTCTGTCTTGAGATCTAACAGACCTCA 761
QY 220 GlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSer 239
DB 762 GGCCTGCAAACTGTCTCAGATGGCACTTGGGTTTCTGTGCCACCTGATCAAACTTCC 821

QY 240 PhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerVal 259
DB 822 TTTTTCATCAATGTTGGTGACACTCTTCAGGTAATGACTTAATGGGAGGTTTAAAGTGTA 881
QY 260 LysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGly 279
DB 882 AAGCATAGAGTTTGGCTGACCCAAACCAAGTCAAGGTTGTCAATGATCTACTTTGGAGA 941
QY 280 ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCys 299
DB 942 CCACCTTGTGTGAAAGATAGACCTTTTACCTTCACTCATGTTTAAAGGAGAGAGAGT 1001
QY 300 LeuTyrlsGluPheThrTrpCysGluTyrlsLysAlaAlaTyrThrSerArgLeuAla 319
DB 1002 TTCTACAAAGAGTTTCAATGTTGGGATACAAAGAGGCTGGTACGCTCAAGGCTAGCG 1061
QY 320 AspAsnArgLeuAlaProPheGlnLysSerAlaAla 331
DB 1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCT 1097
RESULT 5
US-09-938-842A-1350
; Sequence 1350, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1350
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1350
Alignment Scores:
Pred. No.: 6.49e-133 Length: 1026
Score: 1092.50 Matches: 210
Percent Similarity: 76.81% Conservative: 45
Best Local Similarity: 63.25% Mismatches: 72
Query Match: 62.50% Indels: 5
DB: 3 Gaps: 3
US-10-670-454-2 (1-331) x US-09-938-842A-1350 (1-1026)
QY 1 MetValValLeuSerGlnProAlaLeu-----AsnGlnPhePheLeuLeuLysProPhe 18
DB 1 ATGGTGGTTCGTCACAGCCAGTCACTTTAGATACCACTCTCCCTAATCCCCACATAC 60
QY 19 LysSerThrProLeuPheThr-----GlyIleProValValAspLeuThrHisProAsp 36
DB 61 AAACCGGTTCGGTTCCTCCTCCCATTCACCTCCCGTCGTCACCTAGCCGATCCGGA 120
QY 37 AlaLysAsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHis 56
DB 121 GCGAAACCCGAATCGTAAAGCCCTGCGAGGAGTTCCGGTCTCTTCAAGTCTGAACAC 180
QY 57 GlyValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLys 76
DB 181 GGAGTCCGACCCGAACACTCATGCTCGTTAGAGCAGGAGGCTATTGGCTTCTTCTCGGCTTG 240

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Qy 77 SerGlnSerGluLysAspArgAlaGlyProProAspPropheGlyTyrGlySerLysArg 96
Db 241 CCTCAGTCTCTTAAACACGGCGCGTCCACCTGAACCGTACGGTTATGTTAAATAAACGG 300
Qy 97 IleGlyProAsnGlyAspValGlyTyrValGluTyrLeuLeuAsnThrAsnProAsp 116
Db 301 ATTGGACCAACACGGTGAGTGGTTGGATTGAGTATCTCCCTCAATGCTTAATCCTCAG 360
Qy 117 ValIleSerProLysSerLeuCysIlePheArgGlnAsnProHisPheArgAlaVal 136
Db 361 CTCCTCTCTCTAAACCTCCGCGCTTTCGGTCAACCCCTCAAAATTTCCGTCAGTCG 420
Qy 137 ValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuLeuMetAla 156
Db 421 GTGAGGAGTACATGAAGGAGATTAAAGGAAGTGTCTGTAACAAGTGTTCGAGATGTTGCC 480
Qy 157 GluGlyLeuGlyIleArgGlnAsnThrLeuSerArgLeuLeuLysAspGluLysSer 176
Db 481 GAAGAACTAGGGATAGACCCAAAGGACACTCTGAGTAAATGCTGAGAGATGAGAAGAGT 540
Qy 177 AspSerCysPheArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsnArg 196
Db 541 GACTCGTCCCTGAGACTAAACCAATATCCGGCGCGGAGGAA--GAGCGGAGAGATG 597
Qy 197 AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn 216
Db 598 GTGAAGGTGGGGTTTGGGGAACACACAGACCACAGATAATCTCAGTCTAAGATCTAAT 657
Qy 217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAsp 236
Db 658 AACACGGGGGTCTTCAAAATCTGTGTGAAGATGGAAGTGGTGGTGGTGGTGGTGGTGGT 717
Qy 237 GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
Db 718 CACTCTCTCTTCAATTAATGTTGAGATGCTCTCAGGTATGAGTTATGACTAACGGAGGTT 777
Qy 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyr 276
Db 778 AAGAGTGTAAACACAGCGTCTTAGCCGATACAAGGAGATCGAGGATTTCAATGATAT 837
Qy 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296
Db 838 TTCGCGGACCGCCATTGAGCCAGAGATCGCACCAATTGCCATGCTTGTCCCTGAGCAA 897
Qy 297 GluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSer 316
Db 898 GATGATTGGCTTTTCAAAAGAAATTCATCTGGTCTCAATACAAATCTTCTGTACAGTCT 957
Qy 317 ArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
Db 958 AAGCTTGGTGATTATAGACTTGGTCTCTTTGAGAA 993

RESULT 6
US-09-938-842A-1350
; Sequence 1350, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
```

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; SEQ ID NO 1350
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1350

Alignment Scores:
Pred. NO.: 6,49e-133 Length: 1026
Score: 1092.50 Matches: 210
Percent Similarity: 76.81% Conservative: 45
Best Local Similarity: 63.25% Mismatches: 72
Query Match: 62.50% Indels: 5
DB: 3 Gaps: 3

US-10-670-454-2 (1-331) x US-09-938-842A-1350 (1-1026)

Qy 1 MetValValLeuSerGlnProAlaLeu-----AsnGlnPhePheLeuLeuLysProPhe 18
Db 1 ATGTGTGGTTTGGCCACAGCCAGTCACCTTTAGATAAACACATCTCCCTTAATCCCCACATAC 60
Qy 19 LysSerThrProLeuPheThr-----GlyIleProValValAspLeuThrHisProAsp 36
Db 61 AAACCGGTTCCGGTTCTCCTCCATTCATCCCGTCGTCAACCTACCGATCCGGAA 120
Qy 37 AlaLysAsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLeuLysValAsnHis 56
Db 121 GCGAAACCCGAAATCGTAAAGCCCTGCGAGGAGTTCGGGTCTTCAAGGTCTAAACCCAC 180
Qy 57 GlyValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLys 76
Db 181 GGAGTCGACCCGAACTCATGCTCGGTAGCAGCAGGAGGTATTTGGTCTTCTCGGCTTG 240
Qy 77 SerGlnSerGluLysAspArgAlaGlyProProAspPropheGlyTyrGlySerLysArg 96
Db 241 CCTCAGTCTCTTAAACACGGCGCGTCCACCTGAACCGTACGGTTATGTTAAATAAACGG 300
Qy 97 IleGlyProAsnGlyAspValGlyTyrValGluTyrLeuLeuAsnThrAsnProAsp 116
Db 301 ATTGGACCAACACGGTGAGTGGTTGGATTGAGTATCTCCCTCAATGCTTAATCCTCAG 360
Qy 117 ValIleSerProLysSerLeuCysIlePheArgGlnAsnProHisPheArgAlaVal 136
Db 361 CTCCTCTCTCTAAACCTCCGCGCTTTCGGTCAACCCCTCAAAATTTCCGTCAGTCG 420
Qy 137 ValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuLeuMetAla 156
Db 421 GTGAGGAGTACATGAAGGAGATTAAAGGAAGTGTCTGTAACAAGTGTTCGAGATGTTGCC 480
Qy 157 GluGlyLeuGlyIleArgGlnAsnThrLeuSerArgLeuLeuLysAspGluLysSer 176
Db 481 GAAGAACTAGGGATAGACCCAAAGGACACTCTGAGTAAATGCTGAGAGATGAGAAGAGT 540
Qy 177 AspSerCysPheArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsnArg 196
Db 541 GACTCGTCCCTGAGACTAAACCAATATCCGGCGCGGAGGAA--GAGCGGAGAGATG 597
Qy 197 AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn 216
Db 598 GTGAAGGTGGGGTTTGGGGAACACACAGACCACAGATAATCTCAGTCTAAGATCTAAT 657
Qy 217 SerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAsp 236
Db 658 AACACGGGGGTCTTCAAAATCTGTGTGAAGATGGAAGTGGTGGTGGTGGTGGTGGTGGT 717
Qy 237 GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
Db 718 CACTCTCTCTTCAATTAATGTTGAGATGCTCTCAGGTATGAGTTATGACTAACGGAGGTT 777
Qy 257 LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyr 276
Db 778 AAGAGTGTAAACACAGCGTCTTAGCCGATACAAGGAGATCGAGGATTTCAATGATAT 837
Qy 277 PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly 296
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Db      838   TTGCGGGAGCCGCCATTGACGCAGAAGATCGCACCAATTGCCATGCTTGTTCCTTGAGCAA    897
Qy      297   GUGluCyAeLyTyLysGlUpheThrTrpCysGLuTYrLYSLYslYSAlaaLaTYrThRSer    316
Db      898   GATGATTGGCTTTACAAGAATTCACTTGGTCTCAATACAAACTTCTGCTTACAAGTCT    957
Qy      317   ArgLeuAlaAsnArgLeuAlaProPheGlnLys    328
Db      958   AAGCTTGGTGATTATAGACTTGGTCTCTTTGAGAAA    993

RESULT 7
US-10-670-454-7
; Sequence 7, Application US/10670454
; Publication No. US20040229357A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L
; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/10/670,454
; PRIORITY FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1993-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-670-454-7
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Qy	117	Val	Leu	Ser	Pro	Ly	Ser	Leu	Cys	Val	Leu	Arg	Glu	Asn	Pro	His	His	Val	136
Db	469	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	528
Qy	137	Val	Glu	Asn	Tyr	Trp	Leu	Ala	Val	Leu	Val	Asn	Met	Cys	Tyr	Ala	Val	Leu	156
Db	529	GT	G	A	G	A	G	A	T	A	G	A	G	A	T	A	G	A	589
Qy	157	Glu	Gly	Leu	Gly	Leu	Arg	Gln	Arg	Asn	Thr	Leu	Ser	Arg	Leu	Leu	Leu	Asp	176
Db	589	GA	GA	AA	CT	AG	GA	TAG	AG	CA	CA	GG	CA	CT	CT	GAG	TAA	AT	648
Qy	177	Asp	Ser	Cys	Phe	Arg	Leu	Asn	His	Tyr	Pro	Cys	Pro	Glu	Val	Gln	Ala	Leu	196
Db	649	GAC	T	CG	T	CG	T	CG	T	CG	T	CG	T	CG	T	CG	T	CG	705
Qy	197	Asn	Leu	Val	Gly	Phe	Gly	Glu	His	Thr	Asp	Pro	Gln	Ile	Leu	Ser	Val	Leu	216
Db	706	GT	GA	AG	T	GG	GT	T	GG	GA	AA	CA	CA	CA	CA	CA	GA	TA	765
Qy	217	Ser	Thr	Ser	Gly	Leu	Gln	Ile	Cys	Leu	Thr	Asp	Gly	Thr	Trp	Val	Ser	Val	236
Db	766	AA	CA	CG	CG	CG	GT	CT	T	CA	AA	T	CT	GT	G	T	CA	AA	825
Qy	237	Gln	Thr	Ser	Phe	Leu	Asn	Val	Gly	Asp	Ala	Leu	Gln	Val	Met	Thr	Asn	Gly	256
Db	826	CAC	T	CT	CT	CT	T	CT	CA	T	AA	T	GT	T	GG	AG	T	GC	885
Qy	257	Ly	Ser	Val	Ly	His	Arg	Val	Leu	Ala	Asp	Thr	Thr	Ly	Ser	Arg	Leu	Ser	276
Db	886	AA	GA	GT	G	T	T	AA	CA	CA									

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RESULT 8
US-09-371-307-64
; Sequence 64, Application US/09371307A
; Patent No. US20020053095A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371.307A

```

Db	1091	AATAGCGCTTGGACATTTTGAGAGAAATGTGCT	1112
RESULT 9			
US-10-401-321-64			
; Sequence 64, Application US/10401321			
; Publication No. US2003023679A1			
; GENERAL INFORMATION:			
; APPLICANT: Brown, Sherri M.			
; APPLICANT: Heck, Gregory R.			
; APPLICANT: Piller, Kenneth J.			
; APPLICANT: Kileshore, Ganesh M.			
; APPLICANT: Elich, Tedd D.			
; APPLICANT: Logusch, Eugene W.			
; APPLICANT: Rao, Sudabathula			
; APPLICANT: Ream, Joel E.			
; APPLICANT: Logusch, Sherry J.			
; APPLICANT: Baerason, Scott R.			
; TITLE OF INVENTION: Methods for Controlling Gibber			
; FILE REFERENCE: 11899.0216.DVUS01 (WO/216--1)			
; CURRENT APPLICATION NUMBER: US/10/401.321			
; CURRENT FILING DATE: 2003-03-27			
; NUMBER OF SEQ ID NOS: 89			
; SOFTWARE: Patentin version 3.2			
; SEQ ID NO 64			
; LENGTH: 1403			
; TYPE: DNA			
; ORGANISM: Glycine max			
US-10-401-321-64			
Alignment Scores:			
Pred. No.:		2,066-128	Length:
Score:		1060.00	Matches:
Percent Similarity:		76.44%	Conservative:
Best Local Similarity:		60.43%	Mismatches:
Query Match:		60.64%	Indels:
DB:		6	Gaps:
US-10-670-454-2 (1-331) x US-10-401-321-64 (1-1403)			
Qy	1	MetValValLeuSerGlnProAlaLeuAsnGlnPhePh	
Db	149	ATGGTGTCTCTCCACCAATTTCCAGGCAACACACAACTACTCT	
Qy	21	ThrProLeuPheThrGlyIleProValValAspLeuThr	
Db	209	ACGGCATTCTCTCAACCAATTTCCGTTAGTGGACCTCTCT	
Qy	41	IleValAsnAlaCysArgAspPheGlyPhePheIysLeu	
Db	269	ATAGTGAAGCGCTTGTGAGGAATTTGGATTCTTCAAAGT	
Qy	61	GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhe	
Db	329	GAACATATATCCCAATTTGGATCTGGAAGCCTTCAAGTT	
Qy	81	LysAspArgAlaGlyProProAspProPheGlyTyrGln	
Db	389	AAGGAAAAAGTAGGCCCTCCCCAACCATATGGGTATGG	
Qy	101	GlyAspValGlyTyrValGluTyrIleLeuLeuAsnThr	
Db	449	GGGGATGTGTGGTGGGTGGTGTGAGTACCTTCTCTCAACAC	
Qy	121	LysSerLeuCysIlePheArgGluAsnProHisIlePhe	
Db	497	CACACTTCTCTGTATTTGGCAAAACCGCTGAGAAATTT	
Qy	141	IleThrAlaValIysAsnMetCysTyrAlaValLeuGln	
Db	557	ATGCTCTCTGTGAGGAAATGGCATGTGAGATTTCTTGA	
Qy	161	IleArgGlnArgAsnThrLeuSerArgLeuLeuIysAsn	

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Db      617 ATACAAACAAAAATGTTTGTAGCAAGCTTCTTATAGGATAAAGAGAGTGAAGTCTCTGTTTTT 676
Qy      181 ArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      677 AGGGTGAATCACTACCTCTGCTGCTGAACCT--GTGAATGGTCAAAACATGATAGGG 733
Qy      201 PheGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGly 220
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      734 TTTGGAGAACACACGAGCCACAAAATCAATTTCTCTACTTAGGTCCAAACAATACTTTCAGGC 793
Qy      221 LeuGlnIleCysLeuThrAspGlyThrTropValSerValProAspGlnThrSerPhe 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      794 CTTTCAGATTTTCTTAGAGATGGAACACTGCATTTTTCAGTCCCTCCATCACAACAAATCTTTTC 853
Qy      241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      854 TTCATTAATGTTGGTGATTTCTCTTCAGGTATAGCCATGGAAGTTTCGAAGTGTGAA 913
Qy      261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      914 CACAGAGTTTTCACAAATGGATTTAAGTCTAGACTCTCAATGATTTACTTTTCGAGGTCCA 973
Qy      281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      974 CCATTGAGTGAAGAAATAGTACCATTATCTTCACCTATG---AAAGGAAAGAAAGCTTA 1030
Qy      301 TyrLysGluPheThrTyrCysGluTyrLysAlaAlaTyrThrSerArgLeuAlaAsp 320
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1031 TACAAAGAGTTTACGTGGTTCGAGTATAAAATTTAACTATGCTTCAAGATTGCTGAT 1090
Qy      321 AsnArgLeuAlaProPheGlnLysSerAlaAla 331
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1091 AATAGCTTGGACATTTTCAGAGAATTTGTGCT 1123

RESULT 10
US-10-424-599-21951
; Sequence 21951, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic David K
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 21951
; LENGTH: 1390
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_119826C.1
US-10-424-599-21951

Alignment Scores:
Pred. No.:      6,17e-118      Length:      1390
Score:          980.50      Matches:      195
Percent Similarity: 75.68%      Conservative: 57
Best Local Similarity: 58.56%      Mismatches:  74
Query Match:     56.09%      Indels:       7
DB:              7              Gaps:         3

US-10-670-454-2 (1-331) x US-10-424-599-21951 (1-1390)

Qy      1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLysProPheLysSer 20
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      175 ATGGTGTTCTGTCCTCCAAACACACAGAACATCTCTACATCAGAACATACATGCCA 234
Qy      21 ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db      235 ACTGCATTTCTCTCCAAACAATTTCCCATAGTGGACCTCTCCAAACCTGATGCAAGACCCTT 294
Qy      41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      295 ATAGTGAAGGCTTGTGAGGAGTTTGATTTCTTCAAGTCATCAACCATGGTGTGCCCATTT 354
Qy      61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArg-PhePheLysLysSerGlnSerGly 80
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      355 GAAGCTATATCCCAATTTGGAATATGAAGCCTTTCAAACTTCTTCTCTATGCCACTCAATGA 414
Qy      80 uLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAs 100
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      415 GAAA---AAAGTAGAGACCTCCCAATTTGTTGGGTGTAGCAAGAAATTTGGACACAA 471
Qy      100 nGlyAspValGlyTropValGluTyrLeuLeuAsnThrAsnProAspValIleSerPr 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      472 TGGGAGCGTTGGTGGATGGAGTACTTCTTCTCAACCAAGCAA-----TCAAG 522
Qy      120 oLysSerLeu-CysIlePheArgGluAsnProHisPheArgAlaValValGluAsnT 140
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      523 AACACAACCTTCTCTGTTATGGCAAAAACGCTGAGAAATTCAGGTGTCTGTTGAACAGTT 582
Qy      140 yrIleThrAlaValLysAsnMetCysTyrAlaValLeuLeuLeuMetAlaGlyValLeuG 160
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      583 ACATGCTTCTGTGTAGGAGATGGCATGTGAGATTTCTTGGTTGATGGCAGAGGGTTGA 642
Qy      160 lYleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysP 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      643 AGATTCAAGAAAGAGATGTTTACCAAGCTTCTAATGGATAAACAAGTGAATCTATT 702
Qy      180 heArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsnArgAsnLeuValG 200
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      703 TCAGGCTGAATCATTTACGCTGCTTCTCTGAAATGACTCTGAAATGATCAGAACTTGAATG 762
Qy      200 lYpHeGlyGluHisThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerG 220
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      763 GGTTTTGGAGAACACACACACCCCAAAATCATCTCTGTTAAGATCCCAACACTTCAG 822
Qy      220 lYLeuGlnIleCysLeuThrAspGlyThrTropValSerValProAspGlnThrSerP 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      823 GCCTTCAGATTTATCTTAGAGATGGAATTTGATTTCCAGTCCACAGCTCCAGCGCTT 882
Qy      240 hePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerVal 260
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      883 TTTTATTAAAGTGTGATCTCTTCAGGTATGACAAATGCAAGTTCGAAAGTGTGA 942
Qy      260 ysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyP 280
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      943 GACACAGAGTGTGGCAAAATGGGTTTCAAGTCCAGGCTTTCATGATTTACTTTGGAGGTC 1002
Qy      280 roAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluCysL 300
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1003 CACCTTTGAGTGAGAAAATAGCCCATTTATCTCTCTCATG---AAAGGAAAGAAAGTC 1059
Qy      300 euTyrLysGluPheThrTropCysGluTyrLysAlaAlaTyrThrSerArgLeuAla 320
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1060 TATATAAAGAGTTTACCTGGTTTGGATCAAAAATCAATCTACGCTTACGCTTCAAGATTATCTA 1119
Qy      320 spAsnArgLeuAlaProPheGlnLysSerAlaAla 331
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1120 AAAATAGACTTGAACATTTTGAAGAAATTCAGCT 1154

RESULT 11
US-10-392-325-3
; Sequence 3, Application US/10392325
; Publication No. US2004006080A1
; GENERAL INFORMATION:
; APPLICANT: Tanaka, Hiroshi
; APPLICANT: Kayano, Toshiaki
; APPLICANT: Matsuo, Makoto
; APPLICANT: Kobayashi, Masatomo
; APPLICANT: Saito, Tamio
; APPLICANT: Sakamoto, Tomoaki

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; APPLICANT: Sakai, Miho
; TITLE OF INVENTION: GIBBERELIN 2-OXIDASE GENE, FUNCTIONS AND USES THEREOF
; FILE REFERENCE: SHZ-014
; CURRENT APPLICATION NUMBER: US/10/392,325
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 7
; PRIOR APPLICATION NUMBER: JP 2002-276051
; PRIOR FILING DATE: 2002-09-20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Oryza sativa
; NAME/KEY: CDS
; LOCATION: (1)..(984)
; OTHER INFORMATION:
US-10-392-325-3

Alignment Scores:
Pred. No.: 3,48e-117 Length: 984
Score: 973.00 Matches: 190
Percent Similarity: 72.67% Conservative: 52
Best Local Similarity: 57.06% Mismatches: 79
Query Match: 55.66% Indels: 12
DB: 7 Gaps: 3

US-10-670-454-2 (1-331) x US-10-392-325-3 (1-984)

Qy 1 MetValValLeuSer---GlnProAlaLeuAenGlnPhePheLeuLeuLysProPheLys 19
Db 1 ATGGTGGTCTCGCTGGCCCGCCCGCTCGATCATCCCGCTCGAGTTCGCGCGGAC 60
Qy 20 SerThrProLeuPheThrGlyLeuProValValLeuAspLeuThrHisProAspAlaLysAsn 39
Db 61 CCCGGCGAGCTCTTCTCCGGGTGCGGTGCGGTGCGACCTCGCGAGCCCGCGCGCGAGG 120
Qy 40 LeuLeValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValPro 59
Db 121 GCCGTGGTGGACGCTCGCGAGCGGTACGGTTCCTTCAGGTGCTCAACACCGCGTGGCC 180
Qy 60 LeuGluLeuMetAlaAsnLeuGluAenGluAlaLeuArgPhePheLysLysSerGlnSer 79
Db 181 ACGGACACAGTACCAAGCCGAGTCCGAGGCGGTCTTCCTCCAGACGCGGCC 240
Qy 80 GluLysAspAlaCysArgProAspProPheGlyTyrGlySerLysArgIleGlyPro 99
Db 241 GACAAAGGACCGCTCCGGCCCGCCCTACCGGTTCGGGTACGGCAGCAAGCGGATCGGTTTC 300
Qy 100 AenGlyAspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsn-----Pro 115
Db 301 AATGGGACATGGGTGGTTCGAGTACCTCTCTCGCCCTCGACGCGGTCTCGCC 360
Qy 116 AspValIleSerProLysSerLeuCysIlePheArgGluAenProHisPheArgAla 135
Db 361 GACGCTGACCGCTCCGCTCTCGCGGTC-----TTCCGGGCGC 399
Qy 136 ValValGluAenTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuLeuMet 155
Db 400 GCTCTGAACGATGATCTCGGGGTGCGGAAGGTGCGGTGCGGTGATGAGCGGATG 459
Qy 156 AlaGluGlyLeuGlyIleArgGlnArgAenThrLeuSerArgLeuLysAspGluLys 175
Db 460 TCGGAGGGCTGGGATTCGCGAGCGGACGCGCTGAGCGCTGTGTCAGCGCGAAGGG 519
Qy 176 SerAspSerCysPheArgLeuAenHisTyrProCysProGluValGlnAlaLeuAen 195
Db 520 AGCGACCAAGTGTTCGCGGTGAACCACTACCGCGCGTGCAGGCGGTGCGGGGCTCGGC 579
Qy 196 ArgAenLeuValGlyPheGlyIleHisThrAspProGlnIleIleSerValLeuArgSer 215
Db 580 TGCAGCGTCAACCGGGTTCGGCGAGCACACCGACCGGCTCTCTCGTCTCGGCTCA 639
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Qy 216 AenSerThrSerGlyLeuGlnIleCysLeuThrAepGlyThrTrpValSerValProPro 235
Db 640 AACGGCAGCTCCGCGCTGCAGATCGCGTCCGACGCGCGAGTGGGTCTCGGTGCCCTCC 699
Qy 236 AspGlnThrSerPhePheIleAenValGlyAspAlaLeuGlnValMetThrAenGlyArg 255
Db 700 GACCGCGACTCCTCTCTCGTCAAGTCGCGGACTGTTGCGAGTCTCCACCATGGGAGG 759
Qy 256 PheLysSerValLysHisArgValLeuAlaAepThrThrLysSerArgLeuSerMetIle 275
Db 760 TTCAGAGCGGTGAAGCACAGCGGTGTGGCCACACGCTAAAGTCTAGGTTTCCCTTCATC 819
Qy 276 TyrPheGlyGlyProAlaLeuSerGluAenIleAlaProLeuProSerValMetLeuLys 295
Db 820 TACTTTGGAGGGCCACCGCTTAGCAGAGGATTCACCATTTGCCACAGCTCGCGGGGAG 879
Qy 296 GlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLeuAlaAlaTyrThr 315
Db 880 GGAGAGCAGAGCGCTGTACAGGAGTTACATGGGATGATGATACAGAGGCTCCCTACAAA 939
Qy 316 SerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
Db 940 TCAAGGCTTGGAGACACACAGCGCTGGCCAGTTTGAGAG 978

RESULT 12
US-10-437-963-78659
; Sequence 78659, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_78444C.1
US-10-437-963-78659

Alignment Scores:
Pred. No.: 5,15e-117 Length: 1260
Score: 973.00 Matches: 190
Percent Similarity: 72.67% Conservative: 52
Best Local Similarity: 57.06% Mismatches: 79
Query Match: 55.66% Indels: 12
DB: 7 Gaps: 3

US-10-670-454-2 (1-331) x US-10-437-963-78659 (1-1260)

Qy 1 MetValValLeuSer---GlnProAlaLeuAenGlnPhePheLeuLeuLysProPheLys 19
Db 140 ATGGTGGTCTCGCTGGCCCGCCCGCTCGATCATCCCGCTCGAGTTCGCGCGGAC 199
Qy 20 SerThrProLeuPheThrGlyLeuProValValLeuAspLeuThrHisProAspAlaLysAsn 39
Db 200 CCCGGCAGCTCTTCTCCGGGTGCGGTGCGGTTCGACCTCGCGAGCCCGCGCGCGGAGG 259
Qy 40 LeuLeValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValPro 59
Db 260 GCCGTGGTGGAGCGCTCGAGCGGTACGGGTTCCTTCAAGGTGCTCAACCGCGCGGTGGCC 319
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Db 991 TTCATCTACTTCGCGGGCGCGCTGGGGCAGCGATGCGCCGCTCGCAGGTGCTG 1050
Qy 294 LeuLysGlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAla 313
Db 1051 GCGGAGGAGAGAGAGAGCTGTACAGGAGTTTCACTGGGGCGAGTACAGNAGGCCGGG 1110
Qy 314 TyrThrSerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
Db 1111 TACAAGACGAGCTCGCGCACACACAGGCTGGGCCAGTTTGAGAAG 1155

RESULT 14

US-10-670-454-9

; Sequence 9, Application US/10670454
; Publication No. US20040229357A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Stephen G
; APPLICANT: Hedden, Peter
; APPLICANT: Phillips, Andrew L

; TITLE OF INVENTION: Gibberellin 2-Oxidase
; FILE REFERENCE: 0623.0970000
; CURRENT APPLICATION NUMBER: US/10/670,454
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/719,108
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01857
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: GB 9812821.8
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: GB 9815404.0
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9

; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-670-454-9

Alignment Scores:

Pred. No.: 1,57e-114 Length: 1008
Score: 953.00 Matches: 186
Percent Similarity: 70.12% Conservative: 44
Best local Similarity: 56.71% Mismatches: 96
Query Match: 54.52% Indels: 2
DB: 8 Gaps: 1

US-10-670-454-2 (1-331) x US-10-670-454-9 (1-1008)

Qy 1 MetValValLeuSerGlnProAlaLeuAsnGlnPheLeuLeuLysProPheLysSer 20
Db 1 ATGGTAATTTGTTACAGCCAGCCAGTTTGTATAGCAACCTCTATGTTAATCCAAATGC 60
Qy 21 ThrProLeuPheThrGlyLeProValValAspLeuThrHisProAspAlaLysAsnLeu 40
Db 61 AAACCGCGTCCGGTTTTAATCCCTGTTATAGACTTAAACGACTCAGATGCCAAACCCAA 120
Qy 41 IleValAsnAlaCysArgAspPheGlyPheLysLeuValAsnHisGlyValProLeu 60
Db 121 ATCGTCAAGGCATGGAAGAGTTTGGGTTCTTCAAGTCATCAACCATGGGGTCCGACCC 180
Qy 61 GluLeuMetAlaAsnGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
Db 181 GATCTTTTGACTCAGTTGGAGCAGAGCCATCACTCTTTGCTTTCATCCTCTCTC 240
Qy 81 LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
Db 241 AAAGACAAAGCGGTCACCTGACCCGTTTGGTTAGCGTACTAAAAGGATTGGACCCCAAT 300
Qy 101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
Db 301 GGTGACCTTGGCTGGCTGGAGTACATTCCTCTTAATGCTAATCTTTGCTTGGCTTGCCTCAC 360

Qy 121 LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr 140
Db 361 AAAACCCACCGCATTTTCCGGCACACACCCCTCCAAATTTTTCAGAGAGGCGAGTGAAGATAC 420
Qy 141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
Db 421 ATTTAAGAGATGAGAGATGTCCAGCAATTTCTGGAAATGGTAGAGAAAGAGCTAAG 480
Qy 161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 180
Db 481 ATAGAGCCAAAGAGAGCTGAGCGCTTTGTGAAAGTGAAGAAAGTGAATTCGTGCTGCTG 540
Qy 181 ArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 200
Db 541 AGAATGACCATTTACCCGAGAGAGAGACTCCGGTC-----AAGGAAGAGATTGGG 594
Qy 201 PheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly 220
Db 595 TTCGTGAGCACACTGATCCACAGTTGATATCATCTGCTCAGATCAACGACACAGAGGCT 654
Qy 221 LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhe 240
Db 655 TTGCAATCTGTCTCAAGATGGAACATGGGTGTGATTTACACCTGATCCTCTCTTTC 714
Qy 241 PheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys 260
Db 715 TTCGTTCTTGTGCGGAGATCTCTTCAGGTGATGACAAACGGAAGATTCACAGAGTGA 774
Qy 261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 280
Db 775 CATAGAGTGGTGACAAATACAAAGAGGTCAAGGATTCGATGATCTACTTCGACGCTCT 834
Qy 281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 300
Db 835 CCTTTGACGAGAGATGTCACCATTTATCATGCTGTGTCACCAAGCAAGATGATTCCTT 894
Qy 301 TyrLysGluPheThrTrpCysGluTyrLysLysAlaTyrThrSerArgLeuAlaAsp 320
Db 895 TATAATGAGTTTACTTGGTCTCAATACAAAGTTATCTGCTTACAAACTAAGCTTGGTGAC 954
Qy 321 AsnArgLeuAlaProPheGlnLys 328
Db 955 TATAGGCTTGGTCTCTCTTTGAGAAA 978

RESULT 15
US-10-259-194A-141
; Sequence 141, Application US/10259194A
; Publication No. US20040010815A1
; GENERAL INFORMATION:
; APPLICANT: Lange, Markus B.
; APPLICANT: Ghassemlian, Majid
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 70029-NP
; CURRENT APPLICATION NUMBER: US/10/259,194A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,743
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 662
; SOFTWARE: PatentList.pl version 3.0.4 (c) 2001 Syngenta

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; SEQ ID NO 141
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-194A-141

Alignment Scores:
Pred. No.:      2,93e-114      Length:      927
Score:          950.50         Matches:    186
Percent Similarity: 71.21%      Conservative: 49
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Query Match:      54.38%        Indels:     25
DB:               6            Gaps:         3

US-10-670-454-2 (1-331) x US-10-259-194A-141 (1-927)

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Db      1 ATGGTGGTTCTCGCTGGCCGCCGCCGCGTCGATACATCCCGCTGCTGAGGTGCGCGGAC 60
QY      20 SerThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsn 39
Db      61 CCGGGCGAGCTCTTCTCCGGGTGCGCGGTCTGTCGACCTCGGCGAGCCCGCGCGCGGAGG 120
QY      40 LeuIleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHisGlyValPro 59
Db      121 GCCGTGGTGGACGCTCGCGCGGTACGGGTCTTCAAGGTCTCAACACCGCGGTGGCC 180
QY      60 LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSer 79
Db      181 ACGGACACCATGGACAGGCCGAGTCTGGAGGCGCTCAGGTCTCTCCCGACGACGACGCC 240
QY      80 GluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyPro 99
Db      241 GACAGGACCGCTCCCGCGCGCGCTACCCGTTCCGGTACGCGACGACGCGATCGGGTTC 300
QY      100 AsnGlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSer 119
Db      301 AATGGCGACATGGGTGGTCTGAGTACCTCTC----- 333
QY      120 ProLysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGluAsn 139
Db      334 -----AGGCCCGCTCTGAACGAG 351
QY      140 TyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeu 159
Db      352 TACATCTCGGGGTGCGGAAGGTGGCGGTGCGGGTGATGAGCGCATGTCGAGAGGGGCTG 411
QY      160 GlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCys 179
Db      412 GGCATTGCGCAGCGGACGCGCTGAGCGCGTGTGACGCGGAGGGGAGCGACACGAGTG 471
QY      180 PheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuVal 199
Db      472 TTCGCGTGAACCACTACCCGCGCTGCCGCGCTGCGCGCTGCGCGCTGCGCGCTCAC 531
QY      200 GlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSer 219
Db      532 GGCCTTCGGGAGACACCGACCGCGAGCTCGTCTCGTCTCGCTCAACCGGACGCTCC 591
QY      220 GlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProAspGlnThrSer 239
Db      592 GGCCTGCAGATCGCGTCCGCGAGCGCCAGTGGGTGTCTGCTCCCTCCGACCGGACTCC 651
QY      240 PhePheIleAsnValGlyAspAlaLeu---GlnValMetThrAsnGlyArgPheLysSer 258
Db      652 TTCCTTCGTCACGTCGCGACTCGTTGCGACAGGTTCTGACCAATGGGAGGTTCAGAGC 711
QY      259 ValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGly 278
Db      712 GTGAGACACAGGGTGTGGCCACACGCTTAAGTCTAGGGTTCTCTCATCTTCTTGA 771
QY      279 GlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGlu 298
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Db      772 GGGCCACCGTTAGCACAGAGGATTGCACCATTTGCCAGCTGCTGGGGGAGGAGAGCAG 831
QY      299 CysLeuTyrLysGluPheThrTrpCysGluTyrLysAlaAlaTyrThrSerArgLeu 318
Db      832 AGCCTGTACAAGGAGTTACATGGGATGAGTACAAGAAGGCTGCCTACAAATCAAGGCTT 891
QY      319 AlaAspAsnArgLeuAlaProPheGlnLys 328
Db      892 GGAGACACACAGGCTGCCCCAGTTTGAGAAG 921

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Job time : 984 secs
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GenCore version 5.1.6
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Run on: December 28, 2005, 01:42:45 ; Search time 786 Seconds
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220.763 Million cell updates/sec

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Searched: 4172979 seqs, 262114271 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
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2	288	16.5	1011	US-11-152-892-3
3	173	9.9	3861	US-11-152-892-2
4	169.5	9.7	2171	US-11-152-892-1
5	89.5	5.1	967	US-11-058-817A-3
6	84	4.8	193084	US-11-121-086-82
7	83.5	4.8	1243	US-10-750-185-50357
8	82.5	4.7	5515	US-10-517-605-14

c 9	82.5	4.7	5515	7	US-11-055-309A-2	Sequence 2, Appli
c 10	82.5	4.7	5982	7	US-11-034-771-1	Sequence 1, Appli
c 11	82.5	4.7	153142	7	US-11-121-086-27	Sequence 27, Appl
c 12	81.5	4.7	40000	6	US-10-995-561-13513	Sequence 13513, A
c 13	81	4.6	3587	6	US-10-501-675-8	Sequence 8, Appli
c 14	80.5	4.6	1535	6	US-10-750-185-34363	Sequence 34363, A
c 15	80.5	4.6	15804	6	US-10-995-561-13294	Sequence 13294, A
c 16	80.5	4.6	16963	6	US-10-995-561-13467	Sequence 13467, A
c 17	80.5	4.6	24446	6	US-10-995-561-13436	Sequence 13436, A
c 18	80.5	4.6	175416	7	US-11-121-086-43	Sequence 43, Appl
c 19	79.5	4.5	972	7	US-11-058-817A-1	Sequence 1, Appli
c 20	79	4.5	751	9	US-11-082-389-53	Sequence 53, Appl
c 21	79	4.5	1111	6	US-10-750-185-60397	Sequence 60397, A
c 22	79	4.5	1287	9	US-11-082-389-51	Sequence 51, Appl
c 23	78	4.5	595	6	US-10-980-388-41	Sequence 41, Appl
c 24	78	4.5	1082144	7	US-11-117-187-211	Sequence 211, App
c 25	77.5	4.4	861	6	US-10-467-657-2959	Sequence 2959, Ap
c 26	77	4.4	810	6	US-10-467-657-1629	Sequence 1629, Ap
c 27	76.5	4.4	197096	7	US-11-121-086-107	Sequence 107, App
c 28	76.5	4.4	209822	6	US-10-995-561-13198	Sequence 13198, A
c 29	76	4.3	207908	7	US-11-112-908-21	Sequence 21, Appl
c 30	75.5	4.3	98862	7	US-11-121-086-76	Sequence 76, Appl
c 31	75.5	4.3	215308	7	US-11-121-086-77	Sequence 77, Appl
c 32	75	4.3	2858	6	US-10-750-185-34315	Sequence 34315, A
c 33	74.5	4.3	1245	6	US-10-467-657-7773	Sequence 7773, Ap
c 34	74.5	4.3	2407	6	US-10-750-185-33843	Sequence 33843, A
c 35	74.5	4.3	1125000	6	US-10-995-561-13286	Sequence 13286, A
c 36	74	4.2	625	7	US-11-000-463-554	Sequence 554, App
c 37	74	4.2	970	7	US-11-058-817A-5	Sequence 5, Appli
c 38	74	4.2	1952	6	US-10-750-185-62955	Sequence 62955, A
c 39	74	4.2	215308	7	US-11-121-086-77	Sequence 77, Appl
c 40	73.5	4.2	1449	7	US-11-055-822-401	Sequence 401, App
c 41	73.5	4.2	2119	6	US-10-927-641-92	Sequence 92, Appl
c 42	73.5	4.2	2295	7	US-11-000-463-590	Sequence 590, App
c 43	73	4.2	1161	6	US-10-750-185-64816	Sequence 64816, A
c 44	73	4.2	1359	6	US-10-750-185-55071	Sequence 55071, A
c 45	73	4.2	1443	6	US-10-750-185-31989	Sequence 31989, A

ALIGNMENTS

RESULT 1
US-11-152-892-5
; Sequence 5, Application US/11152892
; Publication No. US20050251883A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M.
; APPLICANT: Schomburg, Richard M.
; APPLICANT: Michaelis, Scott D.
; APPLICANT: Bizzell, Colleen M.
; TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
; FILE REFERENCE: 960296.97605
; CURRENT APPLICATION NUMBER: US/11/152,892
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US/10/155,435
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Arabidopsis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1014)
US-11-152-892-5

Alignment Scores:
Pred. No.: 2,46e-29 Length: 1017
Score: 325.50 Matches: 82
Percent Similarity: 46.6% Conservative: 63
Best Local Similarity: 26.3% Mismatches: 103
Query Match: 18.6% Indels: 63


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Db      703  TTTG--GAAATAATAGGACAATGGATCGAGCTAAACCTTGTGGAAGCCCTTACAGTC 759
Qy      243  AsnValGlyAspAlaLeuValMetThrAnGlyArgPheLysSerValLysHisArg 262
Db      760  AACATTTGGGGATATGTTTCAGGCATCGAGTAAATGGAGTGTACCAAGCGTGAGACATAGA 819
Qy      263  ValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyProAlaLeu 282
Db      820  GTGATTTCTCCAGCAAAATATCGAGAGATGCAATAGCTTCTTGTATGTCCTTATCTC 879
Qy      283  SerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluCysLeu----- 300
Db      880  GAAACTGATC-----GATTGCTTTGGGTAT 906
Qy      301  -----TyrLysGluPheThrTrpCysGluTyrLysLys 311
Db      907  CCAAGAAGATATAGAAGATTTCAGTTTCAGAGAGTACAAAGAG 948

RESULT 3
US-11-152-892-2
; Sequence 2, Application US/11152892
; Publication No. US20050251883A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M.
; APPLICANT: Schomburg, Fritz M.
; APPLICANT: Michaels, Scott D.
; APPLICANT: Bizzell, Colleen M.
; TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
; FILE REFERENCE: 960296.97605
; CURRENT APPLICATION NUMBER: US/11/152,892
; PRIOR FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US/10/155,435
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; TYPE: DNA
; ORGANISM: Arabidopsis
US-11-152-892-2

Alignment Scores:
Pred. No.:          9,08e-10      Length:      3861
Score:             173.00      Matches:      55
Percent Similarity: 36.12%      Conservative: 40
Best Local Similarity: 20.91%      Mismatches: 61
Query Match:       9.90%      Indels:      107
DB:                7          Gaps:          9

US-10-670-454-2 (1-331) x US-11-152-892-2 (1-3861)
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Db      3066  TCAACAATCGAGAAATTTCTTCGGAATCAGAGGCATTAGCATATATGTGCGCAGGTT 3125
Qy      155  MetAlaGluGlyLeuGlyIleArgGlnArgAnThrLeuSerArgLeuLysAspGlu 174
Db      3126  CTTGCAGAAAAATCTGGA-----CAAAAT-----TCAAGTTTCTTCAAGAAAAAC 3170
Qy      175  ---LysSerAspSerCysPhe---ArgLeuAsnHisTyrProCysProGluValGln 192
Db      3171  TGTGTGAGAAATACATGTTATGAGTGAACCGATATCCACCTTGTCCCAACCATCG 3230
Qy      193  AlaLeuAsnArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerVal 212
Db      3231  -----GAGGTGTACGGATTATGCGCACACCGCAGTCAGTTCTCTCACAATC 3278
Qy      213  LeuArgSerAsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSer 232

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Db      3279  TTGTATCAAGATCAAGTCGGAGGACTCCAACCT---ATCAAGACAATAGATGGATCGCT 3335
Qy      233  ValProAspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnVal----- 250
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Qy      250  ----- 250
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Qy      250  ----- 250
Db      3516  TGATCAATAATATAAAATGTGGATTTCTTATAAAGATAACATCTAAGGCAATGTATATAA 3575
Qy      251  -----Met-ThrAsnG1 254
Db      3576  AATGCTTTTAAATTAAGATTGTAATTATATATATGTGTTGTTAGGATGGAGCAATGG 3635
Qy      254  YArgPheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMe 274
Db      3636  CATGTACAAAGTGTGTGAACACCGTGTATGACGACCCCAAGGTGGAGAGATTCTCAAC 3695
Qy      274  tIleTyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLe 294
Db      3696  GGCTTATTTTATGTGTCATCATACGACGCGCTTATA----- 3732
Qy      294  uLysGlyGluGluCys-----LeuTyrLysGluPheThrTrpCysGluTyr 309
Db      3733  -----GAGTGTTCAGTGATCGTCTCTTATAGAAATTTTCAGCTTCAGAGAAATT 3782
Qy      309  tLysLys 311
Db      3783  CAGACAA 3789

RESULT 4
US-11-152-892-1
; Sequence 1, Application US/11152892
; Publication No. US20050251883A1
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M.
; APPLICANT: Schomburg, Fritz M.
; APPLICANT: Michaels, Scott D.
; APPLICANT: Bizzell, Colleen M.
; TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
; FILE REFERENCE: 960296.97605
; CURRENT APPLICATION NUMBER: US/11/152,892
; CURRENT FILING DATE: 2005-06-15
; PRIOR APPLICATION NUMBER: US/10/155,435
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Arabidopsis
US-11-152-892-1

Alignment Scores:
Pred. No.:          1e-09      Length:      2171
Score:             169.50      Matches:      74
Percent Similarity: 30.84%      Conservative: 54
Best Local Similarity: 17.83%      Mismatches: 96
Query Match:       9.70%      Indels:      191
DB:                7          Gaps:          14

US-10-670-454-2 (1-331) x US-11-152-892-1 (1-2171)
Qy      27  IleProValValAspLeuThrHis-----ProAspAlaLys----- 38

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Db 118 CTTCTGTGTCATCTCAGCCATCTAACTAGTGTGAGGAGTCAAAACGCAAAAGATGT 177
Qy 39 ---AsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLeuValAsnHisGly 57
Db 178 GTGAAACAATAGTGTGAGCTCGAAGAGTGGGATTTTTCAAATTTGGAACCAATGA 237
Qy 58 ValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLeuValSer 77
Db 238 ATTCACCAAGACGCTTTTGAGATGATGCTCCTCGAAGAGAGAAACTCTTTGACCAACCT 297
Qy 78 GlnSerGluLysAspArgAla-----Gly 85
Db 298 TTTTCTGTGAAAGTCAGAGAACCGTTTTTCGCGATTATCGAAGAAATAGTTACCGTTGGGA 357
Qy 86 ProPro-----AspProPheGlyTyrGly----- 93
Db 358 AACCCCTAGCGCCACTTCTCCCGCTCAGTACTCCGTTTCGGAAGCGTTTCACATCATCTTT 417
Qy 94 -----SerLysArgIleGlyProAsnGlyAspValGlyTyrValGluTyr----- 108
Db 418 TCAGAGGTTTCAAGGATTTCTGATGATCGCAACAACCTCAGGTTTTTTAATTATAGATT 477
Qy 108 ----- 108
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Qy 109 -----LeuLeuLeuAsnThrAsnProAspValIleSerProLysSer----- 122
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Qy 122 ----- 122
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Qy 127 ----- 127
Db 778 ATAGTAGTATTATAGAAACACTTATAAATCTTTTATGTTTAAAGAAAACTTTTCATACAGT 837
Qy 127 ----- 127
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Qy 128 -----GluAsnProHis----- 132
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Qy 152 LeuGluLeuMetAlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeu 171
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Qy 172 LysAsp-----GluLysSerAspSerCysPheArgLeuAsnHisTyrProCysPro 189
Db 1063 GAAAAACATTTTTCAGCTTGAAAAACAGTTTCTAAGGCTCAATTAAGTACCATCT----- 1116
Qy 190 GluValGlnAlaLeuAsnArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIle 209
Db 1117 -----AGTGTTTTGGTCTGAGTGTGTTGGTTTGTCTTCCATACCGATACAACTTTT 1170
Qy 210 IleSerValLeuArgSerAsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThr 229
Db 1171 CTCACATATCTCTCTCAAGATCAATCGGAGGTTAGAAATTG-----GAAATAATGACAA 1227
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Db 1228 TGGATCAGCGTAAACCTTGTGGAGCCCTTACAGTCAACATGGGATATGTTTCAG 1287
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Db 1288 GTAATTACTTCTACCTTTGATTTTCAAGTTCAAGTCCATTAAAG 1332
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; Sequence 3, Application US/11058817A
; Publication No. US20050262580A1
; GENERAL INFORMATION:
; APPLICANT: Petrukhin, Konstatin
; APPLICANT: Webber, Andrea L.
; TITLE OF INVENTION: Transgenic Mouse with a targeted
; FILE REFERENCE: 21550
; CURRENT APPLICATION NUMBER: US/11/058,817A
; CURRENT FILING DATE: 2005-02-16
; PRIOR APPLICATION NUMBER: 60/545,358
; PRIOR FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 967
; TYPE: DNA
; ORGANISM: human
US-11-058-817A-3
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Pred. No.: 1,81 Length: 967
Score: 83.50 Matches: 72
Percent Similarity: 33.33% Conservative: 39
Best Local Similarity: 21.62% Mismatches: 103
Query Match: 5.12% Indels: 119
DB: Gaps: 16
US-10-670-454-2 (1-331) x US-11-058-817A-3 (1-967)
Qy 12 PhePheLeuLeuLysProPheLysSerThrProLeuPheThrGlyIleProValValAsp 31
Db 925 TTTTCTGCTTTTTCCTTTTCTATCATGAGTGTGTTTCT- - - - -GAT 881
Qy 32 LeuThrHisProAspAlaLysAsnLeuIleValAsnAlaCysArgAspPheGlyPhe 51
Db 880 TTGCTCACACCACTTGTCTGAAATACCATTCATGGCTGTTTTCAGCTTTTGGTTTC- - - 824
Qy 52 LysLeuValAsnHisGlyValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeu 71
Db 823 - - - - -TTAGGCTCTTTGTATGTC 806
Qy 72 ArgPhePheLysSerGlnSerGluLysAspArgAlaGly- - - - -ProProAsp 88
Db 805 CGAATGTACAGAAAGAGAAATATGAAGCTGATTGTCATAGGCAATTAGAGCCAGTGCAT 746
Qy 89 ProPheGlyTyrGlySerLysArgIleGly- - - - -ProAsnGly- - - - - 101
Db 745 CCATTTGGGGAAGGGCGAGTCAGTGTAAAGACAGACAGTGCCTGTGCCAATGTCACATG 686
Qy 102 AspValGlyTyrValGluTyrLeuLeuLeuAsnThrAsnProAspVal- - - - -IleSerPro 120
Db 685 GAATTGAATCAGTTGCAACATAGTCAGGTATCGTTTCCACCAAGATATTTCTGATATCCA 626
Qy 121 LysSerLeuCys- - - - -IlePheArgGluAsnProHisPheArgAlaVal 137
Db 625 TGGGCCAAATGCACTTTAACCCATAGTATGAGTACATAATCAC- - - - - 584
Qy 138 GluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGlu 157
Db 583 - - - - -ATGGATAAA 575
```



```
QY 191 ValGlnAlaLeuAenArgAenLeuValGlyPheGlyGluHisThrAspProGlnIlelle 210
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 824 GTTCAGGCT-----CAGCCACAGGTG--- 804

QY 211 SerValLeuArgSerAenSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrp 230
||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 803 -----TCTTATGCAAGGCTCCCTCTCTGTCTTCCCGAGGTCCCA- 763

QY 231 ValSer-----ValProAspGlnThrSerPhePheIleAenValGly 245
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 762 GTCTCTCCTCTGTAACCACTCCCGCTCCACCTTCTCTCTTCTCATCTCTGGGG 703

QY 246 AspAlaLeuGlnValMetThrAsnGlyArgPheLeysrVallysHisArgValLeuAla 265
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 702 GAC-----ACGTCGGAAGCCAGCTCAGGCC 676

QY 266 AspThrThrLysSerArgLeuSerMetIleTyPheGlyGlyProAlaLeuSerGluAen 285
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 675 GCTACCACATCACCCCACTCGAGGTACATCATCTCAGAGGCCAGCACAAAGTGAANAAC 616

QY 286 IleAlaProLeuProSerValMetLeuLysGlyGlu 298
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 615 ACAGGGCCCTTTGTTCAAGTTTACTAAGAGATGGGGAG 577

RESULT 8
US-10-517-605-14/c
; Sequence 14, Application US/10517605
; Publication No. US20050260124A1
; GENERAL INFORMATION:
; APPLICANT: NAGOYA INDUSTRIAL SCIENCE RESEARCH INSTITUTE
; APPLICANT: GIFU INTERNATIONAL INSTITUTE OF BIOTECHNOLOGY
; APPLICANT: YAMADA, Yoshiji
; APPLICANT: YOKOTA, Mitsuhiro
; TITLE OF INVENTION: Method for diagnosing myocardial infarction risk
; FILE REFERENCE: C0200201
; CURRENT APPLICATION NUMBER: US/10/517,605
; PRIOR FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: JP P2002-181580
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 5515
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-517-605-14

Alignment Scores:
Pred. No.: 190 Length: 5515
Score: 82.50 Matches: 40
Percent Similarity: 36.69% Conservative: 22
Best Local Similarity: 23.67% Mismatches: 64
Query Match: 4.72% Indels: 44
DB: 6 Gaps: 7

US-10-670-454-2 (1-331) x US-10-517-605-14 (1-5515)

QY 75 LysLysSerGlnSerGluLysAspArgAla----- 84
::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 4668 AGGAATATCACAGGGGGAGCCAGCAGATGCGTGAATCTTTATTAAACTAG 4609

QY 85 GlyProAspProPheGlyTyrgLysrLysArgIle----- 97
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4608 GGTCCACCCAGGAGGAGCGGCTGGGGCGGGAGCAGGGTCTCCCGCTGCAGGCTGCCGCGGA 4549

QY 98 GlyProAsnGlyAspValGlyTrp-----ValGluTyrlu 109
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4548 GGCAGGAGGACCGGGTGGGTGGGTGCGATGCGTGCAGGCTTCGGCGTTCAGTGATTG 4489

QY 110 LeuLeuAsnThrAsnProAspValIleSerProLysSerLeuCysIlePheArgGluAen 129
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4488 TCCTGGGCACAGAGGGGGCGGCTGGTG---CCACGCGCAGCTTCTCCACAGC 4432
```

```
QY 130 ProHisHisPheArgAlaValValGluAen----- 139
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4431 CGGGCCCATGGCGCTGCATGTCTTCCACAGGGGCTCGAACCCAGCTCTTGTAGCGGGCC 4372

QY 140 ---TyrlleThrAlaValLysAenMetCysTyrlaValLeuGluLeuMetAlaGluGly 158
::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 4371 TGAAGGCGCTCGGCTGACGGGCTATCTCTGGGCC-----TGCTCTCCAG- 4325

QY 159 LeuGlyIleArgGlnArgAenThrLeuSerArgLeuLeuLysAspGluLysSerAspSer 178
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4324 CTTGGCGCGCACCTCCGCGCACCTGCTCTTCACTCGTCAGGCGTCCGGGTCCGGCT 4265

QY 179 CysPheArgLeuAen-----HisTyrlProProCysProGluValGlnAlaLeuAenArg 196
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4264 GCCCATCTCTTCATCCGCGCGCGGAGCGCTCGCCCGAGGCTGGGCGCGCTCTCTGTAG 4205

QY 197 AsnLeuValGlyPheGlyGluHisThr 205
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4204 CGGCTGGCGCGGCGAGGAGCCACAGT 4178

RESULT 9
US-11-055-309A-2/c
; Sequence 2, Application US/11055309A
; Publication No. US20050282750A1
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Daniel
; APPLICANT: Duncan, Keith
; APPLICANT: Baileyl, Kathy
; APPLICANT: Kane, John
; APPLICANT: Ishida, Brian
; TITLE OF INVENTION: Treatment for Dark Adaptation
; FILE REFERENCE: HO-P02351US5
; CURRENT APPLICATION NUMBER: US/11/055,309A
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 10/428,551
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 10/313,641
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/340,498
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/415,864
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 5515
; TYPE: DNA
; ORGANISM: HUMAN
US-11-055-309A-2

Alignment Scores:
Pred. No.: 190 Length: 5515
Score: 82.50 Matches: 40
Percent Similarity: 36.69% Conservative: 22
Best Local Similarity: 23.67% Mismatches: 64
Query Match: 4.72% Indels: 44
DB: 7 Gaps: 7

US-10-670-454-2 (1-331) x US-11-055-309A-2 (1-5515)

QY 75 LysLysSerGlnSerGluLysAspArgAla----- 84
::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 4668 AGGAATATCACAGGGGGAGCCAGCAGATGCGTGAATCTTTATTAAACTAG 4609

QY 85 GlyProAspProPheGlyTyrgLysrLysArgIle----- 97
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4608 GGTCCACCCAGGAGGAGCGGCTGGGGCGGGAGCAGGGTCTCCCGCTGCAGGCTGCCGCGGA 4549

QY 98 GlyProAsnGlyAspValGlyTrp-----ValGluTyrlu 109
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4548 GGCAGGAGGACCGGGTGGGTGGGTGCGATGCGTGCAGGCTTCGGCGTTCAGTGATTG 4489
```

```
QY 110 LeuLeuAenThrAsnProAspValIleSerProLysSerLeuCysIlePheArgGluAen 129
Db 4488 TCGCTGGGCACACGGCGCGCTGGTG---CCACGGCAGCGCTGCACCTTCTCCACCAGC 4432
QY 130 ProHisHisPheArgAlaValGluAen----- 139
Db 4431 CCGGCCCACTGGCGCTGCATGTCCTCCACAGGGGCTCGAACACAGCTCTTGAGCGGGGCC 4372
QY 140 ---TyrIleThrAlaValLysAenMetCysTyrAlaValLeuLeuMetAlaGluGly 158
Db 4371 TGGAGGGCTCGGCTGCAGGGGTATCTGCTGGGC-----TGCTCTCCAG- 4325
QY 159 LeuGlyIleArgIleArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSer 178
Db 4324 CTTGGCGGCACCTCGGCCACCTGCTCTTACCTCTGCTCCAGCGGTGCGGGTCCGGCT 4265
QY 179 CysPheArgLeuAen-----HisTyrProProCysProGluValGlnAlaLeuAenArg 196
Db 4264 GCCCATCTCTCTCATCCGCGCGCGCAGCGCTCGCCGCCACAGGCTGGGCCCGCTCTGTAG 4205
QY 197 AsnLeuValGlyPheGlyGluHisThr 205
Db 4204 CGGCTGGCGCGCGCAGGAGCCACAGT 4178

RESULT 10
US-11-034-771-1/c
; Sequence 1, Application US/11034771
; Publication No. US20050277129A1
; GENERAL INFORMATION:
; APPLICANT: Aerssens, Jeroen
; APPLICANT: Athanasios, Maria
; APPLICANT: Brain, Carlos
; APPLICANT: Cohen, Nadine
; APPLICANT: Dain, Bradley
; APPLICANT: Denton, R. Rex
; APPLICANT: Judson, Richard S.
; APPLICANT: Ozdemir, Vural
; APPLICANT: Reed, Carol R.
; TITLE OF INVENTION: APOE Genetic Markers Associated with Age of Onset of Alzheimer's
; FILE OF INVENTION: Disease
; FILE REFERENCE: 2300.0130801
; CURRENT APPLICATION NUMBER: US/11/034,771
; PRIOR FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: US 60/538,590
; PRIOR FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 5982
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1102)..(1102)
; OTHER INFORMATION: n is 't' or 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1641)..(1641)
; OTHER INFORMATION: n is 'c' or 'g'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2476)..(2476)
; OTHER INFORMATION: n is 'g' or 'a'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4415)..(4415)
; OTHER INFORMATION: n is 't' or 'c'
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4553)..(4553)
; OTHER INFORMATION: n is 'c' or 't'
US-11-034-771-1
```

```
Alignment Scores:
Pred. No.: 215 Length: 5982
Score: 82.50 Matches: 40
Percent Similarity: 36.69% Conservative: 22
Best Local Similarity: 23.67% Mismatches: 64
Query Match: 4.72% Indels: 44
DB: 7 Gaps: 7

US-10-670-454-2 (1-331) x US-11-034-771-1 (1-5982)

QY 75 LysIleSerGlnSerGluLysAspArgAla----- 84
Db 5151 AGGAATATCACAGGGGAGCGCAGCATGCGTGAACTTGTGTAATCTTTATAAATAG 5092
QY 85 GlyProProAspProPheGlyTyrGlySerLysArgIle----- 97
Db 5091 GGTCCACCCAGGAGGAGCGCTGGGGCGGGGACAGGGTCTCCCGTGCAGGCTGCGCGA 5032
QY 98 GlyProAsnGlyAspValGlyTrp-----ValGluTyrLeu 109
Db 5031 GGCAGGAGCACGGGGTGGCGTGGGGTGCATGGCTGCAGGCTTCGGGCTTCAGTGTG 4972
QY 110 LeuLeuAenThrAsnProAspValIleSerProLysSerLeuCysIlePheArgGluAen 129
Db 4971 TCGCTGGGCACAGGGCGCGCTGGTG---CCACGGCAGCGCTGCACCTTCTCCACCAGC 4915
QY 130 ProHisHisPheArgAlaValGluAen----- 139
Db 4914 CCGGCCCACTGGCGCTGCATGCTTCCACAGGGGCTCGAACACAGCTCTTGAGCGGGGCC 4855
QY 140 ---TyrIleThrAlaValLysAenMetCysTyrAlaValLeuLeuMetAlaGluGly 158
Db 4854 TGGAGGGCTCGGCTGCAGCGGTATCTGCTGGGC-----TGCTCTCCAG- 4808
QY 159 LeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSer 178
Db 4807 CTTGGCGGCACCTCGGCCACCTGCTCTTACCTCTGCTCCAGCGGTGCGGGTCCGGCT 4748
QY 179 CysPheArgLeuAen-----HisTyrProProCysProGluValGlnAlaLeuAenArg 196
Db 4747 GCCCATCTCTCCATCCGCGCGCGCAGCGCTCGCCGCCACAGGCTGGGCCCGCTCTGTAG 4688
QY 197 AsnLeuValGlyPheGlyGluHisThr 205
Db 4687 CGGCTGGCGCGCGCAGGAGCCACAGT 4661

RESULT 11
US-11-121-086-27/c
; Sequence 27, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 153142
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-27

Alignment Scores:
Pred. No.: 3,16e+04 Length: 153142
Score: 82.50 Matches: 40
Percent Similarity: 36.69% Conservative: 22
Best Local Similarity: 23.67% Mismatches: 64
Query Match: 4.72% Indels: 44
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DB: 7 Gaps: 7

US-10-670-454-2 (1-331) x US-11-121-086-27 (1-153142)

QY 75 LysLysSerGlnSerGluLysAspArgAla----- 84

DB 72920 AGGAATACACAGGGGAGCCAGCATCGTGAACCTTGGTGAATCTTTATTAAACTAG 72861

QY 85 GlyProAspProPheGlyTyrGlySerLysArgIle----- 97

DB 72860 GTTCACCCAGGAGACGGCTGGGCGGGGACAGGGTCTCCCGTGCAGGCTGCGCGGA 72801

QY 98 GlyProAsnGlyAspValGlyTrp-----ValGluTyrLeu 109

DB 72800 GGCAGGAGCCAGGGGTGGCGTGGGTTCGATGGCTGCAGGCTTCAGTGATTG 72741

QY 110 LeuLeuAsnThrAsnProAspValIleSerProLysSerLeuCysIlePheArgGluAsn 129

DB 72740 TCGCTGGGCACAGGGCGCGCTGGTG---CCACGGCAGCCTGCACCTTCTCCACCAGC 72684

QY 130 ProHisPheArgAlaValValGluAsn----- 139

DB 72683 CCGGCCACTGGCGTGCATGTCTTCCACAGGGGCTCGAACAGCTCTTGAGGGGGGCC 72624

QY 140 ---TyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGly 158

DB 72623 TGGNAGGCCTCGGCCTGCAGGGGTATCTCTGGGCC-----TGCTCCTCCAG- 72577

QY 159 LeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSer 178

DB 72576 CTTGGCGCGCACCTCGCGCACCTGTCTCTTCACTCTGCAGCGGTCCGGGTCCGGCT 72517

QY 179 CysPheArgLeuAsn-----HisTyrProCysProGluValGlnAlaLeuAsnArg 196

DB 72516 GCCATCTCTCATCCGCGCGGCGAGCGCTGCGCCAGGCTGGGCGCGCTCTGTAG 72457

QY 197 AsnLeuValGlyPheGlyGluHisThr 205

DB 72456 CGGCTGGCGGCGCAGGAGCCACAGT 72430

RESULT 12

US-10-995-561-13513/c

Sequence 13513, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

PRIOR FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13513

LENGTH: 40000

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(40000)

OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-13513)

US-10-995-561-13513

Alignment Scores:

Pred. No.: 5,31e+03 Length: 40000

Score: 81.50 Matches: 40

Percent Similarity: 34.04% Conservative: 24

Best Local Similarity: 21.28% Mismatches: 69

Query Match: 4.66% Indels: 55

DB: 6 Gaps: 8

US-10-670-454-2 (1-331) x US-10-995-561-13513 (1-40000)

QY 75 LysLysSerGlnSerGluLysAspArgAla----- 84

DB 23840 AGGAATACACAGGGGAGCCAGCATCGTGAACCTTGGTGAATCTTTATTAAACTAG 23781

QY 85 GlyProAspProPheGlyTyrGlySerLysArgIle----- 97

DB 23780 GTTCACCCAGGAGACGGCTGGGCGGGGACAGGGTCTCCCGTGCAGGCTGCGCGGA 23721

QY 98 GlyProAsnGlyAspValGlyTrp-----ValGluTyrLeu 109

DB 23720 GGCAGGAGCCAGGGGTGGCGTGGGTTCGATGGCTGCAGGCTTCAGTGATTG 23661

QY 110 LeuLeuAsnThrAsnProAspValIleSerProLysSerLeuCysIlePheArgGluAsn 129

DB 23660 TCGCTGGGCACAGGGCGCGCTGGTG---CCACGGCAGCCTGCACCTTCTCCACCAGC 23604

QY 130 ProHisPheArgAlaValValGluAsn----- 139

DB 23603 CCGGCCACTGGCGTGCATGTCTTCCACAGGGGCTCGAACAGCTCTTGAGGGGGGCC 23544

QY 140 ---TyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGly 158

DB 23543 TGGNAGGCCTCGGCCTGCAGGGGTATCTCTGGGCC-----TGCTCCTCCAG- 23490

QY 159 LeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSer 178

DB 23489 ---CGCACCTKCGCCACCTGCTCTTCCACCTCGTCCAGGCGGTG 23448

QY 179 CysPheArgLeuAsnHisTyrProCysProGluValGlnAlaLeuAsnArgLeu 198

DB 23447 CCGGCTCGGCTG-----CCCATCTCTCCATCCGCGCGCGCAGCGCTCGCCC 23400

QY 199 ValGlyPheGlyGluHis-----ThrAspProGlnIleIleSerVal 212

DB 23399 YAGGCTGGGCGCGCTCTGTAGCGGTGGCGRCCAGGAGCCACAGTGGCGGCGCC 23340

QY 213 LeuArgSerAsnSerThrSerGly 220

DB 23339 ACGCGGCCCTSTTCCACCAGGGGC 23316

RESULT 13

US-10-501-675-8

Sequence 8, Application US/10501675

Publication No. US20050282161A1

GENERAL INFORMATION:

APPLICANT: TANABE SEIYAKU CO., LTD.

TITLE OF INVENTION: A Novel Phospholipase A2 and the gene thereof.

FILE REFERENCE: 03-004-PCT

CURRENT APPLICATION NUMBER: US/10/501,675

PRIOR FILING DATE: 2004-07-16

PRIOR APPLICATION NUMBER: JP2002-008435

PRIOR FILING DATE: 2002-01-17

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 8

LENGTH: 3587

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (99)..(2552)

OTHER INFORMATION: (99)..(2552)

US-10-501-675-8

Alignment Scores:

Pred. No.: 150 Length: 3587

Score: 81.00 Matches: 69

Percent Similarity: 35.81% Conservative: 42

Best Local Similarity: 22.26% Mismatches: 104

Query Match: 4.63% Indels: 95

DB: 6 Gaps: 18

US-10-670-454-2 (1-331) x US-10-501-675-8 (1-3587)

QY 84 AlaGlyProPro-AspProPheGlyTyrGlySerLysArgIleGlyProAsn----- 100
 Db 1139 GCTGGGCTCTAGACTGTGTGACCTACTTCACTGGCATCTCTGCTAGTGGACAAT 1198
 QY 101 -----GlyAspValGlyTyr-----ValGlyTyr 108
 Db 1199 GGGCCACCTGTACGGGGACCTCTAGTGTGCGAGGACCTGGAGGACCTATCAGATA 1258
 QY 108 rLeu-----LeuLeuAsnThrAsnProAspValIleSerProLysSerLeuCysIle 125
 Db 1259 GCGCGGAGACCTGGCCAGAGCAAGCTGGAGTCTTTCCAGAGAGCGCTGGCGAG 1318
 QY 125 ePheArgLeuAsnProHisPheArgAlaValValGluAsnThrIleThrAlaVally 145
 Db 1319 CTACCGCGGAG---CTGAGCTCGGCT---GAGCAGGCGCCACCCACGACCTTGT 1372
 QY 145 sAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGlyIleArgGlnArgAs 165
 Db 1373 GAGCTGTGGGCGCTAGTGTGAGTCTCAATGTGCACGCGCAGGTGATGATCAGAACT 1432
 QY 165 nThrLeuSerArgLeuLeuLysAspGluLysSerAspCysPheArgLeuAsnHisTy 185
 Db 1433 GTACGACAGAGCGCGCTCGAAGCGGCTCAGAAC----- 1469
 QY 185 rProProCysProGluValGlnAlaLeuAsn-----ArgAsnLeu----- 198
 Db 1470 ---CCTGCGCCCTACTTGGAGCTCAATGTCAAAGAGAACATCTGGAGACACTGGA 1525
 QY 199 -----ValGlyPhe-----GlyGluHI 204
 Db 1526 CTTCAAGGAGTGGTGTGAGTCTCCCGCTATGAGTCTGCTTCTGGAAGTACGGGCGCT 1585
 QY 204 sThrAspProGlnIleLeuSerValLeuArgSerAsnSerThrSerGlyLeu----- 221
 Db 1586 COTCCCTCTGAGCTCTTGGC-----TCCAGTCTTCATGAGGACGGCTGATGAG 1636
 QY 222 -----GlnIleCysLeuThrAspGlyThrTrpValSerValProAs 236
 Db 1637 GAGGATCCCGAGCGCGGATCTGCTTCTGGAAGCCATCTGGAGCAACATT----- 1688
 QY 236 pGlnThrSerPheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGly----- 254
 Db 1689 -----TTCTCCCTGAACCTGTGAGTCTGAGTCTGATGACCTCACCAGTCTGGGGA 1738
 QY 255 -----ArgPheLysSerValLysHisArgValLeuAlaAs 266
 Db 1739 GTCTGGAAACAGCATCAAGACAGACAGGAGCTTAGAGAGGAGCGCCCTGACCCAC 1798
 QY 266 pThr---ThrLysSerArgLeuSerMetIleTyrPhe---GlyGlyProAlaLeuSerG 284
 Db 1799 CTCGGGACCTCTCTGGGCTGGAGGCTCTGCTGCTGAGCAGCAGCAGCGCTGCCCA 1858
 QY 284 uAenIle-----AlaPro-----LeuPr 290
 Db 1859 GGCATTAAAGGCTTCTGACAGGAGGCGCCCTCCACAGCGCAGCCCACTCTCTCCA 1918
 QY 290 oSerValMetLeuLysGlyGluGlyCysLeuTyrLysGluPhe---ThrTrpCysGluTy 309
 Db 1919 GGGCTCTCAGCTGACACGAGTACTGTAGCCACAAAGACTTCTCCACCTGGGCGACTA 1978
 QY 309 rLysLysAlaAlaTyrThrSerArgLeu 318
 Db 1979 CCAGCTTGACTCCATGCCCGCAGCAGCTG 2006

RESULT 14

US-10-750-185-34363/c
 ; Sequence 34363, Application US/10750185
 ; Publication No. US20050260603A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: Denise, Sue K.
 ; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: WM1100-2
 ; CURRENT APPLICATION NUMBER: US/10750,185
 ; PRIOR FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 34363
 ; LENGTH: 1535
 ; TYPE: DNA
 ; ORGANISM: Bovine 19866880928513
 US-10-750-185-34363
 Alignment Scores:
 Pred. No.: 46.6 Length: 1535
 Score: 80.50 Matches: 67
 Percent Similarity: 33.79% Conservative: 31
 Best Local Similarity: 23.10% Mismatches: 93
 Query Match: 4.61% Indels: 99
 Gaps: 15
 Db:
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 QY 79 SerGluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGly 98
 Db 1243 GCTGAGAAAGATGAGGCTTGTGTGAGGCTCTGTGTGAGTATGTTGCA-----AAC 1193
 QY 99 ProAsnGlyAspValGlyTrpValGluTyrLeuLeuAsnThrAsnProAspValIle 118
 Db 1192 CCCAATGCA-----CTGGATGGTAACCGAGAC----- 1166
 QY 119 SerProLysSerLeuCysIlePheArgGluAsnProHisPheArgAlaValValGlu 138
 Db 1165 ACCCGACTTCACTGGCAGCGCTTTAAGAAACAATGCTGAGTGTGTGCGGCGCTCTAGAG 1106
 QY 139 AsnTyrIleThr-----ThrLeuSerArgLeu-----Ala 143
 Db 1105 AGCGGGGCTCTGTCAAGCGCTGTGATTACAAATGACACCCCGCTTAGCTGGGCTGCC 1046
 QY 144 ValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGlyIleArgGln 163
 Db 1045 ATGAAGGGAATCTTGAGAGGCTCAGCATCTTCTTGATTATGTTGTCAGAGGTCAGAGTC 986
 QY 164 ArgAsn-----ThrLeuSerArgLeu-----Leu 171
 Db 985 ATCAACTTAAAGGCGCAGACGCCCATCTCCGCGCTGTGTGCTCTGCTAGTCAGGGGACTT 926
 QY 172 LysAspGluLysSerAspSerCysPheArgLeuAsnHisTyrProProCysProGluVal 191
 Db 925 GGGACAGAGAAGAGGACTCTTGCTTGAAGTCTCTCCAC----- 887
 QY 192 GlnAlaLeuAsnArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSer 211
 Db 886 -----AGAGCTGTTGGACACTTGA----- 866
 QY 212 ValLeuArgSerAsnSerThrSerGlyLeuGlnIle----- 223
 Db 865 ---TTAAGGAAATATGGCACCATGTCACAGAGAGTGGCCAAAGACAGCAGCTGTGTGAA 809
 QY 224 -----CysLeuThrAspGlyTrpValSerValProProAspGlnThr 238
 Db 808 AAGCTGACTGTTTATGCTCAGCCCCCAGGAGCTCTAAACACACTT-----TCT 761
 QY 239 SerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSer 258
 Db 760 CGCTATGCTGTGGCGGAGGCTGGGACTTCCAGTATCTGCCAGAT-----GCC 713
 QY 259 ValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGly 278

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Db 712 GTCAAGGGCTGCTCTGACAGCTTCTCTGAAGGAATACCTGTACTCATAGATAGCCT 653
QY 279 Gly-----ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeu 294
Db 652 GGAGGAGAGCTCAGCGCGGCACTCTGCGTAAGGTTTTCCTGTAGACACCGTC----- 599
QY 295 LysGlyGluGluCysLeuTyrLysGlu-----PheThrTrpCys-----Glu 308
Db 598 -----TGCTTGGAAACAGGAAGCAGTGTCTCTGTGTGTGTTTATAT 551
QY 309 TyrLysLysAlaAlaTyrThrSerArgLeu 318
Db 550 TTCAAGGCAACATGTCACAAACAGTAACCTT 521
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RESULT 15

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US-10-995-561-13294/c
; Sequence 13294, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13294
; LENGTH: 15804
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(15804)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13294
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Alignment Scores:

Pred. No.:	1.69e+03	Length:	15804
Score:	80.50	Matches:	40
Percent Similarity:	34.04%	Conservative:	24
Best Local Similarity:	21.28%	Mismatches:	69
Query Match:	4.61%	Indels:	55
DB:	6	Gaps:	8

US-10-670-454-2 (1-331) x US-10-995-561-13294 (1-15804)

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Db 9829 AGGAATACAGGGGGAGGCCAGACATGCGTGAACTTGGTGAATCTTTATTAAACTAG 9770
QY 85 GlyProAspProPheGlyTyrGlySerLysArgIle----- 97
Db 9769 GGTCCACCCACAGGAGCGCTGGGGCGGGACAGGGTCTCCCGTGCAGGCTGGCGCGGA 9710
QY 98 GlyProAsnGlyAspValGlyTrp-----ValGluTyrLeu 109
Db 9709 GGCAGAGGACGCGGGTGGCGTGGGGTGCATGGGTGCAGGGCTTCGGCGTTTCAGTGATG 9650
QY 110 LeuLeuAsnThrAsnProAspValIleSerProLysSerLeuCysIlePheArgGluAsn 129
Db 9649 TCGCTGGGCACAGGGCGCGCTGGTG-----CCACGGCAGCTGCACCTTCTCCACCAGC 9593
QY 130 ProHisHisPheArgAlaValValGluAsn----- 139
Db 9592 CCGGCCCACTGGCGCTGCATGTCTTCCACAGGGGCTCGAACCCAGCTCTTGAGGGGGGCC 9533
QY 140 ---TyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGly 158
Db 9532 TGAAGGCCTCGCGCTGCAGGGCGTATCTGCTGGGCGCTGCTCTCTYACGCTTGGCG----- 9479
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QY 159 LeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSer 178
Db 9478 -----CGCACCTTCGCCCACTCTCTTCACTCGTCCAGGCGGTGG 9437
QY 179 CysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeu 198
Db 9436 CGGGTCCGGCTG-----CCCATCTCTCCATCCGGCGCGGACGCCGCTCGCCC 9389
QY 199 ValGlyPheGlyGluHis-----ThrAspProGlnIleIleSerVal 212
Db 9388 YAGGCTGGGCCCGCTCTCTGTAGCGGTGGCGGCCAGGAGCCACAGTGGCGGCCCGC 9329
QY 213 LeuArgSerAsnSerThrSerGly 220
Db 9328 ACGCGGCCCTSTTCCACCAGGGGC 9305
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Search completed: December 28, 2005, 05:19:57
Job time : 891 secs